Universidad Autónoma de Madrid
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FILOGENIA DE LA ALIANZA GENÉRICA DE *MALVA*: UN ENFOQUE MOLECULAR

Memoria presentada por

PEDRO ESCOBAR GARCÍA

Para optar al título de doctor.
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Javier Fuertes Aguilar	Gonzalo Nieto Feliner	Roberto Gamarra Gamarra
Director	Codirector	Tutor

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1. INTRODUCCIÓN

Desde hace unos diez años la sistemática molecular se ha convertido en una herramienta al alcance de cualquier grupo de investigación. Una prueba de ello es que el cuerpo de conocimentos generado por esta disciplina no ha parado de crecer, como atestigua la secuenciación a gran escala de ciertos marcadores como los ITS (Álvarez & Wendel, 2003). Hoy día, el uso de una creciente gama de secuencias diferentes, entre ellas diversos genes y espaciadores cloroplásticos y sobre todo, los genes nucleares de bajo número de copias, ha conducido a una acumulación de información sin precedentes. Gracias a esto las bases de datos públicas en que se incluye esta información, como GenBank, sobrepasan ampliamente la cifra de 100 gigabases, y crecen a ritmos de más de 3 millones de secuencias al mes (GenBank, 2007).

Tal cantidad de información nueva supone un aporte histórico para el conocimiento de la biodiversidad, y ha llevado a muchos a replantearse no sólo los sistemas tradicionales de clasificación (Stevens, 2006; APG, 1998, 2003) sino el propio uso que se ha hecho de los caracteres morfológicos (Judd & Manchester, 1997). En aquellos casos donde la evidencia ha resultado contundente, las clasificaciones formales han sido abandonadas en favor de grupos informales, fácilmente modificables a medida que avanza el conocimiento (Bates, 1968; Tate & *al.* 2005).

Las *Malvaceae* son un buen ejemplo de esta situación a todos los niveles de la jerarquía taxonómica. La escasez de caracteres morfológicos, así como las múltiples apariciones y pérdidas sucesivas de epicálices, pólenes espinulados y otros caracteres de importancia clave en su sistemática impiden la delimitación objetiva de taxones. Desde la extensión del orden Malvales hasta la circunscripción de los géneros *Malva* y *Lavatera*, pasando por los límites de la propia familia, todos los niveles taxonómicos se resienten por la existencia de un elevado grado de arbitrariedad. Esto se manifiesta en que los diferentes niveles están desde antiguo sujetos a polémica sin que hasta tiempos muy recientes fuera posible tomar partido objetivamente por la propuesta de uno u otro autor. Por ello el estudio con caracteres moleculares es particularmente necesario, ya que el establecimiento de grupos naturales es una condición previa indispensable para conocer no sólo las relaciones filogenéticas, sino también cómo han evolucionado los caracteres morfológicos.

Este capítulo inicial pretende resumir brevemente los problemas sistemáticos del grupo (escasez de caracteres morfológicos, falta de consistencia en su uso), desde la delimitación del orden y sus familias hasta la circunscripción genérica, tomando como ejemplo ilustrativo el género *Malva* y afines (*Alcea*, *Althaea*, *Lavatera* y *Malope*, componentes de la alianza genérica de *Malva* o *Malva alliance*). Desde antiguo este grupo ha estado sujeto a controversia sin que hasta tiempos muy recientes fuera posible decantarse por una u otra propuesta sin ambigüedades. Se hace además una sucinta discusión de los diferentes ordenamientos taxonómicos propuestos para la alianza genérica de *Malva*, desde un punto de vista cronológico.

1.1. Los límites del orden Malvales.

El orden Malvales está compuesto tradicionalmente por cuatro familias, *Bombacaceae*, *Malvaceae*, *Sterculiaceae* y *Tiliaceae* (el núcleo de las Malvales). Sin embargo, su circunscripción ha sido históricamente polémica, dado que más allá de estas cuatro familias los diversos autores clásicos no se han puesto de acuerdo a la hora de resolver qué otras deberían ser incluidas. Las clara relación que existe entre las cuatro familias nucleares fue reconocida ya en tiempos de Linné, y cuenta con el apoyo de los últimos trabajos que han utilizado técnicas moleculares (Alverson, 1998; Bayer & *al.*, 1999; Nyffeler & *al.*, 2005). La cuestión de cuál es el grupo más cercano a ellas ha sido también controvertida, debido a que ningún carácter morfológico liga claramente otras familias al núcleo de las Malvales.

Debido a ello, el orden Malvales ha sido definido de diversas maneras, en circunscripción restringida a las *Malvaceae* en sentido estricto (Hutchinson, 1967) o las cuatro familias nucleares más las *Elaeocarpaceae* (Cronquist, 1988), aunque cierto número de autores han incluido también las *Bixaceae*, *Diegodendraceae*, *Cistaceae* y *Thymelaeaceae*, entre otras (Dahlgren, 1983; Thorne, 1983; Takhtajan, 1997).

Los estudios moleculares de los años noventa (Alverson & *al.*, 1998, 1999) aclaran la relación existente entre las cuatro familias que componen el núcleo del orden y otras hasta ahora incluidas entre las Capparales y Sapindales *sensu lato*, apoyando el establecimiento de un orden Malvales extendido que incluiría no sólo las tradicionales *Tiliaceae*, *Sterculiaceae*, *Bombacaceae* y *Malvaceae*, sino también las *Cistaceae*, *Thymelaeaceae* y *Bixaceae*, ésta última aparentemente grupo hermano del núcleo del orden. Otras familias quedan definitivamente excluidas, como las *Elaeocarpaceae*.

Aunque la estrecha relación entre las cuatro familias del núcleo está ampliamente apoyada por datos moleculares, existen muy pocos caracteres morfológicos sinapomórficos que las vinculen. Los únicos caracteres no ambiguos son: estructura de la inflorescencia (unidad *bicolor*, Bayer, 1999) y nectarios formados por tricomas glandulares en la superficie adaxial de las piezas del perianto (Vogel, 2000). Los diversos grupos que integran el orden han experimentado múltiples pérdidas y ganancias de androginóforos, hojas palmadas, flores apétalas, apocarpia, hábito herbáceo, tubos estaminales, venación foliar palmada, polen espinoso o espinuloso, frutos o semillas alados o anteras monotecadas. Y ninguno de los caracteres tradicionalmente diagnósticos es exclusivo de él, como las hojas palmatinervadas, presencia de tricomas estrellados, existencia de mucílago, cálices valvados, estambres numerosos o presencia de ácidos grasos ciclopropeniles.

1.2. La delimitación de las familias.

Pese a que las cuatro familias siempre se han supuesto íntimamente ligadas, el estudio de sus relaciones evolutivas ha sido particularmente desafiante, con múltiples problemas de delimitación. Particularmente difíciles de dibujar son los límites entre las *Malvaceae* y las *Bombacaceae*, así como entre las *Sterculiaceae* y las *Tiliaceae*. Existe cierto número de taxones que han sido emplazados de diversa manera en los esquemas taxonómicos tradicionales, como es el caso de las tribus *Fremontodendreae*, *Gossypieae*, *Hibisceae* y de los géneros *Camptostemon*, *Corchoropsis*, *Craigia*, *Hampea*, *Maxwellia*, *Nesogordonia* y *Uladendron*, dando lugar a aproximaciones normalmente incompatibles.

El esquema utilizado tradicionalmente es una progresión desde las más primitivas *Tiliaceae*, a través de las intermedias *Sterculiaceae* y *Bombacaceae*, a las avanzadas *Malvaceae*. Esta progresión se basa en el creciente grado de fusión de los estambres y la progresiva tendencia al hábito herbáceo, muy extendido en las *Malvaceae*. Sólo Warming (1895) y Ventaka Rao (1952) se han desviado de este modelo considerando como basales a las *Sterculiaceae*.

Ninguna de las familias tradicionales del núcleo de las Malvales está definida de manera no ambigua por caracteres morfológicos, con el agravante de que la distribución de cierto número de caracteres distintivos no es consistente con las clasificaciones tradicionales. Las *Tiliaceae* son desde antiguo un cajón de sastre utilizado para emplazar taxones que no encajan en ningún otro grupo. De este modo, el polen espinoso o espinuloso aparece en las cuatro familias, como también ocurre con los epicálices. Basándose en la presencia de flores unisexuales apétalas con apocarpia secundaria Thorne (1983) y Takhtajan (1997) subdividen la familia *Sterculiaceae* en *Sterculioideae* y *Byttnerioideae*. Sin embargo, la existencia de unos cuantos taxones con flores hermafroditas provistas de corola y a la vez de ovarios apocárpicos suponen un reto más.

Dentro de las cuatro familias existen problemas similares a la hora de delimitar subfamilias y tribus. Los nuevos estudios moleculares han reportado sorpresas mayúsculas, como la posición inesperada de algunos géneros cuyo emplazamiento en las clasificaciones tradicionales no había sido cuestionado jamás. De este modo, *Durio* quedaría fuera de las *Bombacaceae*, mientras que los géneros *Neotessmannia*, *Dicraspidia* y *Mutingia*, tradicionalmente incluidos en la familia *Tiliaceae*, resultan no estar directamente relacionados con ninguna de las cuatro familias nucleares (Nyffeler & *al.*, 2005). Por su parte, *Byttneria* y *Theobroma* se separan de las *Sterculiaceae* componiendo el grupo hermano de las Malvales nucleares. Este grupo, las *Byttneriaceae* de Edlin (1935), han sido siempre un taxón reconocido dentro de las *Sterculiaceae*.

En este estado de la situación, y aunque parezca sorprendente, está claro que no hay suficiente evidencia morfológica (Judd & Manchester, 1997) para la subdivisión del núcleo de las Malvales en las cuatro familias tradicionales. Los caracteres moleculares, por su parte, tampoco apoyan la clasificación tradicional. Sólo las *Malvaceae* tradicionales son claramente monofiléticas. De este modo, y a la vista de los resultados presentados por Bayer & *al.* (1999), Judd & Manchester (1997), Alverson & *al.* (1998, 1999) y Nyffeler & *al.* (2005), parece que mantener la clasificación tradicional no tiene sentido. Inmediatamente aparece la cuestión de cómo establecer una clasificación alternativa. La ampliación de los límites de las *Malvaceae* para incluir las *Bombacaceae* haría el grupo resultante muy difícil de diagnosticar en base a caracteres morfológicos, particularmente porque las *Dombeyoideae* son intermedias entre las familias *Bombacaceae* y *Sterculiaceae*.

La ampliación de las *Tiliaceae* o *Sterculiaceae* tradicionales llevaría al establecimiento de familias parafiléticas. Tratar a los clados como familias resulta a la vez poco práctico, dado que algunas de las familias resultantes deberían ser descritas como nuevas y la atomización en gran número de familias pequeñas no parece ser la solución más recomendable. Así mismo, muchos géneros *incertae sedis* quedarían sin filiación. La solución más conveniente parece ser tratar las alianzas genéricas de los nuevos estudios como subfamilias de una familia *Malvaceae* extendida (*Malvaceae sensu lato*), con la ventaja adicional de que muchas de las tribus podrían mantenerse en el sentido que se les ha dado hasta ahora, si bien ciertos cambios de circunscripción se hacen necesarios (Bayer & Kubitzki, 2003). Las clasificaciones precedentes no han hecho un uso extensivo del rango infrafamilial, de modo que la categoría podría ser usada sin necesidad de cambiar muchos de los nombres utilizados comúnmente.

1.3. La necesidad de estudios moleculares.

Las sinapomorfías que agrupan los grupos infrafamiliares en las *Malvaceae* son escasas, haciendo la delimitación de los taxones muy difícil (Judd & Manchester, 1997). El empleo de algunos caracteres morfológicos como diagnósticos de los taxones infrafamiliares, ha llevado al establecimiento de clasificaciones artificiales. A veces, un carácter morfológico que ha sido ignorado se revela útil gracias a fuentes independientes de evidencia. En el caso de la tribu *Malveae*, la presencia o ausencia de epicáliz, no usado hasta ahora en clasificaciones infratribales, se revela como el carácter clave que delimita dos grandes grupos naturales (Tate & *al.*, 2005).

La mayoría de clasificaciones tradicionales no han sido capaces de evitar altos niveles de homoplasia, lo que se ha traducido en la proliferación de grupos arbitrariamente definidos. En algunos casos los autores han sido conscientes de ello, como en la familia *Tiliaceae*. En otros casos, la posición de ciertos taxones nunca fue discutida y posteriores análisis han revelado que un carácter morfológico aparentemente útil está sujeto a homoplasia, como en el caso de las *Durioneae*. También es necesario tener en cuenta el hecho de que la mayoría de las clasificaciones fueron propuestas en unos tiempos en que el grado de naturalidad, así como el que la clasificación fuera reflejo de la filogenia, no era necesariamente una prioridad. Es importante también considerar que en los últimos tiempos algunos sistemáticos han propuesto la aceptación de los grupos parafiléticos en taxonomía, como es el caso de Grant (2003).

Un gran desafío para las nuevas clasificaciones es la herencia de taxones altamente estructurados establecidos a veces en tiempos relativamente lejanos. Por ejemplo De Candolle (1824) construyó una clasificación de las *Malvaceae* muy elaborada que ha sido mantenida con pocos cambios hasta nuestros días. Los monumentales trabajos de síntesis de finales del siglo XIX (sin los cuales no hubiera sido posible progresar a lo largo del siglo XX, como el tratamiento de la tribu *Malveae* por Bentham y Hooker

[1862], o Baker [1890]) han contribuido decisivamente a que estos esquemas taxonómicos se perpetúen.

Otro de los problemas es que el muestreo de caracteres morfológicos muy importantes en la sistemática del grupo (anatómicos, del desarrollo, químicos) no han sido observados en todos los representantes, particularmente en géneros críticos de posición incierta. Ello puede deberse a que hoy día el estudio morfológico está subestimado en favor de los caracteres moleculares. En las *Malvaceae*, los nuevos grupos que emergen de los estudios moleculares son muchas veces diagnosticables sólo gracias a exámenes morfológicos recientes muy concienzudos, como los trabajos de Bayer (1999) sobre morfología de las inflorescencias y Vogel (2000), sobre anatomía de los nectarios.

La estructura filogenética de las Malvoideae apoya las conclusiones de Judd & *al.* (1994), referentes a ciertos grandes clados en los cuales una gran familia tropical de plantas leñosas aparece parafilética frente a una familia monofilética de plantas herbáceas que se distribuyen por las regiones templadas (como es el caso de los dobletes *Apiaceae*-*Araliaceae*, *Brassicaceae*-*Capparidaceae*, *Malvaceae*-*Bombacaceae*, etc.). Este fenómeno es una consecuencia de la práctica taxonómica tradicional, que en ocasiones muestra una tendencia a separar arbitrariamente los grupos herbáceos de los leñosos en un gran clado monofilético.

En nuestro caso, la posesión de características morfológicas distintivas, unidas al hecho de que los taxones de distribución templada son mejor conocidos que los representantes tropicales, ha llevado a la segregación de un grupo monofilético como las *Malvaceae sensu stricto* de un gran complejo para- o polifilético como las *Bombacaceae* tradicionales. Esto es el resultado de la aplicación de los procedimientos clásicos de agrupación y jerarquización, que requieren del pesado de ciertos caracteres, como la forma del polen (Cronquist, 1981) o el tipo de fruto (Edlin, 1935).

Los diferentes grupos que componen la subfamilia *Malvoideae* no son diagnosticables por sinapomorfías claras, por lo que se hace necesario recurrir a combinaciones de caracteres. Las *Malvoideae* comparten polen espinoso o espinuloso, tubo estaminal con 5 dientes apicales y la presencia de epicáliz. Sin embargo, ninguna de estas características es exclusiva del grupo, como tampoco ninguna de ellas es observable en todos sus representantes. El polen espinoso, muy importante en las clasificaciones tradicionales, aparece también en las *Bombacoideae*, *Dombeyoideae* y en ciertas *Sterculioideae*. Los dientes del tubo estaminal desaparecen en las *Malveae*. El epicáliz está ausente de un gran clado de las *Malveae*, y aparece en las *Bombacoideae*, *Fremontodendreae*, *Dombeyoideae* y en algunas *Grewioideae* como *Luehea*. Las *Malvoideae* incluyen también algunos representantes cuya posición es ambigua, como *Hampea*, un género de arbustos dioicos incluido a veces en las *Bombacaceae* (Hutchinson, 1967; Takhtajan, 1987).

Camptostemon es un género de mangles normalmente emplazado en las *Bombacaceae* (*Durioneae*), en base a su indumento lepidoto, pero en los análisis moleculares aparece como grupo hermano de las *Malvoideae*. Dentro de esta subfamilia, las *Hibisceae* son basales y parafiléticas, mientras que las *Gossypieae*, caracterizadas por las glándulas de gosipol, son monofiléticas. La tribu *Malveae* se caracteriza por la presencia de esquizocarpos, mericarpos normalmente numerosos, en número que iguala al de estilos libres, y ápice de la columna estaminal anterífero, sin dientes estériles adicionales. Dentro existen dos grupos principales, el de *Sida*, sin epicáliz, y el de *Malva*, provisto de epicáliz.

¿Estamos ante un verdadero conflicto entre morfología y datos provenientes de DNA?

En absoluto. La ausencia de sinapomorfías claras que permitan establecer una clasificación basada en la morfología de las *Malvoideae* sin introducir una perspectiva subjetiva, fue demostrada por Judd & Manchester (1997), tras un muestreo de caracteres morfológicos completo. El proceso taxonómico tradicional lleva en muchas ocasiones al establecimiento de grupos parafiléticos o polifiléticos, mientras que las clasificaciones evolutivas basadas en caracteres moleculares producen muchas veces grupos que no son fácilmente diagnosticables, como las *Helicteroideae* o el grupo lavateroide dentro de *Lavatera-Malva*. Más que de un conflicto entre escuela tradicional y datos moleculares estamos ante una reevaluación de los caracteres morfológicos tras la aparición de nuevas fuentes de evidencia en forma de secuencias de DNA.

1.4. *Hibiscus* y la tribu *Hibisceae*.

Los grupos parafiléticos son un frecuentes en los sistemas taxonómicos tradicionales, en los que las plantas son agrupadas por similitud morfológica. El hecho de que dos taxones se parezcan puede sin embargo deberse tanto a lazos de parentesco directos como a la compartición de caracteres plesiomórficos. Un claro ejemplo de este caso es la situación de *Hibiscus* y la tribu *Hibisceae*.

La tribu *Hibisceae* fue descrita por Reichenbach (1828) en base a la presencia de frutos capsulares. Alefeld (1862), tomando en cuenta varias sinapomorfías bien definidas (presencia de glándulas de gosipol, tipo de plegamiento del embrión y presencia de nectarios involucrales, entre otras) transfirió cinco géneros a la actual tribu *Gossypieae*. De este modo, las características que mantienen a las *Hibisceae* son la existencia de cápsulas loculicidas, columna estaminal rematada en cinco dientes y estilos terminales presentes en igual número a los carpelos. Son el grupo con caracteres más plesiomórficos dentro de las *Malvaceae sensu stricto* (*Malvoideae* en lo sucesivo), y no comparten más sinapomorfías que aquéllas que definen la subfamilia.

El caso del género *Hibiscus* es similar al de la propia tribu, con una serie de caracteres definitorios que son compartidos por otros miembros de la familia. Compartidos con las tribus *Malveae*, *Malvavisceae* y *Decaschisteae* aparecen los estilos ramificados; junto con las *Gossypieae* y *Decaschisteae* las cápsulas loculicidas; comparten además con las *Gossypieae*, *Malvavisceae* y *Decaschisteae* el número de carpelos que iguala al número de ramas estilares; y con las *Gossypieae*, *Malvavisceae* y *Decaschisteae* la columna estaminal rematada en cinco dientes. Adicionalmente, ciertas *Gossypieae* presentan también cinco carpelos. De este modo, el género *Hibiscus* y en general las *Hibisceae* sólo pueden ser definidos por caracteres plesiomórficos y por ello comprenden especies remanentes tras segregar grupos con sinapomorfías evidentes. Al carecer de sinapomorfías, es muy difícil establecer hipótesis de parentesco entre los taxones. Por ello, sin datos nuevos e independientes (secuenciación de marcadores moleculares), la mera reevaluación de la variación morfológica no hace más que perpetuar las ambigüedades existentes.

El análisis de secuencias cloroplásticas llevado a cabo por Pfeil & *al.* (2002) llega a la conclusión de que las *Hibisceae* son parafiléticas. La mayoría de las Malvoideae presentan semillas carentes casi por completo de endosperma en la madurez, mientras que tres géneros de la tribu, *Alyogyne*, *Lagunaria* y *Radyera* presentan un endospermo copioso. Estos tres géneros son el grupo hermano de todas las demás *Malvoideae* (*Radyera*, *Lagunaria*) o de las *Gossypieae* (*Alyogyne*). Los miembros de género *Hibiscus* aparecen dentro un clado que además incluye grupos segregados con anterioridad, como *Abelmoschus* y *Fioria*. La tribu *Decaschisteae*, que comparte con *Hibiscus* muchas características pero que presenta claras sinapomorfías, aparece en el clado *Hibiscus* sect. *Furcaria*. El hecho de que algunas *Malvavisceae* (*Pavonia*, *Malvaviscus*) con frutos esquizocárpicos aparezcan estrechamente emparentadas con *Abelmoschus* e *Hibiscus* sect. *Panduriformes* indica que la esquizocarpia apareció dos veces en las *Malvoideae*.

1.5. La tribu *Malveae*. El caso de la alianza genérica de *Malva*.

La tribu *Malveae* ha estado sujeta también a diversos esquemas de clasificación. Bentham y Hooker (1862) dividieron la tribu en cuatro subtribus teniendo en cuenta el número y estructura de los carpelos: *Abutilinae*, *Malopinae*, *Malvinae* y *Sidinae*. Toda una serie de autores posteriores han utilizado estos caracteres, produciendo ligeras variaciones en el esquema inicial. Schumann (1890) elevó las *Malopinae* a tribu, criterio que siguieron también Edlin (1935) y Kearney (1951). A mediados del siglo XX, Bates (1968) y más tarde Bates y Blanchard (1970) eliminaron la clasificación en subtribus estableciendo una serie de alianzas genéricas basadas en diversos caracteres morfológicos y en el número cromosómico. Este critero, con diversas modificaciones fue también seguido por Fryxell (1997) y por Bayer y Kubitzki (2003).

También aquí existen graves problemas a la hora de circunscribir los géneros. Por ejemplo *Sida* es artificial desde el mismo momento de su creación debido a que Linné y sus sucesores lo utilizaron como un cajón de sastre en el que incluir especies que presentaban frutos esquizocárpicos y que carecían de epicáliz. De manera similar, las especies con fruto esquizocárpico provistas de epicáliz acababan integradas en *Malva*. Desde entonces, la historia de ambos géneros está caracterizada por la constante segregación de diversos grupos morfológicamente reconocibles (Fuertes, 2002). Las primeras especies en ser excluidas de *Sida* fueron las de carpelos multiovulados, que fueron transferidas a *Abutilon*. Más tarde, diversos géneros han sido segregados del complejo, hasta que el grupo residual fue dividido en 15 secciones por Fryxell (1985). Pero de acuerdo con los trabajos de Bates (1968), el carácter carpelos uniovulados versus pluriovulados podría estar sobrevalorado, punto de vista que ha sido apoyado por el trabajo de Tate & *al.* (2005). En este trabajo se genera un árbol de ITS en el que las *Malveae* se dividen claramente en dos clados, uno provisto de epicáliz (que incluye, entre otros muchos géneros a *Malva* y *Lavatera*) y otro carente de él. La utilidad taxonómica del epicáliz queda así apoyada en los estudios moleculares y encuentra su sitio en la sistemática de la tribu *Malveae*.

Los últimos trabajos que incorporan secuencias de DNA (La Duke & Doebley, 1995; Tate & *al.*, 2005) no apoyan la monofilia de muchas de las alianzas genéricas propuestas por Bates (1968) y Bates & Blanchard (1970). No es así en el caso de la alianza genérica de *Malva*, cuya entidad se ve reforzada, incluyendo al género *Malope*, de carpelos en disposición irregular. Si bien está claro que los géneros *Kitaibela*, *Lavatera*, *Malva*, *Malope*, *Alcea*, *Althaea* y *Malvalthaea* están estrechamente emparentados, sólo *Malope* (2-3 especies) y *Kitaibela* (2 especies) presentan fronteras estables. Los demás están sujetos a mayor o menor polémica. *Alcea* y *Althaea*, originalmente descritos como entidades independientes, fueron fusionados a principios del siglo XIX y permanecieron unidos durante más de un siglo y medio (Willdenow, 1800), hasta los trabajos de Zohary (1963a, b) en que volvieron a ser separados. Sin embargo, ningún trabajo ha empleado técnicas moleculares para examinar los límites de ambos géneros. Si Alefeld (1862) y Krebs (1994b) estuvieran en lo cierto, *Althaea* sería un género polifilético compuesto por dos grupos no relacionados directamente, las especies anuales, que presentan afinidad con ciertas especies de *Malva*, y las especies perennes, emparentadas con *Alcea*.

Otra incógnita se refiere al género *Malvalthaea* (1-3 especies), propuesto inicialmente por Iljin (1924) como un notogénero producto de la hibridación de *Malva aegyptia* con *Althaea hirsuta*, e ignorado por la mayor parte de los autores. El hecho de que estas dos especies no hibriden nunca en sus amplias áreas de contacto, así como el que *Malvalthaea* sea una planta perenne de base leñosa, hacen urgente la inclusión de esta planta en un estudio molecular.

Sin embargo, es el caso de *Lavatera* y *Malva* el que más tinta ha derramado. Originalmente descritos por Linné y separados por la naturaleza del epicáliz, de tres piezas más o menos fusionadas en *Lavatera* y tres (o dos) piezas libres en *Malva*, ambos géneros se revelaron artificiales muy pronto (Medikus, 1787). En efecto, un análisis detallado revela que la estructura del fruto proporciona una separación nítida de las especies en dos grupos morfológicos, independientemente de su adscripción a *Malva* o *Lavatera*:

1. Frutos de pericarpo espeso y paredes fusionadas, que se dispersan como una unidad, o a veces en sus mericarpos, pero sin dejar al descubierto la semilla. Este tipo de fruto se denomina malvoide (Ray, 1995), por estar entre las especies que lo presentan *Malva sylvestris*, el tipo nomenclatural de *Malva*.
2. Frutos de paredes hialinas que se fusionan al menos parcialmente, formando una estructura intermedia entre el esquizocarpo y la cápsula. En este tipo de fruto los mericarpos se abren en la madurez liberando las semillas desnudas. Este tipo de esquizocarpo recibe la denominación de lavateroide,

por encontrarse entre las especies que lo presentan *Lavatera trimestris*, el tipo de *Lavatera*.

Ciertas especies presentan frutos que no responden claramente a ninguno de estos dos tipos morfológicos, sino que son similares a los esquizocarpos de *Althaea*, con mericarpos de paredes hialinas que no se desarticulan en la madurez, con bordes que no se tocan entre sí. A los esquizocarpos de este tipo nos referimos como tipo *Dinacrusa*.

De este modo, el género *Malva* en su circunscripción tradicional incluye especies de morfología claramente lavateroide, como la sección *Bismalva* (*M. alcea*, *M. moschata*, *M. tournefortiana*), que pese a su epicáliz de brácteas libres presenta frutos lavateroides; por su parte, muchas especies con morfología indudablemente malvoide, como *Lavatera cretica*, *L. mauritanica* o *L. arborea*, están incluidas en *Lavatera*.

Pese a que esta situación es conocida y discutida desde el siglo XVIII, sólo Webb & Berthelot (1836) y Ray (1998) propusieron parcialmente la transferencia de especies con el fin de unificar *Lavatera* sect. *Anthema* con *Malva* sect. *Malva* y *Fasciculatae*.

1.6. Historia taxonómica.

Los géneros *Lavatera*, *Malva*, *Althaea* y *Alcea*, como resultado de su estrecho parentesco y problemas de delimitación, presentan una historia común hasta tal punto que es imposible hablar de uno de ellos sin mencionar los demás. En sus diversas circunscripciones, se han mezclado de diversas maneras. A continuación se presenta una sucinta síntesis de los tratamientos propuestos por los diferentes autores desde los tiempos clásicos de Tournefort y Linné a Ray, ya en la era de la sistemática molecular.

Linné (1753) utilizando el grado de fusión de las brácteas del epicáliz, redefinió los nombres *Alcea*, *Althaea*, *Malva* y *Lavatera* ya utilizados por Tournefort (1700, 1706) y por otros botánicos prelinneanos. Las descripciones de *Malva* y *Lavatera* en *Genera Plantarum* (1789) son casi idénticas salvo por las características del cáliz: "*duplex, exterius triphyllum*" en *Malva*, "*monophyllum, trifidum*" en *Lavatera* (op. cit. pág. 465-466). Tournefort (1706) describió *Lavatera* como un género monoespecífico para segregar *L. trimestris* del gran género *Malva*, en base a la expansión en forma de parasol que remata el carpóforo de esta especie. Ya en *Hortus Cliffortianus*, Linné (1738) había incluido dos especies en este nuevo género *Lavatera*, seguidas de varias más en *Species Plantarum* (1753). Linné usó también el número y grado de fusión de las brácteas del epicáliz para separar *Althaea* y *Alcea*, que contarían con 9 y 6 brácteas fusionadas, respectivamente.

La importancia que le dio Linné en *Genera Plantarum* a la naturaleza del epicáliz para delimitar los géneros *Lavatera*, *Malva*, *Alcea* y *Althaea* contrasta ampliamente con el tratamiento que da al género *Hibiscus*, que presenta "*perianthium exterius polyphyllum, persistens* [...] *rarius monophyllum, multifidum*" (p. 468 op. cit.), sin segregar ninguna unidad de él pese a la gran diversidad de configuraciones del epicáliz existentes, con piezas en diverso número, libres, soldadas o incluso ausentes (como en *Hibiscus lobatus* o en *H. sidiformis*).

Las primeras críticas a la clasificación linneana fueron tempranas. Medikus (1787), basándose en la estructura del esquizocarpo segregó los géneros *Olbia* y *Anthema* de *Lavatera*, y *Bismalva* de *Malva*. *Bismalva* y *Olbia* presentan frutos lavateroides, en el último caso con las paredes de los mericarpos reducidas y fusionadas, conformando una estructura intermedia entre el típico esquizocarpo y una verdadera cápsula (Ray, 1995). Las brácteas del epicáliz son libres en *Bismalva*, mientras que en *Anthema* y *Olbia* están soldadas en mayor o menor medida. Se trata del primer autor que reconoció la estrecha similitud que existe entre el grupo de especies que componían su género *Anthema* (que consistía en *L. arborea* y *L. cretica*) y las especies que dejó dentro de *Malva*: "*auser der äuseren Blumendecke [...] würde es schwer sein,* Anthema *von* Malva *zu trennen*" (p. 42 op. cit.). *Lavatera mauritanica*, similar a *L. cretica* y que presenta piezas del epicáliz soldadas sólo levemente en la base, era desconocida para él. Medikus también puso de relieve el hecho de que el criterio linneano para separar *Alcea* y *Althaea* era débil, dado que "*bei* Althaea officinalis *habe ich eben so oft die äußere Blumendecke 6mal, als auch mehrmal gespalten angetroffen*" (p. 35 op. cit.). Y aunque Tournefort distinguía ambos géneros utilizando la forma de las hojas, divididas en *Alcea* y enteras en *Althaea* (su concepto de *Althaea* incluía muchas especies de *Malva* y ninguna de las especies conocidas por *Althaea* hoy día), Medikus usó la misma circunscripción de los géneros que Linné, pero observando que la diferencia residía en el fruto: pseudobilocular en *Alcea* y unilocular en *Althaea*.

Desde entonces, algunos autores han estado de acuerdo con la visión linneana y por ello han considerado como muy importantes el número y grado de fusión de las piezas del epicáliz (De Candolle, 1824; Baker, 1890, y la mayoría de las floras modernas), mientras que para otros es la morfología del fruto el carácter decisivo a la hora de delimitar los géneros (Medikus, 1787;

Webb & Berthelot, 1833; Alefeld, 1862; Ray, 1995; Krebs, 1994), proponiendo clasificaciones alternativas a la clásica.

A comienzos del siglo XIX De Candolle (1805) aisló *L. trimestris* y la incluyó en su género *Stegia*. Más tarde, en el *Prodromus*, este mismo autor (1824) revertiría su opinión volviendo a la circunscripción linneana. Sin embargo, la principal aportación de De Candolle fue establecer por primera vez una clasificación infragenérica de *Lavatera*, *Malva* y *Althaea*, muchas de cuyas categorías todavía son de amplio uso en las floras actuales. De Candolle usó la estructura de los mericarpos para establecer la clasificación infragenérica de *Lavatera*, pero la ignoró para subdividir *Malva*, posiblemente dándose cuenta de la similitud existente entre sus *Lavatera* sect. *Anthema* y *Malva* sect. *Fasciculatae*. También abogó por la fusión de *Alcea* y *Althaea* bajo una definición más laxa de este último género, postura que pese a las evidentes diferencias entre ambos no fue revisada hasta bien entrado el siglo XX.

Aunque se trata de géneros claramente separables, *Alcea* y *Althaea* han permanecido unidas dentro de una visión extendida de *Althaea* durante al menos 150 años. Willdenow (1800) comenzó esta práctica, que adquirió continuidad con los trabajos de De Candolle (1824), Bentham y Hooker (1862) y Baker (1890). Aunque muchos autores han optado por el mantenimiento de ambos géneros tal y como los definió Linné en 1753 (Alefeld, 1862; Boissier, 1867), esta tendencia a la unión ha desaparecido sólo tras los trabajos de Iljin (1949) y sobre todo de las revisiones de Zohary (1963a, b) y Riedl (1976). Estos tres autores coinciden en el hecho de que *Alcea* es fácil y claramente distinguible de *Althaea* en diversos caracteres morfológicos, como el tamaño de las flores, la sección pentagonal de la columna estaminal en *Alcea*, y la existencia en este último género de un proceso del pericarpo que configura un mericarpo pseudobilocular.

Más adelante Webb y Berthelot (1833) separaron *L. arborea* y *L. cretica* del género *Lavatera* para incluirlas en *Malva*, basándose en los caracteres del fruto sobre los que ya había llamado la atención Medikus (1787). Se trata del primer intento de incluir las especies malvoides del género *Lavatera* dentro de *Malva*. Estos autores destacan también por su intento de aislar las dos especies arbustivas de *Lavatera* endémicas de Canarias en sendos géneros: *Lavatera acerifolia* en *Saviniona* y *Lavatera phoenicea* en *Navaea*. La primera de estas especies es un claro elemento malvoide próximo a la continental *L. maritima*, mientras que la segunda es un gran arbusto de polinización ornitófila, muy divergente y morfológicamente aislada. Con posterioridad Greene (1912) incluyó las *Lavatera* arbustivas de las islas del Canal de California dentro de

Saviniona. Sin embargo, esta visión no ha contado con el apoyo de autores posteriores.

Alefeld (1862) reorganizó por completo los géneros. Este autor reconoció al igual que Medikus (1787) la similitud existente entre *Malva* sect. *Malva* y *Lavatera* sect. *Anthema*, e incluyó ambos grupos dentro de una versión extendida de *Althaea*. Fue además el primero en reconocer la similitud existente entre las especies anuales de *Althaea* y algunas *Malva* anuales. Para ello utilizó el género *Axolopha*, en el que incluyó además especies morfológicamente muy distantes, como *L. maritima*, por lo cual su propuesta ha contado con un escaso grado de aceptación. Lo más interesante de su visión es que establece un subgénero dentro de *Axolopha*, *Dinacrusa*, para *Althaea hirsuta*, *A. ludwigii*, *Malva aegyptia* y *M. cretica*. Esta visión tendrá gran influencia sobre Krebs, en los años noventa del pasado siglo.

A finales del siglo XIX Baillon (1873) y Kuntze (1891) abogan por una visión totalmente sintética incluyendo todas las especies de *Lavatera*, *Malva* y *Althaea* dentro de un género *Althaea* extendido. Sin embargo, la fusión de géneros resulta en un enorme grado de heterogeneidad y una clasificación infragenérica muy aparatosa, lo cual está muy lejos de solucionar nada desde el punto de vista taxonómico. Como resultado de ello, ningún otro autor ha seguido estas clasificaciones. El siglo XIX se despide con Baker (1890), quien en un trabajo de síntesis monumental que agrupó todo el conocimiento disponible en la época sobre la tribu *Malveae*, es más conservador en el tratamiento de los géneros, siguiendo la delimitación clásica linneana, y tomando los rangos infragenéricos de De Candolle (1824) para su subdivisión.

Pasado el ecuador del siglo XX, R. Fernandes (1968b) revisa la historia taxonómica del género *Lavatera*, pero aunque reconoce la gran cercanía morfológica de *Lavatera* sect. *Anthema* y *Malva* sect. *Malva*, no hace ningún intento formal de reorganizar la clasificación, limitándose a explorar las posibilidades taxonómicas más plausibles. El argumento que da para ello es la falta de evidencia suplementaria para un cambio en la circunscripción de los géneros: "*continuamos a caracterizar esses géneros segundo o critério clássico, visto que nada, por enquanto, justifica que um outro seja mais natural*" (op. cit. p. 94).

En los años noventa, Krebs (1994a, b) redescubre las ideas de Alefeld (1863) y establece una clasificación nueva, segregando las especies anuales de *Althaea*, algunas *Malva* y el notogénero *Malvalthaea* a su género *Dinacrusa*, nombre tomado del trabajo de dicho autor, en base a sus esquizocarpos de paredes finas y redondeadas, cuyos bordes no se tocan entre sí. El género

Dinacrusa incluiría a las especies anuales de *Althaea* (*A. hirsuta*, *A. longiflora* y *A. ludwigii*, los tres integrantes de *Althaea* sect. *Hirsutae*) más tres especies anuales de *Malva*, *M. aegyptia*, *M. trifida* y *M. cretica*. Para acomodar estos taxones subdividió *Dinacrusa* en tres subgéneros: *Liogonia* para las *Malva* segregadas, *Dinacrusa* para las *Althaea* anuales y *Malvalthaea*, en el que se incluye *Malvalthaea transcaucasica*, una especie de morfología intermedia entre *Malva* y *Althaea* descrita por Iljin (1924) como un híbrido intergenérico, de distribución caucásica y que ha sido normalmente ignorado por los autores posteriores.

Ya en la era de la sistemática molecular Ray (1995), con su "*new perspective*" trae el antiguo problema de delimitación de los géneros *Lavatera* y *Malva* de nuevo a los escenarios de la sistemática. En base a caracteres carpológicos y moleculares propuso la existencia de dos grupos: uno de ellos con frutos de pericarpo fusionado y mericarpos indehiscentes, que se dispersan como una sola unidad (grupo malvoide, por incluir a *M. sylvestris*, el tipo de *Malva*), y otro con mericarpos de paredes no totalmente cerradas que liberan las semillas en la madurez (grupo *Lavateroide*, por incluir a *L. trimestris*, el tipo de *Lavatera*). De este modo, la vieja idea de Medikus (1787) sobre la estrecha relación existente entre *Malva* sect. *Malva* y *Lavatera* sect. *Axolopha* vuelve a estar de actualidad.

1.7. Objetivos.

En los trabajos previos que afectan a la alianza genérica de *Malva* ha predominado un enfoque morfológico, mientras que los estudios moleculares preexistentes adolecen de muestreo específico limitado. El objetivo de esta tesis doctoral es realizar un estudio filogenético con un muestreo específico representativo, maximizando así mismo el número de marcadores moleculares, con el fin de reinterpretar la variación morfológica presente en el marco de una filogenia robusta. Para ello se han realizado análisis de un total de 62 taxones (18 *Alcea*, 6 *Althaea*, 1 *Kitaibela*, 20 *Lavatera*, 12 *Malva*, 2 *Malope*, 1 *Malvalthaea*) utilizando seis marcadores distintos: nucleares de alto número de copias (ITS), cloroplásticos no codificantes (*trn*L-*trn*F, *psb*A-*trn*H) cloroplásticos codificantes (*mat*K, *ndh*F) y nucleares de bajo número de copias (*ces*A1b), incluyendo un total de más de nueve mil caracteres.

El trabajo desarrolla los siguientes puntos:

1. Exploración de la relación existente entre *Lavatera* sect. *Anthema* y *Malva* sec. *Malva* y *Fasciculatae*. Estos tres grupos presentan frutos de

pericarpo espeso que no libera la semilla en la madurez. Así mismo, pretendemos poner de relieve el parentesco existente entre *Malva* sec. *Bismalva* y *Lavatera* sec. *Olbia* y *Glandulosae*, que presentan frutos similares de mericarpos de paredes hialinas parcialmente fusionadas que liberan la semilla una vez maduros.

2. Clarificación de la posición filogenética de especies morfológicamente aisladas, como *Lavatera trimestris* y los demás taxones de la sección *Lavatera*. Esta especie es el único diploide del grupo y presenta una morfología muy divergente. El caso de *Lavatera* (*Navaea*) *phoenicea* es similar, se trata una especie endémica de Canarias morfológicamente aislada, no directamente emparentada con el otro endemismo canario, *L. acerifolia*.

3. Identificación de sucesos de especiación alopoliploide, muy probables en un grupo de plantas con niveles de ploidía diversos (2 a 16x), y con tendencia a producir híbridos interespecíficos con cierta frecuencia.

4. Realización de un muestreo lo más completo posible de los números cromosómicos de las especies del grupo, en busca de taxones con niveles de ploidía bajos (2 o 4x).

5. Estudio de la evolución de la cantidad de DNA (valores-*2C*) de los taxones del grupo, explorando su variación y reconstruyendo su evolución.

6. Determinación del grado de naturalidad del género *Althaea*, que puede ser un agregado polifilético, tal y como datos morfológicos previos sugieren.

7. Establecimiento de las relaciones existentes entre *Althaea* y *Alcea*, dos géneros que si bien son morfológicamente distinguibles han permanecido unidos durante más de un siglo.

1.8. Contenidos.

La presente memoria doctoral presenta un contenido en forma de capítulos publicables. Por ello su estructura difiere de una memoria tradicional no sólo en la distribución de los apartados que a componen, sino que además el idioma elegido para su escritura ha sido el inglés. Debido a la relativa independencia de cada uno de los capítulos, así como a la diversidad de enfoques metodológicos, cada uno de ellos presenta una estructura autónoma en introducción, material y métodos, resultados y discusión. Las tablas y figuras acompañan a cada capítulo. A continuación se realiza un breve resumen de cada uno de ellos así como una justificación de su contenido.

Capítulo 2. Molecular systematics of the *Lavatera-Malva* complex and related genera (*Malveae*, Malvaceae) based on nuclear and plastid sequence data.

El estado de conocimiento del complejo *Lavatera-Malva*, con un muestreo incompleto en trabajos anteriores (Ray, 1995), que utiliza tan sólo un marcador molecular (ITS), hacía urgente la realización de un estudio filogenético del grupo completo, en el que se ampliaran no sólo las especies muestreadas sino que además se hiciera uso de varios marcadores moleculares. En el presente capítulo se realiza un estudio de 47 taxones integrados en la alianza genérica de *Malva* con marcadores nucleares de alto número de copias (nrDNA ITS) y con secuencias cloroplásticas no codificantes (los espaciadores *trn*L-*trn*F y *psb*A-*trn*H). Los resultados sugieren una diversificación rápida del complejo *Lavatera-Malva*, con la aparición casi simultánea de varios linajes lavateroides y un linaje malvoide de frutos indehiscentes.

Capítulo 3. New Chromosome Counts in the *Malva* Alliance (*Malveae*, Malvaceae).

Si bien los estudios cariológicos en Malvaceae se remontan a principios del siglo XX, a pesar de que existen numerosos trabajos abordando taxones incluidos en la alianza genérica de *Malva*, cierto número de especies presentan números cromosómicos desconocidos. Debido al hecho de que la alianza es un complejo compuesto en su mayoría por taxones hexaploides, con sólo una especie diploide (*Lavatera trimestris*) y dos tetraploides (*Althaea hirsuta*, *Malva hispanica*) es crítico para el conocimiento del grupo el tener datos cariológicos de las especies hasta ahora no estudiadas.

Capítulo 4. Evolution of Genome Size in the *Malva* Alliance (*Malveae*, Malvaceae).

El tamaño del genoma (medido como valor-2*C*) es un carácter de gran interés en sistemática porque tiene repercusiones en el ciclo vital y ecología de las plantas. La existencia de dos grupos de especies, las lavateroides con genoma de gran tamaño, y las malvoides de genomas pequeños pone de manifiesto el interés que tiene la exploración de la variabilidad de este carácter en el grupo, así como su reconstrucción filogenética utilizando *squared change* *parsimony*, rastreando sucesos de ampliación y de miniaturización del contenido nuclear.

Capítulo 5. Low Variability in Three Molecular Markers, DNA Amounts and Chromosome Number Suggest High Phenotypic Plasticity and Extensive Hybridisation within *Alcea* L. (*Malveae*, Malvaceae).

La gran diversidad del género *Alcea*, de distribución predominantemente este-mediterránea e irano-turánica, su complejidad taxonómica así como el hecho de que nunca había sido estudiado con anterioridad mediante técnicas moleculares, aconsejaban el tratamiento del género en un capítulo aparte. La baja variabilidad encontrada en todos los marcadores moleculares analizados, así como la ausencia de variación en niveles de ploidía y cantidades de DNA sugieren, junto con la plasticidad fenotípica extrema que presentan muchas de las especies la existencia de hibridación extensiva entre sus diferentes taxones.

Capítulo 6. Low Copy Nuclear Marker *ces*A1b Reveals Previously Unsuspected Phylogenetic Relationships Within the *Malva* Alliance (Malvaceae).

Pese a la importante labor de muestreo y secuenciación realizada para el capítulo 1, los árboles obtenidos no fueron capaces de resolver las relaciones filogenéticas en dos puntos críticos: la base del clado *Lavatera-Malva* y los taxones ruderales del clado malvoide. Con el fin de obtener un mayor número de caracteres con los que trabajar decidimos secuenciar un marcador nuclear de bajo número de copias, *ces*A1b, así como dos nuevos marcadores cloroplásticos, *mat*K (incluyendo parte de *trn*K) y *ndh*F, para analizar si la falta de resolución se debe a una limitación por el número de bases secuenciadas (politomía blanda) o a un fenómeno de especiación rápido en el cual varios linajes divergen casi simultáneamente de tal manera que es imposible dilucidar el orden de especiación mediante un cladograma dicotómico convencional (politomía dura). Los resultados obtenidos no sólo apoyan la hipótesis de la politomía dura, sino que suponen una evidencia añadida a sucesos de especiación híbrida alopoliploide detectados en el capítulo1. El marcador de copia simple revela la existencia de otro evento de especiación híbrida que no había sido sospechado hasta ahora, y que afecta al dodecaploide *Malva alcea*.

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2. MOLECULAR SYSTEMATICS OF THE *LAVATERA-MALVA* COMPLEX AND RELATED GENERA (MALVACEAE) BASED ON NUCLEAR AND PLASTID SEQUENCE DATA

2.1. INTRODUCTION

The Malvaceae *s. str.* (Bayer et al. 1999) are a good example of morphologically well-defined group, isolated enough to show clear boundaries and easy to be diagnosed. But the taxonomy at the infrafamilial level is far away from being fully resolved. Some authors have even renounced to propose formal hierarchical classifications (Bates 1968; Bates and Blanchard 1970), advocating informal alliances that are easy to modify as new data are gathered. Nowadays, different authors have clarified the evolutionary relationships within several groups (Andreasen and Baldwin 2003; Cronn et al. 2002; Pfeil et. al. 2002, 2004; Small and Wendel 2002; Small et al. 2004; Tate et al. 2005), but there is still much to be done. Current generic definitions are not satisfactory (Fernandes 1968a, b; Krebs 1994a) and the placement of some species is still problematic (Ray 1995, 1998). Some genera (*Alcea*, *Althaea*, *Malvalthaea*) have never been studied with molecular markers. It seems therefore that new, independent molecular data are needed to clarify the phylogenetic relationships and solve long-standing systematic problems.

The genera *Malva*, *Lavatera*, *Althaea* and *Alcea* have classically integrated the so-called *Malva* alliance (Bates 1968; Bayer and Kubitzki 2003). *Malope*, though directly related to *Malva* and *Lavatera*, has normally been placed in the *Malope* alliance together with *Kitaibela* (Bates 1968; Bates and Blanchard 1970), whereas *Malvalthaea*, a small genus restricted to the Caucasus and Northern Iran, has been largely ignored. The *Malva* alliance comprises mainly perennial herbs of Mediterranean distribution, which extend northwards to Atlantic Europe and eastwards to south-western Asia, with main centres of diversity in the western Mediterranean Basin and the Middle East. *Alcea* is the most diverse (about 60 species, Pakravan 2001; Riedl 1976; Zohary 1963b) and includes perennial herbs native mainly to the eastern Mediterranean Basin and south-western Asia. *Althaea* (5-6 species, Tutin 1968) is mainly Mediterranean, with two broadly distributed species spreading over the salt-rich wetlands of most Eurasia. *Malope* (2-3 species, Nogueira et al. 1993; Cullen 1966, Webb 1968) and *Lavatera* (about 20 species, Fernandes 1968b) are mostly Mediterranean herbs with their largest diversity in the western Mediterranean. *Lavatera* comprises also shrubby elements growing in mild climates. Some species of *Lavatera* present a disjunct distribution area and are native to California and Mexico, Ethiopia and Western Australia. *Malva* (about 12 species, Morton 1937; Dalby 1968) is the widest-distributed of all them and ranges from its western Mediterranean centre of diversity to the rest of Eurasia, the ruderal species occuring widely across Australia and America due to recent anthropic introduction. It comprises mainly perennial and annual species. *Malvalthaea* is a genus of putative hybrid origin (1-3 spp, Iljin 1974; Riedl 1976) which includes shrubby elements of south-western Asian distribution.

The history of generic circumscription of the genera *Alcea*, *Althaea*, *Lavatera* and *Malva* has been controversial (table 1). The generic boundaries have varied along the last two centuries based on the relevance given to characters such as epicalyx and fruit morphology. It was first Linnaeus (1753) who, using the nature of epicalyx as diagnostic character, redefined the names *Alcea*, *Althaea*, *Malva* and *Lavatera* already established by Tournefort (1700, 1706). The linnean descriptions of *Malva* and *Lavatera* in *Genera Plantarum* (1789) are almost identical, being the calyx of *Malva* "*duplex, exterius triphyllum*" whereas that of *Lavatera* "*monophyllum, trifidum*" (op. cit. p. 465, 466). Tournefort described *Lavatera* as a monospecific genus, to segregate *Lavatera trimestris* from his large genus *Malva*, on the basis of the expanded, umbrella-like carpophore unique to this species. But Linnaeus included already two species in his *Hortus Cliffortianus* (1737) and several more in *Species Plantarum* (1753). He separated *Alcea* and *Althaea* on the same basis, both presenting fused epicalyx bracts, but in number of 9 and 6, respectively.

Soon Medikus (1787) first criticized the work of Linnaeus for establishing arbitrary generic boundaries and recognized the close fruit morphology link between his genus *Anthema* (consisting of *L. arborea* and *L. cretica*) and a reduced genus *Malva*. He also noticed that the linnean criterion to separate *Althaea* and *Alcea* was rather weak, and retained the generic circumscription but noting that the difference between both genera lies in the fruit shape.

Since then, some authors have agreed with Linnaeus and therefore considered the number and degree of fusion of the epicalyx bracts of great taxonomical interest (De Candolle 1824; Baker 1890, and most modern floras), whereas others have found the fruit morphology to be of greater importance

(Medikus 1787; Webb and Berthelot 1836; Alefeld 1862; Krebs 1994b; Ray 1995), proposing alternative classifications. De Candolle used the mericarp structure to establish the first infrageneric division of *Lavatera*, but ignored it to divide *Malva*, maybe aware of the similarity of his *Lavatera* sect. *Anthema* and his *Malva* sect. *Fasciculatae*. Webb and Berthelot (1836), also upon this great similarity, included both species in *Malva*. An overview of the taxonomic history of the group is provided in table 1.

Genera delimitation within the *Malva* alliance has been revised in recent times, when new data were gathered and new proposals were stated. In a series of two morphological papers, Krebs (1994a, b), focuses the genera *Alcea* and *Althaea* and brings back to stage some ideas from Alefeld (1862). He highlights the fact that some *Malva* are morphologically closer to the annual *Althaea* than the perennial *Althaea* themselves, and proposes new generic boundaries, closely linking this species group to the genus *Malvalthaea*, discovered by Iljin in 1924 and since then largely neglected.

The most relevant of modern contributions is that of Ray (1995), who first used molecular techniques to retrieve new data. He found that *Malva* and *Lavatera* were polyphyletic, both splitting in two well-supported groups which he named Malvoid and Lavateroid, as they included the type species for the genera *Malva* and *Lavatera*, respectively. *Lavatera*, as traditionally circumscribed, includes annual mallows closely related to *Malva sylvestris*, being also several species of lavateroid morphology included within *Malva*.

The phylogenetic and systematic questions remaining to be clarified can be summarised as follows:

1) The placement of *Lavatera trimestris*. This is a morphologically very diverging species which is also the only diploid of the group (Luque & Devesa 1986). It is the typus species of genus *Lavatera* and some authors have opted for taxonomically isolating it on the basis of its particular epicalyx shape and the umbrella-like carpophore. In fact, the original, tournefortian concept of *Lavatera* is a monotypic genus, segregated from *Malva* (Tournefort 1706) to include this taxon. Some authors have agreed with this monotypic definition (Medikus 1787, De Candolle 1805, Alefed 1862) while others support the permanence of this species in a larger genus *Lavatera*, due to the fused epicalyx bracts or the morphology of the schizocarps (De Candolle 1824, Baker 1890, Fernandes 1968a, b and Ray 1995).

2) The close morphological similarity between the species of *Lavatera* sect. *Anthema* and *Malva* sect. *Malva* (Medikus 1787, Webb and Berthelot 1836, Alefeld 1862, Fernandes 1968a, Ray 1995). Both share a unique fruit

structure, with sharp-edged mericarps which do not release the seed when ripe. The mericarp walls are thick and enclose completely the seeds, and detach from the carpophore without leaving any portion attached. This fruit type was named malvoid by Ray (1995) and is shared by species of both *Malva* and *Lavatera*, like these from *Lavatera* sect. *Anthema* (*L. cretica* and *L. arborea* among others) and *Malva* sect. *Malva* (*M. sylvestris* and allies). In fact, without observing the epicalyx it would be difficult to separe species so close morphologically as *L. cretica* and *M. sylvestris* (as it has repeatedly noted by Medikus 1787 and Fernandes 1968a, b), which are often misidentified not only in herbaria, but also in some field flower guides. Both *Lavatera* sect. *Anthema* and *Malva* sect. *Malva* show a tendency to occupy ruderal habitats such as dumps, wastelands and crop fields.

3) The resemblances in fruit morphology among *Malva* sect. *Bismalva* (including *Malva moschata*), *Lavatera* sect. *Olbia* (which includes *Lavatera olbia*), *L.* sect*. Lavatera* (the group of *L. trimestris*) and some morphologically isolated species such as *Malva hispanica* (Medikus 1787; Fernandes 1968a; Ray 1995), which displays two epicalyx bracts attached to the flower stalk rather than to the calyx. In all of them the mericarp walls are fused and do not enclose completely the seed, opening when ripe and releasing the uncovered seeds (lavateroid schizocarp, Ray 1995). The mericarp walls remain attached to a more or less developed carpophore, as tiny hyaline flaps.

4) The morphological singularity of the shrubby Canary Islands endemic *Lavatera* (*Navaea*) *phoenicea* and its relation to other woody representatives of *Lavatera*, already segregated to *Navaea* by Webb and Berthelot (1836) and recently addressed by Fuertes et al. (2002).

5) The development of woody habit in *Lavatera*. It has lead some authors (Webb and Berthelot 1836) to propose the genus *Saviniona*, which included not only the shrubby canary endemic *L. acerifolia*, but later (see Greene 1912) the woody *Lavatera* from the Californian Channel Islands.

6) The heterogeneity of the genus *Althaea*, where the annual species are morphologically similar to certain *Malva* (*M. aegyptia, M. cretica;* Alefeld 1862) and the genus of putative hybrid origin *Malvalthaea*. These taxa share mericarps with hyaline walls, almost enclosing the seed, with edges not touching each other. Recently Krebs (1994b) proposed the creation of the genus *Dinacrusa* to include these taxa.

7) The relationship between the genera *Althaea* and *Alcea*. Although both linnaean genera are easily diagnosed by epicalyx, carpel and staminal column characters, some authors have preferred to merge them within a single,

expanded genus *Althaea*, like Willdenow (1800), who initiated a tendency to merger later followed by De Candolle (1824), Bentham and Hooker (1862) and Baker (1890). Despite the attempts of segregating *Alcea* from *Althaea* made by Alefeld (1862) and Boissier (1867), this tradition was only broken after the fifties of past century by the works of Iljin (1974), Zohary (1963b, c), Riedl (1976) and Townsend (1980). Most modern floras and generic syntheses (Pakravan 2001) incorporathe this vision.

As there are no fully acceptable classifications of the taxa included in the *Malva* alliance, this paper aims to:

1) Conduct phylogenetic analyses of three molecular data sets (ITS, *psb*A-*trn*H, *trn*L-*trn*F), extending the sampling as compared to previous studies (Ray 1995, Fuertes et al. 2002, Tate et al. 2005) to address the critical questions listed above within the *Malva* alliance.

2) Review the different evolutionary interpretations and taxonomic proposals under the evidence of new molecular data, to stablish stable generic boundaries.

3) Reinterpret the morphological characters (nature of epicalyx, fruit traits, woodiness) already used by the different authors against a solid phylogenetic framework to determine synapomorphies that are useful to diagnose natural groups.

4) Identify events of hybrid speciation which are very likely to occur in a plant group with such different and high levels of ploidy, comparing ITS and chloroplast phylogenies to detect incongruence.

2.2. MATERIAL AND METHODS

2.2.1 Taxon Sampling:

Forty-seven species of *Malveae* have been studied (4 *Alcea*, 6 *Althaea*, 19 *Lavatera*, 1 *Navaea*, 2 *Malope*, 12 *Malva*, 1 *Malvalthaea*). *Anisodontea malvastroides* and *Malvella sherardiana* were chosen as outgroup species based on results of previous work (Fuertes et al. 2002; Tate et al. 2005). A total of 347 sequences (120 to ITS, 115 to *psb*A-*trn*H, 112 to *trn*L-*trn*F) belonging to 46 species have been generated and analysed (table 2). The ITS sequence of *Anisodontea malvastroides* comes from Fuertes et al. (2003), and was downloaded from GenBank.

Authority names follow Brummit and Powell (1992). Samples came from field collection in the Mediterranean area (Spain, Portugal, Morocco, France, Italy), living material grown by the authors in the experimental greenhouse at the Real Jardín Botánico, Madrid, or herbaria specimens. For some species, material from *index semina* was cultivated and only included into the analyses when the plants were securely identified. Vouchers of all specimens used were deposited at the herbarium MA (Real Jardín Botánico, Madrid). For a complete list see table 2. Multiple individuals per species were analysed when material was available. All DNA sequences are available at GenBank (http://www.ncbi.nlm.nih.gov, accession numbers EF419430 to EF419769, table 2).

2.2.2 DNA isolation, PCR and sequencing:

For DNA isolation DNeasy Plant Mini Kit (Qiagen) was used according to the manufacturer's recommendations. Total DNA was checked in 1.5 % agarose gels to test the amount and quality of the extractions. PCR products were obtained using puReTaq Ready-To-Go PCR Beads (Amersham Biosciences), with diluted or native stock DNA, depending on concentration. 1 μl DMSO per reaction was added, and for old or difficult herbarium material 4% BSA was used. PCR programs were run in a GeneAmp PCR System 9700 (PE Applied Biosystems) and a MJ Research PTC 200 (Peltier) thermocyclers. The **ITS** region was amplified using the P1A (5´-GGA AGG AGA AGT CGT AAC AAG-3´) and P4 (5´-TCC TCC GCT TAT TGA TAT GC-3´) primers (Fuertes & al. 1999), running an initial denaturation step at 95º for 1 min, followed by 35 cycles of denaturation at 95º for 1 min, annealing at 52ºC for 30 s and extension at 72º for 1 min. An additional extension step at 72º for 10 min was included. For ***psb*A-*trn*H** region, primers used were PSB (5´-CGA AGC TCC ATC TAC AAA TGG-3´) and TRN (5´-ACT GCC TTG ATC CAC TTG GC-3´), at an annealing temperature of 53ºC. The ***trn*L-*trn*F** region was amplified using universal primers TE (5´-GTT TCA AGT CCC TCT ATC CC-3´) and TF (5´-ATT TGA ACT GGT GAC ACG AG-3´) (Taberlet et al. 1991), at 50ºC annealing temperature. PCR products were checked on 1,5% D-1, low EEO agarose gel (Pronadisa), stained with Ethidium Bromide; and then purified with UltraClean PCR Clean-up Kit (MoBio). Cleaned PCR products were sequenced at the DNA Sequencing Service of CIB, CSIC (Madrid, Spain).

2.2.3. Data analysis:

Sequences were assembled with the program BioEdit version 7.0.5.2 (Hall 1999), and aligned with ClustalX (Thompson et al. 1997) followed by ocular inspection. Four datasets were analyzed, ITS with 121 sequences, *psb*A-*trn*H with 115, *trn*L-*trn*F with 112 and combined *psb*A-*trn*H plus *trn*L-*trn*F, including 101 combined sequences isolated from the same individual. Character congruence analyses using ILD tests (Incongruence Length Difference, Farris et al. 1994) implemented by PAUP*4.0b10 (Swofford 2000) were carried out to test for possible data partition incompatibilities.

To check possible contaminations, the Basic Local Alignment Search Tool (BLAST search, Altschul 1990) was used to check our sequences in GenBank. As ITS are a powerful tool to infer phylogeny, but due to the presence of paralogs or pseudogenes the phylogenetic analyses may be distorted (Álvarez and Wendel 2003, Buckler et al. 1997, Mayol and Rosselló 2001), once the possibility of having isolated alien sequences was discarded, we checked for the preserved regions of Liu and Schardl (1994) in ITS1 and Hershkowitz and Zimmer (1996) in ITS 2, to exclude possible pseudogenes from our analyses.

The molecular data sets were analysed using PAUP*4.0b10 (Swofford 2000). Parsimony analyses of four data sets were performed (ITS, *psb*A-*trn*H, *trn*L-*trn*F, *psb*A-*trn*H+*trn*L-*trn*F). Gaps were coded with the simple method of Simmons and Ochoterena (2003), as implemented in IndelCoder provided by the software SeqState 1.25 (Müller 2005). For each data set, heuristic searches were conducted with 1000 random stepwise addition replicates, and tree bisection-reconnection (TBR) branch swapping holding and saving 10 trees per replicate (ACCTRAN optimization). Bootstrap support analyses (Felsenstein 1985) were performed running 100 replicates of random sequence addition, equal weighting and TBR branch-swapping.

Polymorphic positions were coded using IUPAC ambiguity codes. A site is designated as polymorphic when more than one peak is present in the electropherogram and the weakest signal reached at least 25% of the strength of the strongest signal (Fuertes et al. 1999). To avoid the inclusion of misreads as polymorphic sites only double peaks that appeared at the same position in both direct and reverse sequences were considered. Additive polymorphic positions (APS) were also recorded when the two bases of the polymorphic site appeared separately in different accessions of the data matrix, whether or not they turned to be parsimony informative. APS are found to be useful in phylogenetic inference at reticulate scenarios, even when they are parsimony-uninformative (Fuertes and Nieto 2003, Whittall et al. 2000).

Bayesian analyses (Huelsenbeck et al. 2001; Larget and Simon 1999) were implemented in MrBayes 3.1 (Huelsenbeck and Ronquist 2001).

Hierarchical likelihood ratio tests conducted in Modeltest version 3.06 (Posada and Crandall 1998, 2001) yielded the General Time-Reversible (GTR) model (Rodríguez et al. 1990) with gamma distribution as the sequence evolution model best fitting our datasets. Four simultaneous Markov chains starting with a random tree were run for 1,000,000 generations, with tree sampling every 100 generations. This was more than enough to allow standard deviation of split frequencies to stabilize at levels lower than 0.01. The first 2000 trees (20%) were discarded as burnin and thus not taken into consideration to build the 50% majority-rule consensus tree.

2.3. RESULTS

2.3.1. SEQUENCE VARIATION

a) ITS

The ITS1 preserved domain of Liu and Schardl (1994) was found to have the sequence GGCGCGAATCGCGTCAAGAA. All the six conserved regions of Hershkowitz and Zimmer (1996) are present in ITS2, starting with c1, an 11 bp region with the sequence ATCGTYGCCCC. A variable region changing from C- to G-rich towards the 3´ end is followed by the second conserved region c2 (GGGCGGAATTGSYYTCCCG). After 10 variable bp c3 (CGCYYRYGGTTGRYC YAAA) is found, followed by a variable 6-8 bp region and TCCTY. After a short AG rich region the preserved domains c4 (YGCCRCGACNATYGGTGGGA) and the not so constant c5 (KYGYGYWCGT) appear. The last conserved and shortest region (c6, 6 bp) presents the sequence GACCCY. As a result of conserved regions integrity analysis, one accession of *L. mauritanica* was discarded due to extensive presence of punctual mutations.

The average GC content is 58,4% with some variations, being slightly lower in the perennial species of *Althaea* than in the annuals. The annual *Malva* species and the perennial *Lavatera* tend to present higher GC contents.

Our ITS dataset presents a remarkably high number of additive polymorphic sites (APS), 73 in total (9.2% of total positions), appearing in 27 out of 40 studied taxa. Most of them are autapomorphies, but 16 appear to be shared and support the hypothesis of reticulation at different points of the phylogenetic trees. Polymorphic C, G (Y) and A, G (R) sites account for the 42.8 and 34.6% (respectively) of all observed indeterminations, followed far away by the much less common M (A, C, 11.2%), K (G, T, 7.1%), W (A, T, 3.6%) or S (C, G, 1%). The appearance of polymorphic sites does not seem to be ligated to particulary high chromosome numbers, being most of affected species hexaploid. This is particularly evident in the case of the ruderal mallows, which show a marked tendency to share polymorphisms. *Malva parviflora* and *M. sylvestris* share 3 of these polymorphic positions, while *Lavatera arborea* and the 12-ploid *L. mauritanica* share 4. This latter species is apparently a hybrid, as well as *Malvalthaea transcaucasica*, another taxon with a high number of polymorphisms, some of which (positions 676, 713 and 773) are shared with both *Althaea hirsuta* and *Malva aegyptia*.

b) Plastid markers

***psb*A-*trn*H**: Sequence variation in this spacer is complex due to the presence of multiple indels, some of them autapomorphic. Some malvoid sequences present insertions which can be repeated sequences or not. The annual *Althaea*, *M. cretica* and *M. aegyptia* present large deletions in the region spanning from positions 462 to 559. An AT microsatellite of reduced size appears between positions 354 and 387. But maybe the most characteristic feature of this plastid marker is the hairpin inversion found between positions 28 and 101. This region has been usually removed from phylogenetic analysis in groups where it is present, like *Paeonia* (Sang et al. 1997) or *Tarasa* (Tate & Simpson 2003) among others, but in view of new results proving the informativeness of the structure (Bain & Jansen 2006) we decided to include it. Despite this relative sequence complexity, no region was found to be ambiguously aligned and therefore all the nucleotides sequenced were used in the analysis.

***trn*L-*trn*F**: This spacer shows far less complexity than the preceding, with some length polymosphism due to a terminal repeat occurring among the malvoid taxa, from 466 to 556 bp. Alignment was straighforward and only few indels were detected. The most significative are a 7 bp insertion at position 215 exclusive to *Alcea*, and a 9 bp insertion at position 95 which is characteristic of perennial *Althaea*. A reduced AT microsatellite spans from positions 152 to 176, interrupted by a GTG conserved triplet.

2.3.2. Analysis

a) ITS

The bayesian 50% majority rule tree (not shown) was essentially identical to the parsimony strict consensus. Only minor differences in the terminal taxa were found regarding the ruderal malvoid taxa (such as *Malva neglecta* or *Lavatera cretica*), some of them failing to cluster monophyletically in both analyses. Posterior probabilities were more supportive than bootstrap values, both appear displayed in figure 1.

The **ITS parsimony analysis** included 793 total characters, of which 506 were constant, 51 variable characters were parsimony-uninformative and 236 were parsimony-informative, yielding 3150 most parsimonious trees with a length of 699, consistency index (CI) = 0.5823, retention index (RI) = 0.9313 and homoplasy index (HI) = 0.4177.

The ITS analyses produced well-resolved trees (see figures 1 and 3), in which *Malva* and *Lavatera* cluster together with the annual *Althaea* species within a single, well-supported clade (bootstrap support, BS = 99, bayesian posterior probability = 100) sister to which *Malope*, the perennial *Althaea* and *Alcea* appear. Nested within this clade, the terminal part (*Lavatera*-*Malva* clade, LM) splits into two morphologically well-diferentiated groups of species including most *Malva* and *Lavatera* species, one with the malvoid taxa and other with the lavateroid ones, which will be successively called Malvoid and Lavateroid groups (Ray 1995). All remaining species are sister to the terminal LM clade.

The malvoid group is strongly supported by bootstrap analyses (BS98, 100), but the lavateroid, despite the morphological link, is not (BS < 50, 94). Five clades of lavateroid taxa display high BS support values, containing the perennial *Lavatera* (BS81, 100), *L. trimestris* (BS100, 100), *Malva hispanica* (BS100, 100), *L. thuringiaca* (BS98, 100) and *Malva* sect. *Bismalva* (BS100, 100). The position of *L. punctata* at the base of *Bismalva* is not supported, falling to a basal *Lavatera*-*Malva* polytomy in the BS analysis.

Within the malvoid group, the *Lavatera acerifolia* - *L. maritima* clade (BS86, 83) is sister group to the remaining taxa, a high-supported clade (BS100, 100) grouping the ruderal *Malva* species. At the base of the ruderal *Malva* clade, there appear two annual to perennial species (BS100, 100), the (sub-) shrubby *L. arborea* and *L. mauritanica*. The terminal group is a polytomy including several clades. The shrubby endemics *L. assurgentiflora*, *L. plebeia* and *L. abyssinica*, from California, Australia and Ethiopia, respectively, appear together in a single, well-suppported clade (BS93, 100), and are not closely related to the also shrubby Canary Island endemics *L. acerifolia* and *L. phoenicea*, which are also not closely related to each other (as in Fuertes et al. 2002). Another group arising from this polytomy is the *M. parviflora* - *M. verticillata* clade, whose close link is recognized since many years, here including one accession of *M. neglecta*. Another clade links *L. cretica* with the similar but small-flowered *M. nicaeensis*, and one acession of *M. neglecta*, species which displays polyphyletic ITS. The two accessions of *M. sylvestris* arise directly from the polytomy.

The sister group of the LM clade is integrated by the annual species of *Althaea* (sect. *Hirsutae*) plus *Malva cretica* ssp. *althaeoides*. The link between *Malva cretica* and the annual *Althaea* sect. *Hirsutae* is not well-supported (BS63, 100), neither is the position of this clade with respect to the LM clade (BS < 50, 98).

Immediately downwards in the tree *Malvalthaea transcaucasica* is basal to the *Malva aegyptia* - *M. trifida* group, shaping a well-supported clade (BS100, 100). Though not supported by bootstrap analysis, this triplet of species is sister-group to both the malvoid and lavateroid groups, plus the annual *Althaea* clade. Separated from all the other species, the morphologically very diverging *Lavatera phoenicea* is basal to all other *Lavatera* and *Malva* species, and also to the annual *Althaea* and *Malvalthaea*.

Well-supported and basal to the group appear both *Malope* and *Althaea* clades (BS100, 100 for both clades). The *Althaea* clade includes the perennial species of *Althaea* as well as all *Alcea* species analysed.

b) Plastid markers

Chloroplast data are in general informative at higher levels than ITS (Sang et al. 1997) and the spacers used for these analyses yielded big unresolved regions in the resulting trees.

The ***psb*A-*trn*H** parsimony analysis included 659 total characters, from which 572 were constant, 41 variable characters were parsimony-uninformative and 46 were parsimony-informative. 99 indels were included. The parsimony analyses resulted in 400 most parsimonious trees, with a length of 109, CI = 0.8624; RI = 0.9667 and HI = 0.2206.

The topologies resulting (not shown) were largely unresolved, with all major clades arising from a single, basal politomy. Elimination of the hairpin sequence, microsatellite or insertions did not have any positive effect in the tree scores. A clade comprising most malvoid species receives low support (BS60, 90), while the lavateroid taxa do not fall in a single clade, although all the perennial species from *Lavatera* sect. *Olbia* cluster together. The annual *Althaea* cluster with *Malva cretica* (BS79, 100), including *Malvalthaea transcaucasica*, which was linked to *Malva aegyptia* in the ITS analysis. *Malva aegyptia* and *Malva trifida* are closely related (BS99, 100).

The ***trn*L-*trn*F** matrix included 464 total characters, from which 414 were constant, 15 variable characters were parsimony-uninformative and 35 were parsimony-informative. The parsimony analyses resulted in 9860 most parsimonious trees, with a length of 51, CI = 0.9608; RI = 0.9934 and HI = 0.0513.

This spacer yielded better-resolved trees (not shown), as it is more informative and less homoplasic than *psb*A-*trn*H. Large regions from the consensus trees appear unresolved as large polytomies. The perennial *Althaea* are closely related to *Alcea* (BS93, 100) and sister taxa to the remaining. *Malope* is not directly linked to *Althaea*-*Alcea* and is sister to annual *Althaea*, *Malvalthaea*, *Lavatera* and *Malva*.

Most malvoid species appear grouped and highly supported by bootstrap values (BS82, 100). As *L. maritima* and *L. acerifolia* collapse into the big polytomy, *L. arborea* appears as sister taxon to all remaining malvoid species (BS62, 80).

Regarding the lavateroid species, all perennial *Lavatera* from sect. *Olbia* appear together in a single clade, including also other lavateroids like *L. maroccana* and *L. thuringiaca*, but not *L. trimestris*, which collapses to the basal polytomy.

To increase the number of parsimony-informative characters and improve resolution, we merged **both plastid** matrices, including 1126 total characters, from which 995 were constant, 55 variable characters were parsimony-uninformative and 76 were parsimony-informative. The parsimony analyses resulted in 7700 most parsimonious trees, with a length of 163, CI= 0,8589; RI= 0,9640 and HI = 0,2130. The bayesian analysis of separated chloroplast datasets yielded also poorly resolved trees fully compatible with the parsimony topologies. Dataset combination improved resolution, though large polytomies remained. Posterior probability values appear mapped on the parsimony topology in figure 2.

The topology of the combined *psb*A-*trn*H + *trn*L-*trn*F tree is better-resolved though large polytomies remain, due to short branch length at critical points (figure 4). The perennial *Althaea-Alcea* clade and the remaining species arise from a basal polytomy. The *Malope* are sister to all other taxa studied, but not with high support (BS69, 99), as in the ITS analysis. All remaining taxa cluster together (BS75, 100) and arise from a large basal polytomy.

The lavateroid taxa do not cluster together any more. Most perennial *Lavatera* appear to be linked, as they did in the ITS analysis, but this relation is poorly supported (BS < 50), as it is their association with *M. hispanica*. The *Bismalva* clade also remains highly supported (BS98, 100), as the *M. aegyptia* - *M. trifida* clade (BS100, 100).

All malvoid species but *L. acerifolia* occur in a single, low-supported (BS77, 100) clade. Within it, *L. arborea*, *L. abyssinica*, *L. plebeia* and *L. assurgentiflora* appear placed in the lower positions. All remaining *Malva* and malvoid *Lavatera* are nested together, also with low support scores.

Althaea hirsuta remains associated with *Malva cretica* (BS59, 100), which appears also strongly linked to *Malvalthaea transcaucasica*, in a clear case of incongruence between datasets.

For a comparison between the ITS and plastid topologies see figure 5.

2.4. DISCUSSION

2.4.1. Natural lineages in the *Malva* alliance: synapomorphies and group definition.

The picture drawn by molecular data contrasts sharply with the traditional systematic approach to the group, based upon the number and degree of fusion of the epicalycinal bracts. The species possessing thick-walled, undehiscent schizocarps (figure 6) cluster together in a well-supported clade (BS 98 in ITS analysis, 77 in joint plastid), regardless of their inclusion in traditional *Lavatera* or *Malva* and conforming the Malvoid group (Ray 1995). The fact is that, outside the degree of fusion of the epicalyx, *Lavatera* sect. *Anthema* and *Malva* sect. *Malva* and *Fasciculatae* are essentially almost identical. Sometimes the apparently clear difference separating them is blurred - *Lavatera cretica* and *Malva sylvestris* show diverse degrees of fusion among the pieces of the involucre - what results is that this pair of species is normally misidentified at the shelves and desks of not only botany students, but also at the biggest herbaria.

The close morphological resemblance among the malvoid *Lavatera* (the species traditionally included in sections *Anthema* and *Axolopha*: *L. acerifolia*, *L. arborea*, *L. cretica*, *L. maritima*, *L. mauritanica* as well as the non mediterranean *L. abyssinica*, *L. assurgentiflora*, and *L. plebeia*) and the ruderal mallows (from traditional sect. *Malva* and *Fasciculatae*: *M. neglecta*, *M. nicaeensis*, *M. parviflora*, *M. sylvestris* and *M. verticillata*) has been noted since long ago. Already in 1787, Medikus splitted some malvoid *Lavatera* to the genus *Axolopha*. All the species included share the unique structure of malvoid schizocarp (Ray 1995), with characteristic thick-walled, sharp-edged mericarps enclosing completely the seed, which are dispersed as a single unit. All these species are high polyploids of basal number x = 7, ranging from the widespread hexaploid level to the 16-ploid *L. cretica* (Luque & Devesa 1986). The chromosomes are always small and the DNA amounts are highly reduced, as compared with these of the lavateroid taxa (Escobar et al. 2007).

Despite this high bootstrap support scores for the Malvoids, the taxa displaying dehiscent schizocarps with thin, fused walls (lavateroids in Ray 1995) fail to cluster together in our bootstrap analyses. Instead, up to five independent lineages arise from a *Lavatera*-*Malva* polytomy (figures 1 and 2).

Within traditional *Malva*, sect. *Bismalva* (*M. moschata*, *M. tournefortiana* and *M. alcea*) presents lavateroid fruits. These species form a natural group recognized since very long (Medikus 1787), with perennial herbs occurring in forest margins, showing dimorphic indumentum of stellate and simple hairs, and solitary flowers subtended by leaf-like bracts, more shortly pedunculated and more divided toward the apex of the racemose inflorescence. In our analyses the monophyly of *Bismalva* group is highly supported (BS100 in ITS analysis, 98 in plastid), but its placement and relations are not so clear. ITS data suggest it is sister to the perennial *Lavatera* (*Olbia* clade) and closely related to sect. *Lavatera* and *Malva hispanica*. The plastid data set also suggests a basal position not only to the *Olbia* clade but also to the malvoid species, and links it tightly to *Lavatera trimestris* from sect. *Lavatera*. Neither of these relationships are strongly supported (bootstrap support < 50) so with our present dataset we are only able to recognize its basal position within the *Lavatera*-*Malva* clade.

Among the lavateroids the perennial *Lavatera* clade obtains support only in the ITS analysis (BS81). The shrubs from section *Olbia* (*L. bryoniifolia*, *L. oblongifolia* and *L. olbia*) are sister to the remaining species but with low scores (BS53). This traditional section is integrated by evergreen shrubs with solitary flowers which appear in terminal bracteate racemes. All present monomorphic indument of stellate hairs, and a very characteristic carpophore longer than the mericarps. There is an exception, *L. plazzae*, a tall perennial herb endemic to Sardinia (Atzei 1995), with paniculate terminal ebracteate inflorescences and an unique epicalyx of 3-6 lobes. These species are sister taxa to a high supported clade (BS90) including perennial herbs traditionally classified within the *L. triloba* aggregate, including *L. triloba* s. str., *L. flava*, *L. agrigentina* and *L. stenopetala*, the latter not included in this study. All of them present dimorphic indument of glandular and stellate hairs, and fasciculate flowers, axilar to leaf-like bracts. All the species of the clade present fruits with 13-20 mericarps, while all the remaining *Lavatera-Malva* have up to 10 (-15). These species share also chromosome numbers (2n = 6x = 44) and the occurrence of large chromosomes with high DNA amounts, as compared with the malvoid species.

Three more lavateroid clades polytomize in the bootstrap analysis. That containing *L. trimestris* is well-supported in both ITS and plastid analyses (BS100). The clades including *L. thuringiaca* and *M. hispanica* are also well-supported by ITS (BS 98 and 100, respectively), but not so much in the plastid joint analysis (BS < 70). The other species of lavateroid morphology fail to resolve satisfactorily an polytomize at the base of the large *Lavatera-Malva* clade. Along with these some other species (*L. punctata*, *L. maroccana*) appear loosely attached to the lavateroid clades, polytomizing in the bootstrap support analysis (BS < 50).

Sister to the remaining *Lavatera* and *Malva*, the annual species of *Althaea* cluster together with *M. cretica* and *Malvalthaea transcaucasica*. This is a major point of incongruence, because *Malvalthaea* clusters with *Malva trifida* and *M. aegyptia* in the plastid joint analysis. These taxa fall outside the *Lavatera-Malva* clade and are sister to the remaining species. Only bayesian posterior probabilities support this relationship, as bootstrap analysis fails to find signifficant support. The plastid joint tree lacks information at this level and polytomizes. Contrastingly, the perennial *Althaea* are more related to *Alcea* and are sister taxa of all remaining studied taxa.

Lavatera (*Navaea*) *phoenicea* is sister to all so far mentioned taxa in the ITS dataset, as the joint chloroplast analysis lacks information at this level. The closest relative of the *Lavatera-Malva* clade plus *Navaea* is the genus *Malope*. It has been included in the tribe *Malopeae* (Schumann 1890), with the genera *Kitaibela* and *Palaua*, on the basis of verticillate or spirally-arranged mericarps. Bates (1968), in his unranked classification of generic alliances, retained *Kitaibela* and *Malope* as the *Malope* alliance, transferring *Palaua* to the *Sphaeralcea* alliance; but this is not supported by later work (Tate et al. 2005), in which *Malope* appears to be closely linked to *Lavatera* and *Malva*.

Sister to *Malope* and all remaining species, a highly supported clade grouping the perennial *Althaea* plus *Alcea* occurs. This relationship is highly supported by ITS (BS > 90), being the joint plastid analysis less supportive (BS between 60 and 80).

2.4.2. Phylogenetic incongruence, hybrid speciation and introgression among the Malvoids.

The malvoid group appears phylogenetically highly structured, both in the ITS and chloroplast datasets. Sister to the other malvoid taxa a clade containing *L. acerifolia* and the diverse accessions of *L. maritima* appears. Both constitute the traditional *Lavatera* sect. *Axolopha* and are characterised by their single indumentum of stellate hairs and their solitary or geminate flowers, subtended by leaf-like bracts. Carpophores surpassing the mericarp surface are present. *Lavatera acerifolia*, endemic to the Canary Islands, with maple-like almost glabrous leaves is sister to *L. maritima*, with round grey, whitish-green leaves, more adapted to dry climates. This group is strongly supported by the ITS analyses (BS83, 100) but in the chloroplast analysis its union to the base of the malvoid group is not enough supported and both taxa fall within the large, basal polytomy in the *Lavatera-Malva* clade. The malvoid taxa integrate the most widespread group within the *Lavatera-Malva* clade, ranging from the Mediterranean region northwards to Scandinavia, and as neophytes in both Americas, Africa and Australia, some of them being narrow endemics to remote areas such as Australia, Ethiopia or California.

The small-flowered ruderal mallows appear, as predicted by morphology data, to be very closely related. Both ITS and chloroplast datasets support 1) an association among *L. cretica*, *M. nicaeensis* and *M. neglecta*; 2) hybridisation among hexaploid taxa, as indicate the polyphyly of accessions for *M. neglecta* (ITS data) and *M. parviflora* (chloroplast data); 3) the close link between *M. parviflora* and what appears to be its autopolyploid derivative, *M. verticillata*; 4) the malvoid *Lavatera* are not closely related to each other; 5) the incongruence of both datasets suggests allopolyploidy in both *L. mauritanica* and the group of extramediterranean *Lavatera*.

As ITS results show, the 16-ploid *L. cretica* appears basal to a clade including some accessions of *M. neglecta*, all *M. nicaeensis* and *M. parviflora*. Arising also from the malvoid polytomy there is another highly-supported clade containing an accession of *M. neglecta* and *M. verticillata*, both very similar in overall morphology but the latter being 12-ploid. *M. parviflora* presents two APS, at positions 61 (Y, K) and 105 (Y). This last position is T for most ruderal mallows, but C for some vouchers of *M. parviflora* and for *M. verticillata*, which lack APS.

The observed non-monophyly of *M. neglecta* and *M. parviflora* may be due to hybridisation, a frequent phenomenon among some hexaploid small-flowered mallows (mainly *M. neglecta*, *M. nicaeensis*, *M. parviflora* and *M. sylvestris*). As a result, there are many names to describe the variability and morphological diversity of hybrids (see Sennen 1910, 1932). This species group form a polyploid series of basic chromosome number 2n = 6x = 44, with up to 16-ploids reported within *L. cretica*, while *L. mauritanica* and *M. verticillata* are 12-ploid. They present similar DNA amounts (Escobar & al. 2007), and share ruderal habitats, annual life cycles, and mostly tiny fasciculate flowers subtended by leaf-like bracts. But these high level polyploid mallows lack APS, fact that together with their well-delimited, easy-diagnosable morphology suggests, at least for *L. cretica* and *M. verticillata*, an autopolyploid origin.

Contrary to what was expected only from morphology data, the malvoid *Lavatera* are not closely related which each other. In the ITS cladogram (figure 1) *L. arborea* and *L. mauritanica* appear basal to the remaining malvoid ruderal mallows, but *L. cretica*, quite similar to the latter, appears in a separate clade closely linked to *M. nicaeensis* and some accessions of *M. neglecta*. The plastid analyses (figure 2) lead to similar conclusions, with some incongruence. The three malvoid species of *Lavatera* are monophyletic but neither of them is directly related to each other.

The case of *L. mauritanica* deserves special attention. In the ITS analysis, it appears very well supported in a basal malvoid clade together with *L. arborea*. But with the chloroplast dataset the results are quite different, being deeply embedded within the *M. parviflora-verticillata* clade, whereas *L. cretica* is basal to them, and *L. arborea* remains at low positions within the malvoid clade. This incongruence could be intrepreted as a hybrid allopolyploid speciation event, as both *L. arborea* and *M. parviflora* are sympatric at the neighborhoods of Gibraltar Streit, the native restricted area - with some irradiations westwards in the Iberian Peninsula ans eastwards in Morocco- of *L. mauritanica*. Both species share chromosome number and DNA amounts. Morphologically both *L. mauritanica* and *L. arborea* share dark-eyed flowers, character unique to them within the malvoid group. The ecological requirements of *L. mauritanica* are unique: it colonizes nitrified sandy areas close to the sea, mainly in beaches; though some specimens thrive also at limestone coastal rocky outcrops.

Another focus of incongruence within the malvoid group is found among the extramediterranean, shrubby *Lavatera* species *L. abyssinica* (Ethiopia), *L. assurgentiflora* (Californian Channel Islands) and *L. plebeia* (Australia). As the phylogenetic affinities among these taxa and the Canary Island *L. phoenicea* and *L. acerifolia* have ecological and biogeographical implications we discuss the island endemics further in section 4.

2.4.3. The placement and affinities of *Lavatera trimestris*.

Lavatera trimestris presents a unique umbrella-like carpophore which has led several authors to recognizing it as a separate genus. This species was originally a monospecific segregate from a heterogeneous genus *Malva* (Tournefort 1706). Linnaeus (1753) redefined the genus and included other species placed before in the tournefortian *Malva* and *Althaea*, giving birth to the *künstliche Geschlechter* (Medikus 1787) which has spilled rivers of ink from Medikus to our days. De Candolle (1805) isolated it in his genus *Stegia* and later in the section *Stegia* within *Lavatera*. Also Alefeld (1862) and Medikus (1787) preferred this monotypic definition.

The annual lavateroid species are morphologically close to each other. *Lavatera trimestris*, *L. punctata* and *L. maroccana* present extended, campanulate, fused epicalyces of mucronate bracts with tiny lobes between the three main ones (figure 6). The carpophore of *L. maroccana* is also umbrella-like, but not covering the mericarps as in *L. trimestris*. *L. punctata* shows an extended carpophore as well, but not umbrella-shaped, while the calyx, not as extended as in the preceeding taxa, is also characteristic. Although this morphological homogeneity, neither bayesian nor parsimony analyses support a clade including the three of them. *Lavatera trimestris* is linked in our results to *M. hispanica*, while *L. punctata* is loosely attached (BS<50) to the base of *Bismalva* clade. The relationships among these and the other lavateroid species are not clear. ITS data cluster them with the *Bismalva* clade, whereas the chloroplast markers link just *L. trimestris* with *Bismalva* and *L. maroccana* and *L. punctata* appear closely related to the *Olbia* clade. Neither of these relationships is highly supported by bootstrap analyses, which collapse the branches to a basal polytomy from which the *Olbia*, *Bismalva* and malvoid clades, plus *L. thuringiaca*, *M. hispanica* and the three annual *Lavatera* arise.

Therefore, and despite the relative morphological coherence in fruit morphology, are we really in front of a phylogenetically single lineage or facing a hard polytomy, an early, fast evolving complex which produced the malvoids and up to five distinct lavateroid lineages? With the present data it seems unrealistic to give an assertive answer. The use of other molecular markers, particularly low-copy nuclear genes may be of great utility at this point.

2.4.4. Island endemics. How many times has woodiness appeared in the genus *Lavatera*?

Basal to all the remaining species of *Lavatera*, *Malva* and annual *Althaea* there appears the Canary Island endemic *Lavatera phoenicea*. Although traditionally considered to be a *Lavatera* species, it is morphologically very diverging and was first segregated to the monotypic genus *Navaea* by Webb and Berthelot (1836) on the basis of an unusually high number of mericarps (30-40) that are provided with two horn-like protuberances, deciduous epicalyx, articulate flower stalks and a unique nectary-structure. As it has already been pointed out by other molecular studies (Fuertes et al. 2002), *L. phoenicea* is not directly related to the other shrubby Canary Islands endemic *L. acerifolia*, leading to the conclusion that these species are the fruit of independent island colonisation events. *Lavatera phoenicea* is also not directly related to the extramediterranean malvoid *Lavatera* (*L. abyssinica*, *L. assurgentiflora* aggregate and *L. plebeia*, from Ethiopia, California and Australia, respectively). The fact that the other woody representatives of the genus (figure 6) are also not direcly linked to each other makes us think of woodiness appearing at least twice in the group: at the base of the malvoids, which have evolved towards hebaceous life forms and at the base of the whole *Lavatera* - *Malva* - annual *Althaea* clade.

The extramediterranean *Lavatera* species appear tightly clustered (BS93, 100) in our ITS dataset, nested within the ruderal mallows. But the plastid scenario shows quite a different picture, with these species arising together from a basal polytomy within the malvoid group, position that they share with the hexaploid *L. arborea*. Chomosome counts show 2n = 12x = c. 84 for *L. assurgentiflora* and 2n = 43 for *L. plebeia* (Skovsted 1935), being unfortunately the chromosome numbers of *L. abyssinica* unknown for us. The possible allopolyploid origin of these species, is at this state of our knowledge only an attractive hypothesis that we would like to explore as new data are gathered. The number of polyploidization/hybridisation/dispersal events remains obscure, due to our limited disponibility of material. The possible dispersion routes are also unknown for us, as these three taxa are endemic to very distant areas which are also far away from the Western Mediterranean, home to most

Lavatera-Malva taxa. Sea birds could be involved, as *L. arborea* - a serious candidate for progenitor species - thrives on seashore rocky outcrops nitrified by bird deyections.

Lavatera assurgentiflora and its close relatives from the Californian Channel Islands (*L. insularis*, *L. lindsayi*, *L. occidentalis*, *L. venosa*, all of them resembling *L. assurgentiflora*) are morphologically very similar to *L. acerifolia*, despite not being closely related, with maple-like leaves covered with tiny stellate hairs, and flowers slightly zygomorphic with a flexuous staminal column. This is the reason why they have been included by Greene (1912) in the genus *Saviniona* from Webb and Berthelot (1836), in which they isolated *L. acerifolia*.

2.4.5. Circumscription of *Althaea* and its relation to *Alcea*. The genus *Dinacrusa*.

The names *Alcea* and *Althaea*, which appear scattered in the European medieval tradition, were already used by Tournefort (1700). Linnaeus kept both names for hollyhocks and marshmallows, respectively, and transferred most species of *Althaea* to his conception of *Malva* and *Lavatera*. Though both genera are well-characterised since Medikus (1787), Willdenow (1800) and later De Candolle (1824) and Baker (1898) merged them within a larger *Althaea*. It has not been until recent times when Zohary (1963b, c) proposed the recognition of *Alcea* in the linnaean sense, view which is normally adopted nowadays. *Althaea* includes two distinct morphological groups which appear to be not directly related. One, sect. *Althaea*, includes the perennial species and is sister taxon of *Alcea*. The other, sect. *Hirsutae*, groups annual species, which are more closely related to *Malva cretica* than to the perennial *Althaea.* Our data support the work of modern revisors of *Alcea* (Zohary 1963b, c; Riedl 1976, Townsend 1980 and Pakravan 2001), which consider the genus as a separate entity. Nevertheless, and due to the species richness and importance of *Alcea* in the plant biodiversity of the Middle East (Zohary 1963a), further molecular studies are desirable.

The similarity among the annual *Althaea* and the annual mallows *M. cretica* and *M. aegyptia* has been long recognized. Alefeld (1862) first recognized this morphological link and proposed a new classification alternative to Linnaeus´s, which nobody else has ever used. He retained within *Althaea* the perennial species, and separated the annuals to a new genus which he diagnosed with the candollean name *Axolopha*, where he included also *M. aegyptia* and *M. cretica*. The mentioned taxa share the presence of closed, sharp-edged mericarps similar to these found in the malvoid group, but with side walls that are separated in the maturity. Krebs (1998b) grouped the annual *Althaea*, *M. cretica*, *M. aegyptia* and the nothogenus *Malvalthaea*, which was unknown to Alefeld, within *Dinacrusa*. For the infrageneric classification Krebs used the nature of the epicalyx, grouping together the annual *Althaea* within subgenus *Dinacrusa*, the *Malva* under subgenus *Liogonia* and *Malvalthaea* in a homonymous subgenus. This classification scheme is not supported by our data, which link *M. cretica* with the annual *Althaea*, and *Malvalthaea* either with *Malva aegyptia* (ITS data) or *Althaea hirsuta* (chloroplast) suggesting hybridisation, as it was initially proposed by Iljin (1974). Morphology is therefore not conclusive and it seems not possible to clearly describe these two clades because the species involved lack morphological synapomorphies.

The case of *Malvalthaea* deserves particular attention, as it is closely related either to *Malva aegyptia* - *M. trifida* (ITS) or to *Althaea hirsuta* (chloroplast), in both cases with high BS scores. This incongruence strongly suggests hybridisation. Unfortunately we lack chromorome counts for *Malvalthaea*, and due to the chromosome plasticity of one progenitor species - *A. hirsuta* - we lack evidence to speak about either allopolyploid or homoploid hybrid speciation. In fact, the name *Malvalthaea* was given by Iljin (1924, 1974) who noting the close similarity of this plant to both *Malva aegyptia* and *Althaea hirsuta* proposed the creation of the nothogenus *Malvalthaea*. The *Hirsutae* clade is sister group to both malvoid and lavateroid taxa.

Basal to all other taxa within the *Lavatera*-*Malva* clade there appears the *Malva aegyptia*-*M. trifida* clade. It is highly-supported, both in the ITS and chloroplastic phylogenies (BS83 and 100, respectively), but whereas in the ITS analysis it includes *Malvalthaea transcaucasica*, in the chloroplast analysis just *Malva aegyptia* and *M. trifida* appear. The results with bayesian analysis are identical. We hypotesize, according to Iljin (1974) that this species is an hybrid between the lineages of *Althaea hirsuta* and *Malva aegyptia*. This hybridisation would be chorologically possible, despite no hybrid taxa between these plants is reported anywhere outside the area of *Malvalthaea*. It seems also possible from a karyological perspective, due to the fact that *A. hirsuta* and *M. aegyptia* share at least one of the chomosome numbers of the former species, 2n = 44. The chromosome number of *Malvalthaea transcaucasica* remains unknown to us. The species presents 3-7 linear-lanceolate epicalyx pieces which are never all fused. It is a shrub or scrub which grows in semiarid environments in the Caucasus.

2.4.6. Taxonomic implications.

The classical delimitation of the genera *Althaea*, *Lavatera* and *Malva*, based solely upon the number and degree of fusion of the epicalyx bracts (free for *Malva*, fused for *Lavatera*) is uncompatible with both the distribution of fruit morphology characters and our analyses. The genera as traditionally circumscribed are therefore arbitrarily delimited and polyphyletic, in our opinion no longer tenable. The taxonomic history of both *Malva* and *Lavatera* is illustrative of the fate of artificial groups, where lack of informative characters and new, independent data lead different authors to an apparently neverending circle of arbitrary reshaping of the genera without conclusive consequences. *Malva* is a good example of "waste-bin" genus, receiving species with schizocarpic fruits and three free epicalyx pieces, most of them nowadays included in other genera. The history of *Malva* is a continuous segregation of smaller entities until relatively recent times and comparable to *Sida*, which received schizocarp species lacking epicalyx (Fryxell 1997, Fuertes et al. 2003). *Lavatera* is an example of the opposite, starting as a monospecific genus to accomodate *L. trimestris* and ending up with its 14-18 species recognized today.

At this point we would like to outline some conclusions regarding the systematic arrangement of the group:

1. *Althaea*, *Lavatera* and *Malva* are mainly Old World genera described early in the history of Botany, accepted acritically by most authors and traditionally separated on the basis of the number and degree of fusion of the epicalyx pieces. This character seems to be highly homoplasious and is not compatible with the distribution of fruit traits as well as with molecular characters from nrITS, and the plastid markers *psb*A-*trn*H and *trn*L-*trn*F.

2. Previous molecular data and fruit morphology analysis (Ray 1995) depict a scenery where some *Lavatera* are provided with malvoid traits, and some *Malva* display a clear lavateroid syndrome. Our analyses fully support the entity of the Malvoid group, while the lavateroid is not so well-supported and collapses in the bootstrap analysis splitting in up to five different lineages, suggesting a fast speciation event and a relative older age of the lavateroids over the malvoids.

3. *Lavatera phoenicea* is isolated at the base of a clade containing the annual *Althaea*, *Malvalthaea*, the remaining of *Lavatera* and all *Malva*. Due to both phylogenetic isolation and high morphological divergence it seems more

appropriate to include it within the genus *Navaea*, as proposed by Webb and Berthelot (1836).

4. The genus *Althaea* as traditionally circumscribed is polyphyletic. Two groups can be distinguished, sect. *Althaea*, including two-three perennial species (the marshmallows), sister group of the genus *Alcea*, and the sect. *Hirsutae*, including tiny annual, ruderal plants, which appear to be more closely related to *Malva cretica*.

5. The genus *Alcea*, as traditionally delimited by Linnaeus, is an authonomous monophyletic entity, though closely related to the perennial representatives of genus *Althaea*.

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Table 1. Authorities and main contributions.

Authority	Main contributions
Tournefort (1700, 1706)	*Lavatera* monospecific (only *L. trimestris*), on the basis of unique carpophore structure. Genus *Malva* including many neotropical Malveae. Genus *Althaea* including several *Malva* species, and no modern *Althaea*.
Linné (1738, 1753, 1789)	Tournefortian names *Alcea*, *Althaea*, *Malva* and *Lavatera* redefined on the basis of epicalyx structure. *Lavatera* expanded. Species arrangement used by most modern floras.
Cavanilles (1786)	Describes *Malope trifida*, *Malva cretica* and *Malva althaeoides*
Medikus (1787)	Linnean classification first criticized. *Olbia* and *Anthema* splitted from *Lavatera*, and *Bismalva* from *Malva*, on grounds of fruit structure. Close morphological link between *Anthema* and reduced genus *Malva* first recognized. Linnaean criterion to separate *Althaea* and *Alcea* reassessed.
De Candolle (1805)	*Lavatera trimestris* isolated in the monospecific genus *Stegia*.
De Candolle (1824)	Back to the linnaean vision of *Lavatera-Malva*. Infrageneric classification of *Lavatera*, *Malva* and *Althaea* first established. *Alcea* first merged within *Althaea*.
Webb and Berthelot (1833)	First attempt to include the thick-walled mericarp *Lavatera* species within *Malva*.
Alefeld (1862)	*Malva*, *Lavatera* and *Althaea* included within an expanded *Althaea*. Morphological similitude between annual *Althaea* and some *Malva* first recognized.
Baillon (1873)	*Malva*, *Lavatera* and *Althaea* included within an expanded *Althaea*.

Kuntze (1891)	*Malva*, *Lavatera* and *Althaea* included within an expanded *Althaea*.
Baker (1890)	Synthesis of tribe *Malveae*. Criteria of Linné followed for genera delimitation, De Candolle (1824) for generic subdivision. Many neotropical taxa excluded from *Malva*.
Greene (1912)	American shrubby *Lavatera* species included in *Saviniona*.
Zohary (1963)	*Alcea* and *Althaea* independent.
Fernandes (1968a, b)	Main modern reviewer of *Lavatera*. Close fruit morphology shared by *Malva* sect. *Malva* and *Lavatera* sect. *Anthema* recognized, but linnaean generic boundaries retained.
Krebs (1994a, b)	Alefeld rediscovered, and annual *Althaea*, some *Malva* and the *Malvalthaea* segregated to *Dinacrusa*.
Ray (1995, 1998)	Medikus rediscovered. Analysis of molecular and fruit traits recognizing Malvoid and Lavateroid groups. Several *Lavatera* assigned to *Malva*.

Table 2. Material studied.

Species	Voucher	ITS	*psb*A-*trn*H	*trn*L-*trn*F	Origin
Alcea angulata	ang615	EF419543	—	—	Austria. Wien: Botanischer Garten.
Alcea pallida	PE140	EF419545	EF419661	EF419767	Iran. Quasr-el-Shirin.
Alcea rosea	PE422	EF419544	EF419662	EF419766	Austria. Wien: Botanischer Garten.
Althaea armeniaca	PE427	EF419542	EF419660	EF419735	Ukraine. Danube Delta (Index Seminum).
Althaea cannabina	PE345	EF419540	EF419657	EF419732	Spain. Madrid: Chinchón.
Althaea cannabina	PE471	EF419541	EF419660	EF419734	Greece. Edessa.
Althaea cannabina	PE594	EF419539	EF419657	EF419733	Austria. Wien: Botanischer Garten.
Althaea hirsuta	PE270	EF419510	EF419659	EF419717	Italy. Sardinia: Perdasdefogu.
Althaea hirsuta	PE356	EF419509	EF419658	EF419716	Turkey. Aydin.
Althaea hirsuta	PE454	EF419508	EF419621	EF419718	Italy. Abruzzo: L´Aquila.
Althaea hirsuta	PE455	EF419507	EF419622	EF419719	Spain. Barcelona: Cabacés.
Althaea hirsuta	PE456	—	EF419623	EF419720	Spain. Álava: Orviso.
Althaea hirsuta	PE458	—	EF419624	EF419721	Romania. Dobrogea: Babadag.

Althaea longiflora	PE362	EF419500	—	—	Spain. Ciudad Real: Alhambra.
Althaea longiflora	PE461	EF419502	EF419638	EF419725	Spain. Badajoz: Gévora.
Althaea longiflora	PE462	EF419503	EF419639	EF419726	Spain. Badajoz: Magacela.
Althaea longiflora	PE596	EF419501	EF419640	EF419724	Morocco. Marrakech.
Althaea ludwigii	PE459	EF419504	EF419641	—	Morocco. Taza.
Althaea ludwigii	PE460	EF419505	EF419642	EF419722	Morocco. Ouarzazate.
Althaea ludwigii	PE616	EF419506	EF419643	EF419723	Iran. Tehran.
Althaea officinalis	PE330	EF419537	EF419656	EF419727	Spain. Madrid: Aranjuez.
Althaea officinalis	PE511	—	EF419653	EF419729	Spain. Zamora: Río Duero.
Althaea officinalis	PE512	EF419538	EF419654	EF419730	France. Haute Corse: L´Aliso.
Althaea officinalis	PE513	—	EF419655	EF419731	Bulgaria. Varna: Nos Cernija.
Althaea officinalis	PE604	EF419536	EF419652	EF419728	Spain. Ciudad Real: Alhambra.
Anisodontea malvastroides	PE067	EF419547	—	—	South Africa. Cape Town.
Lavatera abyssinica	PE383	EF419461	EF419579	EF419709	Spain. Madrid: Jardín Botánico.
Lavatera acerifolia	PE134	—	EF419577	EF419687	Spain. Tenerife: Los Gigantes.

Lavatera acerifolia	PE135	EF419459	—	—	Spain. Fuerteventura: Antigua.
Lavatera agrigentina	PE308	EF419430	EF419553	EF419670	Italy. Sicilia: Agrigento.
Lavatera arborea	PE153	EF419466	EF419585	EF419704	Spain. Albacete: Tobarra.
Lavatera arborea	PE239	EF419469	EF419586	EF419706	Italy. Sardegna: Capo Caccia.
Lavatera arborea	PE252	EF419467	EF419587	EF419707	Italy. Sardegna: Alghero.
Lavatera arborea	PE378	EF419468	—	EF419705	Spain. Lugo: Ribadeo.
Lavatera assurgentiflora	PE570	EF419460	EF419578	EF419708	Spain. Madrid: Jardín Botánico.
Lavatera assurgentiflora	PE325	EF419548	—	—	USA. California (Index Seminum).
Lavatera bryoniifolia	PE141	EF419439	EF419550	EF419666	Greece. Crete: Rethimnion.
Lavatera bryoniifolia	PE552	EF419440	—	—	Greece. Agios Ioannis.
Lavatera cretica	PE031	EF419470	EF419589	EF419688	Spain. Badajoz: Don Benito.
Lavatera cretica	PE076	—	EF419588	—	Portugal. Alto Alentejo: Évora.
Lavatera cretica	PE235	EF419471	EF419590	EF419690	Italy. Sardegna: Alghero.
Lavatera cretica	PE599	EF419472	EF419591	EF419689	Morocco. Sidi Yahya.
Lavatera flava	PE000	EF419434	EF419552	—	Morocco. Taourirt.

Lavatera flava	PE414	EF419433	EF419551	EF419669	Morocco. Al-Hoceima.
Lavatera maritima	PE200	EF419457	EF419573	EF419712	Spain. Zaragoza: Calatayud.
Lavatera maritima	PE329	EF419456	EF419572	EF419711	Italy. Sardegna: Cala Gonone.
Lavatera maritima	PE404	EF419458	EF419574	EF419713	Spain. Murcia: Los Belones.
Lavatera maritima	PE405	—	EF419575	—	Spain. Almería: Mojácar.
Lavatera maritima	PE598	EF419455	EF419576	EF419710	Morocco. Gorges du Zegzel.
Lavatera maroccana	PE346	EF419453	EF419563	EF419681	Spain. Sevilla: Las Cabezas de San Juan.
Lavatera maroccana	PE515	EF419454	EF419564	EF419682	Morocco. Taza.
Lavatera mauritanica	PE137	EF419463	EF419581	EF419691	Spain. Almería: Alborán.
Lavatera mauritanica	PE318	EF419464	EF419583	—	Portugal. Algarve. Ponta de Sagres.
Lavatera mauritanica	PE319	—	EF419582	EF419692	Portugal. Algarve. Cabo de São Vicente.
Lavatera mauritanica	PE630	EF419465	EF419584	EF419693	Morocco. Mediouna.
Lavatera oblongifolia	PE144	EF419441	EF419560	EF419665	Spain. Almería.
Lavatera olbia	PE004	EF419442	EF419561	EF419668	Spain. Baleares: Mahón.
Lavatera olbia	PE451	EF419443	EF419562	EF419667	Italy. Sardinia: San Giovanni di Sinis.

Lavatera phoenicea	PE002	EF419526	EF419644	EF419763	Spain. Tenerife. Anaga.
Lavatera phoenicea	PE628b	EF419527	EF419645	EF419764	Spain. Tenerife. Anaga.
Lavatera phoenicea	PE629	EF419528	EF419646	EF419765	Spain. Tenerife: Teno.
Lavatera plazzae	PE285	EF419444	EF419549	EF419664	Italy. Sardegna: Porto Torres.
Lavatera plebeia	PE634	EF419462	EF419580	—	Australia. South Australia. Adelaide.
Lavatera punctata	PE348	EF419446	EF419566	EF419677	Turkey. Aydin.
Lavatera punctata	PE450	EF419445	EF419565	EF419678	Turkey. Aydin.
Lavatera punctata	PE555	—	—	EF419679	Greece. Amfilokhia.
Lavatera thuringiaca	PE353	EF419452	EF419567	EF419680	Russia. Burgistan: Pyatigorsk.
Lavatera thuringiaca	PE559	EF419451	—	—	Austria. Wien: Botanischer Garten.
Lavatera triloba ssp. pallescens	PE354	EF419431	EF419555	EF419672	Spain. Baleares: Sa Foradada.
Lavatera triloba ssp. pallescens	PE564	EF419432	EF419554	EF419671	Spain. Baleares: Isla Colom.
Lavatera triloba ssp. triloba	PE117	EF419435	EF419556	EF419673	Spain. Ciudad Real: Almedina.
Lavatera triloba ssp. triloba	PE169	EF419438	EF419557	EF419676	Spain. Badajoz: Usagre.

Lavatera triloba ssp. triloba	PE357	EF419436	EF419558	EF419674	Spain. Murcia: Alhama.
Lavatera triloba ssp. triloba	PE359	EF419437	EF419559	EF419675	Spain. Almería: Vélez Blanco.
Lavatera trimestris	PE181	EF419448	EF419569	EF419684	Spain. Cáceres: Logrosán.
Lavatera trimestris	PE233	EF419449	EF419570	EF419685	Italy. Sardegna: Alghero.
Lavatera trimestris	PE308	EF419450	EF419568	EF419686	Spain. Cádiz: Alcalá de los Gazules.
Lavatera trimestris	PE595	EF419447	EF419571	EF419683	Morocco. Rif: Chefchaouen.
Malope malacoides	PE279	—	EF419651	—	Italy. Sardegna: Laconi.
Malope malacoides	PE415	EF419535	EF419650	EF419760	Morocco. Rif: Tetouan.
Malope malacoides	PE600	EF419534	—	EF419761	Morocco. Rif: Fnidek.
Malope malacoides	PE605	—	—	EF419762	Spain. Cádiz: Algodonales.
Malope trifida	PE070	EF419532	EF419648	EF419758	Spain. Huelva: El Portil.
Malope trifida	PE394	EF419529	EF419647		Morocco. Sidi Kacem.
Malope trifida	PE499	EF419533	EF419649	EF419759	Morocco. Rif: Khenichet.
Malope trifida	PE550	EF419530	—	—	Morocco. Fès.
Malope trifida	PE601	EF419531	—	EF419757	Morocco. Rif: Khenichet.

Malva aegyptia	PE351	EF419520	EF419632	EF419740	Spain. Zaragoza: Bujaraloz.
Malva aegyptia	PE465	EF419519	EF419630	EF419741	Spain. Alicante: Santa Pola.
Malva aegyptia	PE466	EF419516	—	—	Greece. Crete: Rethimnion.
Malva aegyptia	PE467	EF419518	—	—	Greece. Karpathos.
Malva aegyptia	PE468	EF419517	EF419631	EF419742	Spain. Toledo: Yepes.
Malva alcea	PE338	EF419493	EF419609	EF419747	Spain. Ávila: Mijares.
Malva alcea	PE440	EF419492	EF419610	EF419745	France. Marnay-Sur-Seine.
Malva alcea	PE539	EF419491	EF419611	EF419746	Spain. Toledo: Navamorcuende.
Malva cretica ssp. althaeoides	PE350	—	EF419629	—	Spain. Cádiz: Algodonales.
Malva cretica ssp. althaeoides	PE389	EF419513	EF419626	—	Spain. Jaén: Aldeaquemada.
Malva cretica ssp. althaeoides	PE390	EF419514	—	—	Spain. Alicante: Castell de Castells.
Malva cretica ssp. althaeoides	PE391	EF419515	EF419627	—	Spain. Alicante: Vall de Gallinera.
Malva cretica ssp. althaeoides	PE463	EF419512	EF419628	EF419744	Spain. Málaga: Carratraca.
Malva cretica ssp. althaeoides	PE361	—	—	EF419743	Italy. Sicilia: Palermo.
Malva hispanica	PE149	EF419488	EF419606	EF419715	Spain. Badajoz: Cabeza del Buey.

Malva hispanica	PE602	EF419489	EF419607	EF419714	Spain. Badajoz: Guadajira.
Malva hispanica	PE631	EF419490	EF419608	—	Morocco. Ounara.
Malva moschata	PE322	EF419495	EF419616	EF419750	Spain. La Rioja: Rasillo de Cameros.
Malva moschata	PE493	—	EF419617	EF419748	Spain. Lérida: Bausent.
Malva moschata	PE494	—	EF419618	EF419749	Spain. Lérida: Alins.
Malva moschata	PE496	EF419496	EF419615	EF419751	Spain. Guipúzcoa: Legazpia.
Malva moschata	PE499	—	EF419619	EF419752	Spain. León: La Uña.
Malva moschata	PE593	EF419494	—	EF419753	France. Pyrenées Orientales: Lortet.
Malva neglecta	PE349	EF419478	EF419597	EF419702	Spain. Valladolid: Encinas de Esgueva.
Malva neglecta	PE632	EF419479	EF419598	—	Italy. Sardegna: Lago Cuga.
Malva nicaeensis	PE032	EF419473	EF419592	EF419699	Spain. Badajoz: Talarrubias.
Malva nicaeensis	PE105	—	EF419594	—	Italy. Sardegna: Uri.
Malva nicaeensis	PE097	EF419474	EF419593	EF419700	Spain. Toledo: Yepes.
Malva nicaeensis	PE105	EF419475	—	—	Spain. Ciudad Real: Alhambra.
Malva nicaeensis	PE228	EF419477	EF419596	EF419701	Italy. Sardegna: Lago Cuga.

Malva nicaeensis	PE633	EF419476	EF419595	—	Morocco. Berkane.
Malva parviflora	PE005	EF419483	EF419604	EF419694	Spain. Badajoz: Guadajira.
Malva parviflora	PE059	EF419484	EF419601	EF419696	Portugal. Alto Alentejo: Vendas Novas.
Malva parviflora	PE249	EF419485	EF419603	EF419695	Italy. Sardegna: San Giovanni di Sinis.
Malva parviflora	PE296	EF419486	EF419602	EF419697	Spain. Sevilla: Morón de la Frontera.
Malva sylvestris	PE001	EF419480	EF419599	EF419698	Spain. Madrid: Retiro.
Malva sylvestris	PE515	EF419481	—	—	Morocco. Oujda.
Malva sylvestris	PE635	EF419482	EF419600	—	Portugal. Alto Alentejo: Vendas Novas.
Malva tournefortiana	PE189	EF419497	EF419612	EF419755	Spain. Badajoz: Talarrubias.
Malva tournefortiana	PE479	EF419499	EF419614	EF419754	Morocco. Oukaimeden.
Malva tournefortiana	PE489	EF419498	EF419613	EF419756	Portugal. Tras-os-Montes: Mogadouro.
Malva trifida	PE352	EF419524	EF419634	EF419739	Spain. Navarra: Fraile Alto.
Malva trifida	PE254	EF419525	EF419636	EF419738	Spain. Lérida: Balaguer.
Malva trifida	PE392	EF419522	EF419633	—	Spain. Madrid: San Martín de la Vega.
Malva trifida	PE393	EF419523	EF419635	—	Spain. Huesca: Fraga.

Malva trifida	PE452	—	—	EF419736	Spain. Soria: Monteagudo de las Vicarias.
Malva trifida	PE453	EF419521	—	EF419737	Spain. Madrid: Aranjuez.
Malva verticillata	PE442	EF419487	EF419605	EF419703	Germany. Leipzig (Index Seminum).
Malvalthaea transcaucasica	PE628	EF419511	EF419637	—	Azerbaijan. Saliani: Chaladzh.
Malvella sherardiana	PE325	EF419546	EF419663	EF419768	Spain. Córdoba: Montoro.

3. NEW CHROMOSOME COUNTS IN THE *MALVA* ALLIANCE (*MALVEAE*, MALVACEAE)

3.1. INTRODUCTION

The genera *Malva*, *Lavatera*, *Althaea* and *Alcea* are members of the *Malva* generic alliance, one of the groups of the tribe *Malveae* (Malvaceae) (Bates 1968; Bayer and Kubitzki 2003). *Malope*, though directly related to *Malva* and *Lavatera*, has normally been placed in the *Malope* alliance together with *Kitaibela* (Bates 1968; Bates and Blanchard 1970). The *Malva* alliance comprises perennial and annual herbs as well as some shrubs of Mediterranean distribution, extending to the Atlantic Europe and south-western Asia, with main centres of diversity in the western Mediterranean Basin and the Middle East. *Alcea* is the most diversified (about 60 species, Pakravan 2001; Riedl 1976; Zohary 1963a, b) and includes perennial herbs from the eastern Mediterranean Basin and south-western Asia. *Althaea* (5-6 species, Tutin 1968) is also Mediterranean, with two species spreading over the eutrophic wetlands of most Eurasia. *Malope* (2-3 species, Nogueira & *al.* 1993; Cullen 1966) and *Lavatera* (about 20 species, Fernandes 1968a, b) are mostly Mediterranean herbs with their largest diversity in the western Mediterranean Region. Some species of *Lavatera* occur outside the Mediterranean Basin and are native to California and Mexico, Ethiopia and Western Australia. *Malva* (about 12 species, Dalby 1968) is the widest-distributed of these genera and ranges from its western Mediterranean centre of diversity to most of Eurasia, with some ruderal species occuring widely across Australia and America due to recent anthropic introduction. It comprises mainly perennial and annual species.

The karyology of the *Malva* alliance is well known due to extensive sampling since the thirties of the XX Century (see table 3 for references). Some of the most important contributions are the early studies of Davie (1935) and Skovsted (1935). Later contributions include Dahlgren & *al.* (1971), Löwe & Kjellkvist (1974), Luque & Devesa (1986) and Queirós (1977). Though the wealth of work, the chromosome numbers of some species remain unknown. As only one diploid (*Lavatera trimestris*, 2n = 14) and two tetraploids (*Althaea longiflora* 2n = 22, *Malva hispanica* 2n = 24) are known, the majority of species being hexaploids, it seems critical to fill in the information gaps to complete the karyological picture of the group. This paper aims to retrieve the disperse karyological bibliography regarding the *Malva* alliance and compare the results to our own chromosome counts, providing new data for the cases in which the chromosome number and ploidy level are unknown.

3.2. MATERIAL AND METHODS

Thirty-eight taxa of the *Malva* alliance from the genera *Alcea* (2), *Althaea* (6), *Lavatera* (16), *Malope* (2) and *Malva* (12) were sampled from natural populations in western Europe and Africa (Spain, Portugal, France, Italy and Morocco, see table 1). Two samples come from *index semina* (*Althaea armeniaca*, from the Botanischer Garten der Universität Hohenheim, and *Malva verticillata*, from the Botanischer Garten der Universität Oldenburg) and were not analysed until identification was confirmed. Five species come from herbarium material collected in the Eastern Mediterranean and South-Western Asia.

Seeds were grown in Petri dishes and fresh root tips were excised and treated with a saturated solution of 8-quinolinol (Sigma-Aldrich) for 2 h at room temperature, then stained using Feulgen. For the Feulgen staining (Feulgen & Voit, 1924), root tips were fixed in freshly prepared 3:1 methanol : acetic acid, transferred to 96° ethanol, and then stored at -20°C until use. Root tips were later hydrolytically depurinized in 5M HCl at 20°C for 60 minutes, then stained in Schiff´s reagent prepared from basic fuchsin (Fluka), as described in Greilhuber & Ebert (1994). Hydrolysis was stopped by rinsing the root tips in distilled water. Samples were then stained with Schiff´s reagent over 1.5 h in the dark at room temperature. Afterwards samples were washed with SO_2 water (for 100 ml 0,50 g $K_2S_2O_5$ and 5 ml 1N HCl in 95 ml distilled water), and then squashed in 45% acetic acid. Squashed slides were frozen in liquid N_2 to remove coverslips, ethanol-dehydrated and air dried.

Somatic metaphases were observed under a 63x oil immersion objective. A minimum of ten plates from different infividuals of the same population were examined. The Feulgen-stained slides and digital photographs of the plates are preserved at the Real Jardín Botánico de Madrid, CSIC.

3.3. RESULTS

We report chromosome counts for 38 species (table 2, see also figures 1-15). For 7 of them no previous references were found, so we assume them to be new. These species are *Althaea longiflora*, *A. ludwigii*, *Lavatera assurgentiflora*, *L. punctata*, *Malope malacoides*, *Malva aegyptia* and *M. trifida*.

The chromosome numbers found agree with these reported by previous authors. Most species are hexaploid (x = 7), with 2n = 40, 42, 44. The perennial *Lavatera* (*L. triloba* aggregate, including *L. agrigentina* and *L. triloba* ssp. *pallescens*) share their 2n = 42 with the shrubby members of *Lavatera* sect. *Olbia* (*L. bryoniifolia*, *L. oblongifolia* and *L. olbia*). The annual *Lavatera* of sect. *Lavatera* are variable and include the only diploid of the group, *L. trimestris* (2n = 14), with the other representatives being hexaploids (*L. maroccana* 2n = 40, *L. punctata* 2n = 42). Among the taxa of *Lavatera* sect. *Anthema*, *L. cretica* is a 16-ploid with 2n = 112, while *L. mauritanica* is 12-ploid and displays 2n = 84. *Lavatera maritima* is hexaploid with 2n = 44. Among the extramediterranean *Lavatera* species, the Californian *L. assurgentiflora* is found to be a 12-ploid (2n = 84), contrasting with the Australian and also shrubby *L. plebeia*, with 2n = 43 (Skovsted, 1935).

Among the members of *Malva*, within sect. *Bismalva M. moschata* and *M. tournefortiana* share 2n = 6x = 42, while *M. alcea* is a 12-ploid with 2n = 84. The morphologically isolated *M. hispanica* is a tetraploid with 2n = 24. The remaining species are hexaploids with 2n = 42, 44; with the sole exception of *M. verticillata*, which is found to be a 12-ploid of 2n = 84.

Within *Althaea*, there are two well-defined groups. The annual species of sect *Hirsutae* are hexaploid with 2n = 42 (*A. hirsuta*, *A. ludwigii*) or tetraploid with 2n = 22 (*A. longiflora*). The perennial representatives of sect. *Althaea* are either hexaploids (*A. officinalis*), with 2n = 42, or 12-ploids with 2n = 84 (*A. armeniaca*, *A. cannabina*).

Both *Malope* species (*M. malacoides* and *M. trifida*) are hexaploids and share 2n = 44.

3.4. DISCUSSION

3.4.1 Which is the base chromosome number of the *Malva* alliance?

For Bates (1968) and later for Bates & Blanchard (1970), chromosome number was a character of the greatest taxonomic importance. The latter authors proposed an unranked system of generic alliances, on grounds of both diverse morphological characters and chromosome numbers, abandoning the previous scheme of Bentham and Hooker (1862) for the *Malveae*, with four subtribes (*Abutilinae*, *Malopinae*, *Malvinae*, *Sidinae*) based on the structure of the gynoecium. For Bates (1968) there would be two base chromosome numbers, x = 7 for *L. trimestris*, and x = 11 for the remaining of the group, in a close relationship with the South African *Anisodontea* (2n = 44), which he interpreted as a tetraploid. Thus, the chromosome number of *L. trimestris* would be explained as an isolated lineage which developed independently in the Mediterranean. The fact that *L. trimestris* is closely related to species with higher chromosome numbers like *L. punctata* (2n = 42) or *L. maroccana* (2n = 40) (Escobar & *al.*, 2004), and the fact that it is the only diploid of a generic complex integrated by *Alcea*, *Althaea*, *Kitaibela*, *Lavatera*, *Malva* and *Malope* leads us to think that the base number is only x = 7 and not 11, therefore *Anisodontea* and most of existing species being hexaploids. The number 2n = 40 chromosomes could have appeared by means of chromosome loss or fusion, and 2n = 44 could be explained as a product of chromosome fision. We argue that taxa like *L. maroccana* (2n = 40) or *L. maritima* (2n = 44) are hexaploids, thus being *M. hispanica* (2n = 24) and *A. longiflora* (2n = 22), along with some populations of *A. cannabina* (Devesa & *al.*, 1995) the only tetraploids so far reported in the complex.

3.4.2 Chromosome size and phylogeny in the *Lavatera* - *Malva* complex

Previous studies (Luque & Devesa 1986) already show a marked chromosome size difference among the different species of genus *Lavatera*. Despite some taxa display chromosomes of intermediate size (like *L. arborea*), our results indicate the presence of two size groups, one with big chromosomes, usually bigger than 1.5 μm and another with small punctiform chromosomes, smaller than 1.5-2 μm.

Regardless to their filiation to *Lavatera* or *Malva*, the taxa traditionally included in these two genera fall within two fruit structure categories. A first group displays schizocarps with partially fused walls, which form an inner cavity and release the seeds when ripe. The schizocarp side walls dearticulate when ripe and leave two hyaline flaps attached to the carpophore. As the taxa in this category include *L. trimestris*, the typus of genus *Lavatera*, this schizocarp structure was named lavateroid by Ray (1995). The other group includes species of thick pericarp which do not release the seed when ripe, dispersing the mericarps themselves or the whole schizocarp as a single unit. As these species include *M. sylvestris*, typus of genus *Malva*, Ray (1995) named these species malvoid. Our results indicate that the lavateroids are a basal, early diversified complex which radiated in the Mediterranean area originating the malvoids, a monophyletic, highly-supported clade which evolved toward herbaceous, ruderal biotypes. The species within the lavateroid lineages display large chromosomes, while the malvoids undergo progressive genome reduction. There is a clear chromosome downsizing trend from the early diverging shrubby malvoids, as *L. maritima* or *L. acerifolia*, through the medium sized *L. arborea* to ruderal herbs with punctiform chromosomes, as *L. cretica* or *M. sylvestris*. Parallel to this chromosome miniaturization there is a marked DNA loss, manifested as progressively reduced *C*-values (unpubl. data).

3.4.3. Polyploidization in the *Malva* alliance

The radiation of the lavateroids seems to have been a fast event, as critical short branches in phylogenetic trees are retrieved in both parsimony and bayesian analyses (unpubl. data). The existence of only one diploid species (*L. trimestris*, 2n = 14) as well as only one tetraploid (*M. hispanica*, 2n = 24) indicates that diversification occurred through polyploidization, being the hypothetical diploid and tetraploid progenitors extinct. In fact, most extant species are hexaploids with 2n = 40, 42 and 44, followed by 12-ploids (*Althaea cannabina*, *M. alcea*, *M. verticillata*, *L. mauritanica*) and a single 16-ploid, *L. cretica* (2n = 116). The lack of octoploids could be interpreted as a fast replacement of tetraploid taxa by the fast radiating, better-adapted hexaploids.

Some species from the 12 ploid complex are likely to have appeared through allopolyploidization, as it is the case of *L. mauritanica*, where well-supported incongruence among ITS and plastid markers is a strong indicative of hybrid speciation between an undetermined species of annual mallow and *L. arborea*. In the case of *M. alcea*, incongruence among low-copy nuclear markers and both the ITS and plastid datasets suggests hybridization between *L. thuringiaca* and *M. moschata*. This species additionally display additive DNA *C*-values. Other species of the 12-ploid complex seem to be of autopolyploid origin. The robust and edible *Malva verticillata* seems to be an autopolyploid derivative of *M. parviflora*, a very similar but less vigorous species.

The case of the 16-ploid *L. cretica* is similar to that of *M. verticillata*. It is morphologically close to its hexaploid relatives from the ruderal mallow complex, particularly to *M. sylvestris* and *M. nicaeensis*. Though, its particular chromosome number suggests a cycle of recurrent autopolyploidization, probably from one of the hypothetical tetraploid ancestors, through an octoploid derivative which would be extinct. The diversity of chromosome numbers reported for *L. cretica* (2n = 44 in Davie 1935; 2n = 116 in Luque & Devesa 1986, and reported data) seems difficult to interpret in this scenario and could be due to misidentification with the hexaploid and much more widespread *M. sylvestris*, which is quite a common phenomenon observed nearly in every herbarium.

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Table 1. Material studied.

Taxon	Voucher	Origin
Alcea pallida	PE415	Turkey. Aydin.
Alcea rosea	PE 416	Spain. Madrid: Madrid.
Althaea armeniaca	PE 427	Index Seminum.
Althaea cannabina	PE 429	Spain. Lérida: Solsona.
Althaea hirsuta	PE 270	Italy. Sardinia: Perdasdefogu.
Althaea longiflora	PE 296	Spain. Badajoz: Magacela.
Althaea ludwigii	PE 616	Iran. Tehran.
Althaea officinalis	PE 409	Spain. Madrid: Aranjuez.
Lavatera acerifolia	PE 951	Spain. Tenerife: Los Gigantes.
Lavatera arborea	PE 252	Italy. Sardinia: Alghero.
Lavatera assurgentiflora	PE 570	United States. California.
Lavatera bryoniifolia	PE 141	Greece. Crete: Rethimnion.
Lavatera cretica	PE 599	Morocco. Rif: Sidi Yahya.
Lavatera maritima	PE 598	Morocco. Gorges du Zegzel.
Lavatera maroccana	PE 311	Spain. Sevilla: Las Cabezas de San Juan.
Lavatera mauritanica	PE 319	Portugal. Algarve. Cabo de São Vicente.
Lavatera oblongifolia	PE 144	Spain. Almería.
Lavatera olbia	PE 451	Italy. Sardinia: San Giovanni di Sinis.
Lavatera phoenicea	PE 952	Spain. Tenerife: Teno.
Lavatera punctata	PE 450	Turkey. Aydin.
Lavatera thuringiaca	PE 590	Austria. Wien.
Lavatera triloba subsp. *pallescens*	PE 564	Spain. Baleares: Isla Colom.
Lavatera triloba subsp. *triloba*	PE 606	Spain. Madrid: Arganda del Rey.
Lavatera trimestris	PE 595	Morocco. Rif: Chefchaouen.
Malope malacoides	PE 600	Morocco. Rif: Fnidek.

Malope trifida	PE 601	Morocco. Rif: Khenichet.
Malva aegyptia	PE 681	Greece. Crete: Rethimnion.
Malva alcea	PE 338	Spain. Ávila: Mijares.
Malva cretica subsp. *althaeoides*	PE 950	Spain. Cádiz: Algodonales.
Malva hispanica	PE 602	Spain. Badajoz: Guadajira.
Malva moschata	PE 593	France. Pyrenées Orientales: Lortet.
Malva neglecta	PE 795	Italy. Sardinia: Lago Cuga.
Malva nicaeensis	PE 226	Italy. Sardinia: Uri.
Malva parviflora	PE 603	Spain. Badajoz: Guadajira.
Malva sylvestris	PE 597	Morocco. Oujda.
Malva tournefortiana	PE 185	Spain. Badajoz: Talarrubias.
Malva trifida	PE 605	Spain. Madrid: San Martín de la Vega.
Malva verticillata	PE 442	Index Seminum.

Table 2. Results.

Taxon	2n	Ploidy
Alcea pallida	42	6x
Alcea rosea	42	6x
Althaea armeniaca	84	12x
Althaea cannabina	84	12x
Althaea hirsuta	42	6x
Althaea longiflora	22	4x
Althaea ludwigii	44	6x
Althaea officinalis	42	6x
Lavatera acerifolia	44	6x
Lavatera arborea	40	6x
Lavatera assurgentiflora	84	12x
Lavatera bryoniifolia	42	6x
Lavatera cretica	112	16x
Lavatera maritima	44	6x
Lavatera maroccana	44	6x
Lavatera mauritanica	84	12x
Lavatera oblongifolia	42	6x

Lavatera olbia	42	6x
Lavatera phoenicea	44	6x
Lavatera punctata	42	6x
Lavatera thuringiaca	44	6x
Lavatera triloba subsp. *pallescens*	42	6x
Lavatera triloba subsp. *triloba*	42	6x
Lavatera trimestris	14	2x
Malope malacoides	44	6x
Malope trifida	44	6x
Malva aegyptia	42	6x
Malva alcea	84	12x
Malva cretica subsp. *althaeoides*	44	6x
Malva hispanica	24	4x
Malva moschata	42	6x
Malva neglecta	42	6x
Malva nicaeensis	42	6x
Malva parviflora	42	6x
Malva sylvestris	42	6x
Malva tournefortiana	42	6x
Malva trifida	42	6x
Malva verticillata	84	12x

Table 3. Chromosome numbers compiled from the literature. ? Indicates lack of references. ▲ Chromosome number cited in Nogueira (1993).

Taxon	Count, references
Alcea rosea	2n=26 Burkett 1932, Pogliani & Del Grosso 1972. 2n=42 Kesseler 1932, Skovsted 1935, 1941, Delay 1948, Hindáková 1970, Hazra & Sharma 1971, Queirós 1977. 2n=56 Sugiura 1936.
Althaea armeniaca	2n=84 Darlington & Wylie 1955.
Althaea cannabina	2n=28 Devesa 1995. 2n=84 Markova & Goranova 1993.
Althaea hirsuta	2n=35 Devesa 1995. 2n=41+3B Markova & Goranova 1993.

	2n=42 Devesa 1995. 2n=50 Dahlgren & *al.* 1971, Devesa 1995.
Althaea longiflora	?
Althaea officinalis	2n=40, 44 Davie 1933. 2n=42 Skovsted 1935,Wulff 1937, Ford 1938, Delay 1948, Pólya 1950, Skalinska & *al.* 1971, Queirós 1977.
Lavatera agrigentina	2n=44 Brullo & *al.* 1978.
Lavatera arborea	2n=36 Davie 1935. 2n=40 Nakajima 1936, Luque & Devesa 1986. 2n=42 Skovsted 1935, Kramer & *al.* 1972. 2n=44 Queirós 1977.
Lavatera assurgentiflora	?
Lavatera bryoniifolia	2n=42 Snogerup 1995.
Lavatera cachemiriana	2n=42 Skovsted 1935.
Lavatera cretica	2n=40, 44 Davie 1935. 2n=112 Skovsted 1935, Ford 1938, Queirós 1977, Luque & Devesa 1986. 2n=118-120 Dahlgren & *al.* 1971. 2n=126 Löve & Kjelkvist 1974.
Lavatera maritima	2n=44 Luque & Devesa 1986.
Lavatera maroccana	2n=40 Luque & Devesa 1986.
Lavatera mauritanica ssp*. davaei*	2n=84 Luque & Devesa 1986.
Lavatera oblongifolia	2n=42 Luque & Devesa 1986.
Lavatera olbia	2n=40 Davie 1933, 1935. 2n=42 Nakajima 1936, Delay 1948, Queirós 1977, Luque & Devesa 1986.
Lavatera plebeia	2n=43 Skovsted 1935.
Lavatera punctata	2n=42 ▲
Lavatera thuringiaca	2n=40 Bolkhovskikh 1969. 2n=42 Dmitrieva 1986. 2n=44 van Loon & al. 1980. 2n=44, 46 Sopova & al. 1983.
Lavatera triloba	2n=42 Luque & Devesa 1986. 2n=44 Davie 1933, 1935.
Lavatera triloba ssp. pallescens	2n=42 Cardona & Contandrinopoulos 1983.
Lavatera trimestris	2n=14 Davie 1933, 1935, Sugiura 1931, 1936, Skovsted 1935, Delay 1948, Labadie 1979, Luque & Devesa 1986.

Malope malacoides	2n=44 ▲
Malope trifida	2n=44 Izmaillow 1989, Pogan & al. 1990.
Malva aegyptia	?
Malva alcea	2n=84 Dmitrieva 1986, Lövkvist & Hultgård 1999.
Malva hispanica	2n=24 Queirós 1977, Devesa 1995.
Malva moschata	2n=42 van Loon & al. 1980, Albers & Pröbsting 1998, Lövkvist & Hultgård 1999.
Malva neglecta	2n=42 Mulligan 1984, Montgomery & *al.* 1997.
Malva parviflora	2n=40-42 Delay 1948. 2n=40-44 Davie 1933. 2n=42 Skovsted 1941, Heiser & Whitaker 1948, Reese 1957, Bir & Sidhu 1974, van Loon & al. 1974, Bidak & Brandham 1995, Provatova & al. 1996.
Malva sylvestris	n=21 Sidhu & *al.* 1990. 2n=42 Latter 1932, Davie 1933, Skovsted 1935, 1941, Delay 1948, Roy & Sinha 1961, Uhríková 1970, van Loon & *al.* 1971, Skalinska & *al.* 1971, Fritsch 1973, Queirós 1977, Al-Bermani & al. 1993.
Malva tournefortiana	2n=42 Queirós 1977, González & Elena 1986, Diosdado & al. 1993, Devesa 1995.
Malva trifida	?
Malva verticillata	2n=84 Skovsted 1941.

4. EVOLUTION OF GENOME SIZE IN THE MALVA ALLIANCE

4.1. INTRODUCTION

Current estimates of 1C-value in angiosperms vary by more than 1900-fold, from 0.066 pg for *Genlisea aurea* (Greilhuber & *al*., 2005b) to 127.4 pg in *Fritillaria assyriaca* (Bennett, 1987). Small or very small genomes are by far more common than big ones, with more than half of the angiosperms covered by the literature having C-values smaller than 3.5 pg and a modal value in the range of 0.7 pg (Leitch & *al*., 2005). This lack of correlation between organismic complexity and genome size, the apparent high surplus of DNA over what would be strictly necessary for life, and the lack of correlation between C-value and number of coding genes is what has been called the "C-value paradox" (Thomas, 1971) or also the "C-value enigma" (Gregory, 2005).

The genome size of an organism influences a number of cell, organismic and ecological traits. This fact led Bennett (1971) to develop the "nucleotypic theory", proposing that the bulk of DNA merely by its mass, and irrespective to the information encoded, has effects at the cellular level in traits such as cell cycle length, duration of mitosis and meiosis, cell volume, area and weight or chromosome mass and length at metaphase (Bennett, 1972; Ichikawa & *al*., 1971, but see Cavalier-Smith, 2005, for criticism). Despite the absence of an influence model of genome size at the organismic level, several correlations with some life traits have been suggested, among them fruit and flower size (Stebbins, 1971), but also leaf strategy (Morgan & Westoby, 2005), seed mass (Thompson, 1990), or shoot expansion and phenology (Grime & Mowforth, 1982). Studies about variation in genome size across ecological gradients have shown that mesic habitats allow the largest genomes, being plant species with low genome sizes more common at the Equator and the Poles, as well as at both high and low elevations (for a review see Knight & Ackerly, 2002).

Notably, the DNA amount is correlated with two characters of the utmost importance for plant growth: cell size and minimum cell doubling time (Bennett, 1971, 1987, Van´t Hof & Sparrow, 1963). Both factors interact to determine the growth rate of the plant, and ultimately, its life history and ecological strategy. Bennett (1972) compared the DNA amount of ephemerals, annuals, obligate perennials (plants which need more than a year to produce first seed) and facultative perennials (plants which produce seed already during their first year of life, and may live for longer time), showing a clear relationship between DNA *C*-value and type of life cycle displayed. Species with low DNA amounts include ephemerals and long-lived perennials, while those with very high DNA amount are exclusively obligate perennials. Thus, with increasing C-values, the range of life cycles displayed by plants decreases. Maximum C-values for ephemeral species are much smaller than these of annuals, which have also significatively smaller C-values than obligate perennials, but display similar ones to facultative perennials.

The nuclear DNA content can therefore limit the types of plant life-history. Species with medium DNA amounts could not be ephemerals, while those with very high DNA amounts could not be ephemerals or even annuals. Species with low DNA C-values which complete meiosis within 1 or 2 days have the possibility of colonizing a wider range of habitats, in contrast, species with very high DNA C-values spend so long to complete cell cycle that it would be virtually impossible for them to behave as ephemerals.

Only recently, genome size evolution studies have been carried out, due both to the planned increase in genome size data sampling (Bennett & *al.*, 2000; Bennett & Leitch, 2005; Kapraun, 2005; Obermayer & *al.*, 2002; Voglmayr, 2000), and the progressive accumulation of more robuste phylogenies (Albach & Greilhuber, 2004; Grotkopp & *al.*, 2004; Leitch & *al.*, 2005; Soltis & *al.*, 2003; Weiss-Schneeweiss & *al.*, 2005; Wendel & *al.* 2002).

The genera *Malva*, *Lavatera*, *Althaea* and *Alcea* have classically integrated the *Malva* alliance (Bates, 1968; Bayer & Kubitzki, 2003) within tribe *Malveae*, subtribe *Malvinae*. *Malope*, though directly related to *Malva* and *Lavatera*, has normally been placed in the *Malope* alliance together with *Kitaibela* (Bates, 1968, Bates & Blanchard, 1970). The *Malva* alliance comprises mainly perennial herbs of Mediterranean distribution, which extend northwards to Atlantic Europe and eastwards to south-western Asia, with main centres of diversity in the western Mediterranean Basin and the Middle East. *Alcea* is the most diverse (about 60 species, Pakravan, 2001; Riedl, 1976; Zohary, 1963a, b) and includes perennial herbs native to the eastern Mediterranean Basin and south-western Asia. *Althaea* (5-6 species, Tutin, 1968) is mainly Mediterranean, with two broadly distributed species spreading over the wetlands of most Eurasia. *Malope* (2-3 species, Nogueira & *al.*, 1993; Davis, 1966; Webb, 1968) and *Lavatera* (about 20 species, Fernandes, 1968a, b) are mostly Mediterranean herbs with their largest diversity in the western

Mediterranean. *Lavatera* comprises also shrubs growing in mild climates. Some species of *Lavatera* present a disjunct distribution area and are native to California and Mexico, Ethiopia and Australia. *Malva* (about 12 species, Morton, 1937; Dalby, 1968) is the widest-distributed of all and ranges from its western Mediterranean centre of diversity to the rest of Eurasia, the ruderal species occuring widely across Australia and America due to recent introduction. It comprises mainly perennial and annual species. *Malvalthaea* has a putative hybrid origin (1-2 spp, Iljin, 1974; Riedl, 1976) and includes suffruticose elements of south-western Asian distribution.

Lavatera and *Malva* are two genera established early in the history of Botany and accepted almost acritically until recent times. Medikus (1787) first noted the close similarity existing among annual *Malva* species from sect. *Malva* and the annual *Lavatera* from sect. *Anthema*. More recently, the problem of *Lavatera* and *Malva* being artificial genera was reviewed by Fernandes (1968b) and Ray (1995), the latter giving the names Malvoid and Lavateroid to the morphological groups already distinguished by Medikus and Fernandes.

Despite some representatives of the *Malva* alliance are widely distribued over Europe, and as alien species in North and South America, temperate Asia and Australia, we have found only three previous genome size measurements to our study (Plant DNA C-values database, Bennett & Leitch 2005b), for *Lavatera arborea*, *Malva sylvestris* (Ceccarelli & *al*., 1998), and *M. parviflora* (Bidak & Brandham, 1995), which agree with our results. We think this lack of previous data is due to the widespread presence of thick mucillage in the family *Malvaceae*, which poses a physical difficulty to flow cytometry.

The aims of this study are to provide estimates for the genome size of 36 species of the genera *Althaea*, *Malope*, *Malva* and *Lavatera*, and map them on a nuclear nrDNA phylogeny to explore if any evolutionary patterns arise. Chromosome counts are provided, some of them being new reports for previously non-studied species. The genus *Alcea* will be covered in a separate study, due to its taxonomical complexity and high number of species.

4.2. MATERIAL AND METHODS

4.2.1. Plant material

Thirty-eight species from the closely related genera *Alcea* (2), *Althaea* (6), *Lavatera* (16), *Malope* (2) and *Malva* (12) were sampled from natural populations in western Europe and Africa (Spain, Portugal, France, Italy and Morocco, see table 1). Two samples come from Index Seminum (*Althaea armeniaca*, from the Botanischer Garten der Universität Hohenheim, and *Malva verticillata*, from the Botanischer Garten der Universität Oldenburg) and were also grown but not analysed until conclusive identification was confirmed. Five further species come from herbarium material collected in the Eastern Mediterranean and South-Western Asia. Seeds were grown in Petri dishes and fresh root tips were excised and co-fixed with a standard (*Pisum sativum*, *Secale cereale*, *Zea mays*, see table 2) in 3:1 methanol : acetic acid as indicated below.

4.2.2. Chromosome counts

Immediately after excision, root tips were treated with a saturated solution of 8-quinolinol (Sigma-Aldrich) for 2 h at room temperature and Feulgen-stained as indicated below.

4.2.3. Genome size estimation

Genome size estimation was carried out using both Feulgen densitometry and flow cytometry. Both techniques provide accurate results which agree when best practice reccomendations are followed (Doležel & *al.*, 1998; Greilhuber & Temsch, 2001).

a) Feulgen Densitometry

For the Feulgen staining (Feulgen & Voit, 1924), root tips of both sample and standard (*Pisum sativum* 'Kleine Rheinländerin', 2C = 8.84, Greilhuber & Ebert, 1994) were co-fixed in freshly prepared 3:1 methanol : acetic acid, transferred to 96° ethanol, and then stored at -20°C until use. Root tips were later hydrolytically depurinized in 5M HCl at 20°C for 60 minutes, then stained in Schiff´s reagent prepared from basic fuchsin (Fluka), as described in Greilhuber & Ebert (1994). Hydrolysis was stopped by thoroughly rinsing the root tips in distilled water. Samples were then stained with Schiff´s reagent over 1.5 h in the dark at room temperature. Afterwards samples were washed with SO_2 water (for 100 ml 0,50 g $K_2S_2O_5$ and 5 ml 1N HCl in 95 ml distilled water), and then squashed in 45% acetic acid. Squashed slides were placed over a cold plate to remove coverslips, ethanol-dehydrated and air dried, then stored in the dark until measurement.

Nuclear 2C and 4C values were estimated using the software of image analysis CIRES (Cell Image Retrieval and Evaluation System 3.1, Kontron, Munich, Germany) following Greilhuber & Ebert (1994) and Greilhuber & Temsch (2001). Measurements of nuclei IOD (integrated optical density) were performed using a monochromatic green filter under a 63x oil immersion objective.

b) Flow Cytometry

For nuclei isolation, the protocols of Baranyi & Greilhuber (1996) and Temsch (2003) were followed. Up to 25 mg of leaf tissue from sample and standard (*Pisum sativum* 'Kleine Rheinländerin', 2C = 8.84, Greilhuber & Ebert, 1994; *Secale cereale*, 2C = 15.57, Doležel, 1998; *Zea mays*, 2C = 5.46, Doležel, 1998) were co-chopped in 1.1 ml citric acid isolation buffer (pH 1.5, Galbraith & *al*., 1983). The nuclei suspension was filtered through a 30 μm nylon mesh (Sefar AG, Rüschlikon, Switzerland) to remove cell debris, and then incubated for 30 min at 37°C with RNAse A. Samples were stained with 4 ml propidium iodide (PI) solution (pH 9.5) for 1 h at 4°C in the dark, then immediately measured with a Cell Analyzer (CAII) Partec (Münster, Germany) flow cytometer.

For 2C nuclear DNA content estimation, three to five individuals per species were analyzed, performing 3-5 runs per individual together with the standards (see table 2). Additional runs with standard alone were performed to align the instrument. In each run 5000 cells were analyzed. The 2C-value of each sample was calculated using the position of peaks in relative fluorescence intensity histograms with the following ratio:

$${}_{s}2C = {}_{s}G_1 \times ({}_{st}G_1)^{-1} \times {}_{st}2C$$

Where ${}_{s}2C$ = sample 2C-value, ${}_{s}G_1$ = sample G_1 mean peak, ${}_{st}G_1$ = standard G_1 mean peak and ${}_{st}2C$ = standard 2C-value.

Samples were polysaccharide-rich, making measurements complicated. Pippeting was difficult and in most cases chopped leaf pieces were strongly stuck together without releasing any nuclei. Trials with several plant tissues were made and finally root was chosen, as normally it is not so polysaccharide-rich as the leaves or petals. Peaks with coefficient of variation higher than 3.5 were discarded. This was the case for *Lavatera assurgentiflora*, *L. thuringiaca*, *Malope malacoides* and *M. trifida*, for which flow measurements were thus not possible.

4.2.4. Phylogenetic framework

The reconstruction of genome size evolution was made on a bayesian nrDNA ITS topology product of a wider research proyect on the phylogeny of the *Malva* alliance (Escobar & *al.*, 2007). A subset of the molecular data matrix including ITS data for the species whose 2C-value was measured was taken and re-analysed with MrBayes, obtaining a compatible, simpler topology.

For bayesian analysis, a minimum generation number (about 400,000) was estimated as four times the number required for likelihood convergence (Hall, 2001). The resampled matrix was analyzed using the GTR (General Time Reversible) model for one million generations, saving a tree every 1000 generations. The initial 20% of the saved trees was discarded as burnin. The remaining were used to compute a 50% majority-rule tree in PAUP*. True probabilities of each clade are displayed above each branch in figure x.

4.2.5. Reconstruction of genome size evolution

Since the study group is composed mostly of polyploids, observed 2C-values were divided by the ploidy level for statistical comparison and evolutionary inference (1Cx-values, Greilhuber & *al.* 2005). Nested ANOVA were carried out with the program NESTAN (Applied Biostatistics, Inc., 1991), considering variation at infraspecific, specific, generic and intergeneric levels.

For reconstructing the evolution of genome size three analyses were carried out using a bayesian tree topology obtained from ITS data (Escobar & *al.* 2007). The first used a generalised least squares method (GLS) as implemented in the computer program Continuous (Pagel, 1997, 1999), to compare two models of evolution in continuous characters, Model A corresponding to standard constant-variance random-walk and Model B, directional random-walk. The latter measures the regression of observed values across different taxa against total path length in the tree. Hypothesis testing (H_0 Model A versus H_1 Model B) used a log-likelihood ratio statistic, to compare the goodnes of fit of the model B to the observations with that of Model A.

The second analysis used linear parsimony as implemented in MacClade 4.0 (Maddison & Maddison, 1992). It minimizes the sum of changes along tree branches (Farris, 1970, Swofford & Maddison, 1987), yielding a range of equally parsimonious values at each branch.

Additionally, squared-change-parsimony analysis (Rogers, 1984; Huey & Bennett, 1987) was carried out, which minimizes the sum of squared changes along the tree yielding single values. Since rooting the tree may affect character reconstruction (Maddison, 1989), both the rooted and unrooted program options were considered.

For convenience purposes, a classification of 1Cx-value data in the following ranks is followed instead of that proposed by Leitch & *al.* (1998) for the whole of the angiosperms (fig. 1). 1Cx-values ≤ 0.321 are considered to be very small (11 taxa). Small values are these in the range 0.322 ≤ 1Cx-value ≤ 0.597 (13 taxa), being medium these between 0.598 ≤ 1Cx-value ≤ 1.122 (8 taxa). For 1Cx > 1.123 we classify the taxa as large (6 in total).

4.3. RESULTS

4.3.1. Genome size

2C-values were measured for 38 species (36 ingroup species plus two outgroup) from the genera *Althaea* (6 species), *Lavatera* (15 species plus 1 subspecies), *Malope* (2 species) and *Malva* (12 species), as shown in table 2. The outgroup (2 *Alcea* species) was chosen following results of Tate & *al.* (2005). The observed mean 2C-values ranged between 1.252 pg in *Malva parviflora* to 10.948 in *Malva alcea*, which means an 8.7-fold range of variation. Results from Feulgen densitometry and flow cytometry were very similar, as previous studies have already remarked (Doležel & *al.*, 1998) whenever recommendations for good practice are followed (Doležel & Bartoš, 2005; Greilhuber & Temsch, 2001). Nested ANOVA tests did not find any intraspecific differences, a result which agrees with the general 2C-value homogeneity across single species (Greilhuber, 1988, 1998, 2005). In fact, most intraspecific variation in DNA amount is found to be the result of taxonomic heterogeneity (as in Greilhuber & Speta, 1985), and overcame once classification problems are solved.

4.3.2. Chromosome counts

Chromosome numbers vary from 2n=14 in *Lavatera trimestris*, the only diploid of the group (x = 7), to 112 in *Lavatera cretica*, which corresponds to 16-ploid. From the possible 16 levels of ploidy only five are observed, 2n = 14 (2x), 2n = 28 (4x), 2n = 40 to 44 (6x), 2n = 84 (12x) and 2n = 112 (16x). Chromosome counts for all the studied species appear in table 2. These agreed with observations from previous work. For 7 species we have not found chromosome number reports in the literature, so we assume first recording being done here: *Althaea longiflora* 2n = 22 (4x), *A. ludwigii* 2n = 44 (6x), *Lavatera assurgentiflora* 2n = 84 (12x), *L. phoenicea* 2n = 44 (6x), *Malope malacoides* 2n = 44 (6x), *Malva cretica* subsp. *althaeoides* 2n = 44 (6x), *M. trifida* 2n = 42 (6x).

4.3.3. Genome size evolution

Linear parsimony analysis reconstructed intervals for the 1Cx-values. Lower limits (MINSTATES) are shown in figure 2. Squared-change parsimony inferred almost identical values in both rooted and unrooted analyses (data for rooted analysis shown in figure 2), which also were similar to these inferred by linear parsimony.

Basal nodes are inferred to have small 1Cx-values, with changes occuring at higher levels on the tree. Within the perennial *Althaea* clade, a rise in 1Cx-value from small to medium appears in *A. officinalis*. The annual *Althaea* clade also undergoes a rise to medium in *A. hirsuta*. The 1Cx-value sinks in the *Malope* clade from the basal small to the derived very small, as also happens in the *Malva aegyptia* clade. But where the most striking changes occur within the *Lavatera-Malva* clade. The postulated ancestor of both malvoid and lavateroid groups is inferred to have small 1Cx-value, but both groups followed different evolutionary pathways. The malvoid species evolved mainly loosing DNA, leading to very small genomes despite forming a polyploid series from 6 to 16x. Only basal taxa have small or medium 1Cx-values, as *L. acerifolia* and *L. maritima*, respectively. Within the lavateroid group, there is a distinct trend upwards from the basal small 2C-values inferred to the large observed within this group. All the species of the *Malva* alliance with observed large 2C-values occur within this clade. The only exception appears to be the *Bismalva* group, where a possibly independent, reverse trend to decrease is observed.

The GLS analysis for the whole data set did not yield higher likelihood scores for Model B (directional random-walk), indicating a lack of general trend (increase or decrease) in genome size evolution. Since lavateroid species tend to show much higher 1Cx-values than the malvoids, we performed separate GLS analyses for both groups, significantly higher log-likelihood ($P < 0.05$) was found in malvoids for Model B, indicating the existence of directional evolution.

4.4. DISCUSSION

Lavatera and *Malva* were considered independent genera in the XVIII Century by Linné (1753) on the basis of a single character, the degree of fusion of epicalyx bracts. In the classical view *Lavatera* displays fused epicalyx bracts whereas in *Malva* these pieces are free. But both carpological and molecular data suggest that groups supported by epicalyx morphology are not natural. Instead, the character used by Linnaeus appears to be highly homoplasic, leading to the differentiation of artificial genera, as it has been noted several times in the literature (Medikus, 1787; Webb & Berthelot, 1833; Alefeld, 1862; Fernandes, 1968a, b; Krebs, 1994a, b; Ray, 1995).

Molecular data as nrDNA ITS, the low copy nuclear marker *ces*A1b, cpDNA *trn*L-*trn*F, *psb*A-*trn*H, *mat*K and *ndh*F (Escobar & *al*., 2007) group together all *Lavatera* with most *Malva* and the annual *Althaea* species (sect. *Hirsutae*), in what here is denominated *Lavatera-Malva* Clade (LM). Within this clade three major groups are defined. The lavateroid group comprises most perennial *Lavatera*. The malvoid group comprises the ruderal, highly derived species of *Malva* and *Lavatera* (Ray, 1995), and the *Althaea* sect. *Hirsutae* clade which groups a core of small annual *Althaea* with *Malva cretica* subsp. *althaeoides*.

Many malvoid species are thus included in the classical concept of *Lavatera*, whereas some *Malva* (sect. *Bismalva* and *M. hispanica*) present lavateroid characteristics. Several *Malva* species split from the malvoid and lavateroid groups to appearing more related to the annual species of *Althaea*, or being basal to the group.

4.4.1. Polyploidy and genome size within the *Malva* alliance

DNA amounts are normally constant within a species, but in many groups significant variation among closely related species is observed. Genome size varies 4.3-fold in *Veronica* (Albach & Greilhuber, 2004), and over five-fold differences occur in genera as *Crepis* (Jones & Brown, 1976), *Ranunculus* (Smith & Bennett, 1975) and *Vicia* (Li & Liu, 1996). In others, *C*-values show remarkable constancy, as in the case of *Ficus* (Ohri & Koshoo, 1987). In subtribe *Malvinae* DNA amounts range from 2*C* = 1.25 pg in *Malva parviflora* to 2*C* = 10.94 pg in *Malva alcea*. This means a 8.7-fold overall range of variation.

Chromosome numbers in plants range from 4 to 600 (Bennett, 1987). No plants with 2n = 2 are known, although there are animals with this chromosome number. Two plant species with 2n = 4 exist, *Haplopappus gracilis* (Asteraceae) and *Zingeria biebersteiniana* (Poaceae). In the *Malva* alliance chromosome numbers vary from 2n = 14 in *Lavatera trimestris*, the only diploid of the whole group (x = 7), to 112 in *Lavatera cretica*, a 16-ploid. Five ploidy levels are displayed, 2x = 14 in *Lavatera trimestris*; 4x = 22, 24 in *Althaea longiflora* and *Malva hispanica*, respectively; 6x = 40, 42 or 44, in most taxa (see table 2); 12n in *Althaea cannabina*, *Lavatera mauritanica*, *Malva alcea*, *Malva verticillata*; and 16n restricted to *Lavatera cretica*. At least two species show variable levels of ploidy: in *Malva verticillata* both hexaploids and 12-ploids are known, for *Lavatera cretica* hexaploids and 16-ploids.

The radiation of the lavateroids and the later diversification of the ruderal malvoids seem to have been fast, as critical short branches in phylogenetic trees are retrieved in parsimony and bayesian analyses. The existence of a single diploid species (*L. trimestris*, 2n = 14) as well as only one tetraploid (*M. hispanica*, 2n = 24) among *Lavatera*-*Malva* suggests early polyploidization, being the low-ploidy ancestors extinct. Most extant species are hexaploids followed in number by the 12-ploids (*L. mauritanica*, *M. alcea*, *M. verticillata*), apparently derived from the preceding. The lack of octoploids could be interpreted as a fast replacement of tetraploid taxa by the fast radiating, better-adapted hexaploids. Another point suggesting fast radiation is the fact that among the ruderal malvoids (*L. cretica*, *M. sylvestris* and allies) DNA amounts are additive among ploidy levels. For instance *L. mauritanica* (2n = 84, 12-ploid) has twice as much DNA as the small hexaploid annuals (*M. parviflora*, *M. nicaeensis*, *M. neglecta*), resulting in almost identical 1Cx-values. An additive relationship between DNA amounts and ploidy levels is expected for neopolyploids of recent origin (Leitch & Bennett, 2004), where forces causing genome expansion or contraction have not yet acted.

Some species from the 12-ploid complex are likely to have appeared through allopolyploidization, as it is the case of *L. mauritanica*, where well-supported incongruence among ITS and plastid markers is a strong indicative of hybrid speciation between an unidentified annual mallow and *L. arborea*. Other species of the 12-ploid complex seem to be of autopolyploid origin. The robust and edible *Malva verticillata* seems to be an autopolyploid derivative of *M. parviflora*, a very similar but less vigorous species.

The case of the 16-ploid *L. cretica* is similar to that of *M. verticillata*. It is morphologically close to its hexaploid relatives from the ruderal mallow species complex, particularly to *M. sylvestris* and *M. nicaeensis*, sharing also 1Cx-value with them. Its particular chromosome number suggests a cycle of recurrent polyploidization, probably from one of the hypotetical tetraploid ancestors through an octoploid extinct derivative. The diversity of chromosome numbers reported for *L. cretica* (2n = 44 in Davie, 1935; 2n = 112 in Queirós, 1977; Luque & Devesa 1986, and reported data) is difficult to interpret in this context and could be due to confusion with the hexaploid *M. sylvestris*, a common phenomenon observable in most herbaria.

4.4.2. The complex pattern of genome size evolution and variation across the *Malva* alliance

Using two species of *Alcea* as outgroup, the reconstructed ancestral 1Cx-value in the *Malva* alliance appears to be small, irrespective of the method employed (linear or squared-change parsimony). Within the early diverging lineages 1Cx-values tend to keep comparatively low, with punctual increases or decreases around a value inferred to be about 0.378 pg.

The *Althaea* clade is sister to all the remaining species, with the perennial *Althaea* (*A.* sect. *Althaea*) –a group of perennials closely linked to water– nested within. *Althaea armeniaca* is an Eastern European - Western Asian element with 1Cx = 0.568 (12x). *Althaea cannabina* has a smaller 1Cx-value of 0.546 (12x). Within this lineage, *Althaea officinalis* a widespread herb used traditionally in the European pharmacopoeia (1Cx = 0.609, 6x) is inferred to have undergone punctual genome size increase.

Malope appears to be monophyletic and the closest relative of all remaining *Lavatera* and *Malva*. According to the general trend inferred for the basal groups, 1Cx-values are small. *Malope malacoides* (1Cx = 0.370, 6x) is a widespread Mediterranean perennial plant with showy flowers. *M. trifida*, an annual restricted to southern Spain and Rif (Northern Morocco), appears to have undergone genome reduction to 1Cx = 0.310 (6x).

Lavatera (*Navaea*) *phoenicea* is a summer-deciduous small tree or large shrub endemic to the Canary Islands which appears isolated at the basis of all *Malva*, *Lavatera* and annual *Althaea* species. With 1Cx-value = 0.677 (6x), it is inferred to have undergone genome expansion from the small-genome hypotetical ancestor.

The *Malva aegyptia* clade encomprises two annual species, *M. aegyptia* (1Cx = 0.321, 6x), an inconspicuous widespread weed, and *M. trifida* (1Cx = 0.381, 6x) a showy outbreeder endemic to the Central and Eastern Spain gypsum banks. Within this group, *M. aegyptia* is inferred to have undergone genome reduction, maybe due to its short life cycle associated to ruderal ecology.

At the basis of both malvoid and lavateroid taxa the species of *Althaea* included in sect. *Hirsutae* appear together in a clade, plus a further *Malva* species, *M. cretica* subsp. *althaeoides*. This is a remarkable fact which strongly suggests that *Althaea* is polyphyletic (Escobar & *al*. 2004). The perennial species of *Althaea* (sect. *Althaea*) appear to be basal within the *Malva* alliance. *M. cretica* subsp. *althaeoides*, a showy annual endemic to the Eastern Iberian Peninsula is basal in the group. *Althaea longiflora* (1Cx = 0.549, 4x) is an annual Western Iberian-Moroccan showy species, closely related to *A. hirsuta*, to which some authors assimilate it (Krebs, 1994b; Bolòs, 1995). The latter species, much more widely distributed (1Cx = 0.772, 6x) is similar but with much smaller flowers. *Althaea ludwigii* is an ephemeral to perennial species (depending on ecological factors) ruderal in desert areas of Northern Africa and South-Western Asia, with 1Cx = 0.370 (6x). The ancestral 1Cx-value reconstructed for the group is small, with genome expansion in the branch leading to *A. hirsuta*.

The remaining taxa appear in a single clade comprising all *Lavatera* species and their closest relatives among *Malva*, and splits into two groups: malvoid and lavateroid taxa. The lavateroid taxa are morphologically defined by their schizocarps releasing the seeds at maturity. In this group the distal portion of the carpel is weakly united to the side walls conforming a C-shaped mericarp (Ray, 1995). The malvoid clade is characterized by their undehiscent schizocarps. In this group, the outer layer of the fruit resembles a thick box tightly united to the fruit axis, so that the whole fruit/schizocarp is dispersed instead of simple seeds.

The malvoid group displays the lowest 1Cx-values of all the studied species. At its basis two closely related species appear, *Lavatera maritima* (1Cx = 0.691, 6x) and *Lavatera acerifolia* (1Cx = 0.597, 6x), which are the only representatives of the clade presenting small or medium-sized 1Cx-values. These species are evergreen or summer-decidous shrubs, the former appearing in all the Western Mediterranean region, the latter endemic to the Canary Islands. The rest of the group consists of a polyploid series of mainly annual plants (some of them behave as short-lived perennials in mild habitats) with high requeriments in soil nitrogen. A marked decrease in 1Cx-value inferred from the GLS model and both linear and squared-change parsimony to have occurred at the base of the malvoid group, after the divergence of *L. maritima-acerifolia*. Such decrease has probably happened in very recent times, as suggested by observed additivity in the 2C-value measurements of the different ploidy levels. The 1Cx-values of *L. cretica* (16x) and the ruderal hexaploids (*M. neglecta*, *M. sylvestris*, *M. nicaeensis* and *M. parviflora*) are almost identical, being that of *M. verticillata* slightly higher than expected. This contrasts with the general trend of polyploids, which have comparatively smaller genomes than would be expected merely by ploidy increase (Leitch & Bennett, 2004). Moreover, this decrease in genome size is also associated with a lack of resolution for the relationships of the small-flowered mallows, which we interpret as a hard polytomy, i. e. a fast and recent speciation event.

The lavateroid group includes two clades. The first clade groups *Lavatera triloba sensu lato*, large perennials with big flowers related to wet environments on slightly saline soils. The Iberian populations (subsp. *triloba*, 1Cx = 1.325, 6x) with purple flowers, are segregated from the Balearic populations (*L. triloba* subsp. *pallescens* 1Cx = 1.260, 6x) which are smaller and related to seashore limestone rocky slopes. Closely related to this group are *L. bryoniifolia* and *L. olbia*, the former (1Cx = 1.122, 6x) being a large shrub native to the Eastern Mediterranean Basin. It is similar in overall appearance and ecology to *L. olbia* (1Cx = 1.090, 6x), a tall shrub with showy flowers, widely distributed in the Western Mediterranean Region. *Lavatera oblongifolia*, a small shrub endemic to Granada and Almería provinces in Southern Spain (1Cx = 1.045, 6x) is morphologically divergent within the genus *Lavatera*. Within this clade a strong trend towards genome increase is detected, from medium-sized estimated ancestral 1Cx-values of 0.976 (squared-change parsimony) or 1.045-1.090 (linear parsimony) to the large amounts observed in the *L. triloba* aggregate.

The second lavateroid clade (the *Lavatera trimestris* clade) is not strongly supported and includes 5 species or species groups currently placed in both

Malva and *Lavatera*. Sister to the remaining species are *L. maroccana*, and the clade *L. trimestris*-*M. hispanica*. Upwards in the tree *L. thuringiaca*, *L. punctata* and the *Bismalva* clade appear. As bootstrap support rendered values lower than 50%, the lavateroid group was collapsed to a basal polytomy. Squared-change parsimony and generalised least squares models have the drawback of not tolerating polytomies in the analysis, which we arbitrarily solved with branches of small length (commonly 0.1, Maddison, 1989; Soltis & *al.*, 2003). We have analysed the strict consensus tree of figure 1 and used arbitrary branch lengths of 0.1 to sort this problem out.

L. thuringiaca, a Pontic-Eastern Europaean species with 1Cx = 1.405 (6x), is a showy perennial with large flowers often used in horticulture. The annual Ibero-Moroccan *L. maroccana* (1Cx = 0.356, 6x) appears to be restricted to temporary lagoon shores on deep clay soils, in Sevilla and Cádiz provinces (Spain) and the Rif (Morocco). It is quite similar to *L. trimestris*, but having smaller, paler yellowish lilac flowers. The fruits present a protective disc resembling *L. trimestris*, but not covering the mericarps at fruit maturity. This latter is a showy annual, with a comparatively high 1Cx of 1.690. It is the only diploid of the whole group. The *Bismalva* clade comprises three closely related *Malva* species, *M. alcea, M. moschata* and *M. tournefortiana*. *M. alcea* (1Cx = 0.912, 12x) and *M. moschata* (1Cx = 0.489, 6x), are two perennial species of wide European distribution, *M. alcea* typically found in clearings and along roads in deciduous forests. This species displays the biggest 2C-value of all the group, 2C = 10.948. *M. tournefortiana* (1Cx = 0.491, 6x) is a Western-Mediterranean element, very similar in overall appearance to *M. moschata*, but more exigent in habitat, growing mainly in clearings and margins of well preserved evergreen or deciduous forests.

The lavateroid group includes species whith the largest 1Cx-values. The ancestor of all lavateroid taxa is reconstructed to be of small to medium (linear parsimony) or medium (squared-change parsimony) 1Cx-value, thus not being clear if genome enlargement is the result of a general trend within the lavateroid group or appeared several times independently, one associated with the *L. triloba-olbia* clade and other with the *L. trimestris* clade. The also lavateroid *Bismalva* group shows an opposite trend with a conspicuous decrease in genome size. This decrease appeared independently, from an ancestor of medium-sized 1Cx-value.

The position of different taxa within this second lavateroid clade is also not fully resolved, the clades collapsing to a basal lavateroid polytomy in the Bootstrap support analysis. With the present data, though it is evident that lavateroid taxa (with the exception of *Bismalva*) have undergone extensive genome expansion, it is not possible to decide wether a) *Bismalva* and *L. maroccana* retained a hypotetical small ancestral genome size or b) 1Cx-values in *Bismalva* and *L. maroccana* are the effect of genome downsizing from lavateroid ancestors with medium-sized genomes. It is also unclear whether genome expansion has occurred one, two or more times during the evolution of lavateroid taxa.

If the presented evolutionary scenario for the lavateroids (figure 2) is to be believed, the evolution of genome size within the lavateroids has followed a complex pattern where a small to medium-sized genome ancestor underwent genome expansion leading to *L. trimestris-M. hispanica*, *L. thuringiaca*, *L. punctata* and the *Lavatera triloba-olbia* clade; and genome downsizing in the lines of *Bismalva* and *L. maroccana*.

Genome size in the *Malva* alliance is a trait subject to complex evolution. Basal taxa present generally small 1Cx-values, ancestral genome sizes being reconstructed as equally small. Some punctual increases to medium-sized genomes are inferred, as it is the case of *Althaea officinalis*, *Lavatera phoenicea* and *Althaea hirsuta*. Two genome downsizing events are also likely to have occurred among these basal taxa, as in *Malope trifida* and *Malva aegyptia*.

The *Lavatera-Malva* clade has a small to medium-sized inferred ancestral genome size. Two main trends appear to be clear, genome downsizing within the malvoid group, composed mainly of annuals; and genome expansion in the lavateroid group, which accumulate the most massive 1Cx-values whith the exception of the *Bismalva* species. But due to the not strongly-supported topology of the cladogram it is not clear whether this trend to present large genomes is due to several independent increases or to a single evolutionary event. It is not clear whether the small to medium genomes showed by *Bismalva* and *L. maroccana* are the result of genome downsizing or maintenance of a plesiomorphic trait.

4.4.3. Selective forces in genome size evolution

By the moment, questions as why does extensive genome size variation among closely related species exist remain unanswered. According to some studies (Kubis & al., 1998), most of plant genomes is composed of highly repeated sequences, which would account for the great interspecific variability in genome size.

We are used to talk about genetic information in terms of DNA sequence. But the mere amount of DNA may be a key factor -regardless of the sequence- in the determination of some cellular traits, the most influential of which are cell size and minimum doubling time (Bennett 1971, 1972, Van´t Hof 1963). For a given chromosome number, the species with larger DNA amount have also bigger chromosomes. For example, it would be impossible for the small cell nuclei of *Malva parviflora* (2*C* = 1.25 pg) to house the much larger chromosomes of *Lavatera triloba* (2*C* = 8.01 pg), despite both of them being hexaploids with 2n = 42.

There is an association between the duration of mitosis (Van´t Hof 1963, Bennett 1971), meiosis and DNA amount. Bennett (1971, 1972) studied the relationship between meiosis and DNA amount, finding in *Antirrhinum majus* and *Haplopappus gracilis*, both with 5.5 pg DNA per cell, that the meiosis lasts 24 and 36 h, respectively. In *Lilium longiflorum* (106 pg DNA per cell) it is about 192 h, and in *Trillium erectum* (120 pg DNA per cell), 274 h.

It is also possible to observe a well-defined ecological trend in the distribution of genome sizes. The *C*-values measured are on average high for the Mediterranean perennial and shrubby species (most of them lavateroids); and low for the widespread, ruderal, annual species, which belong to the malvoid group. The ecological specialization leads to the appearance of strong differences in DNA amounts between types of life cycles (table 2). The average DNA amount for species showing ephemeral behaviour, like *Althaea ludwigii*, *Malva aegyptia* or *M. parviflora* is 2*C* = 1.79 pg, less than the average DNA amount for annual plants displaying a minimum lifespan of more than 7 weeks. For such species, like *Lavatera maroccana*, *Malva hispanica* or *M. trifida*, the average DNA amount is *2C* = 2.93 pg, which in fact is quite similar to the DNA content of species which can grow as annuals but which usually, if the environment is not too harsh, can survive for several years and produce flowers and fruits again. This group of species displays an average DNA amount of 2*C* = 2.85 pg and includes species such as *Lavatera cretica*, *L. mauritanica* and *Malva sylvestris*. Within the obligate perennials, both large herbaceous plants (*Lavatera thuringiaca*, *Malva alcea*) and shrubs (*Lavatera maritima*, *L. olbia, L. oblongifolia*) occur, the DNA amount being the largest of all, 2*C* = 6.32, more than twice the formers. In animals it is possible to find comparable examples, for instance the minimum duration of the tadpole stage is positively correlated with DNA *C*-value in frogs. The species whose tadpoles colonize transient puddles have a shorter tadpole stage, and a lower DNA *C*-value (Goin & *al.*, 1968).

The nuclear DNA content can limit the types of life-history which a species can display. For example, species with medium DNA amounts cannot be ephemerals, while those with very high DNA amounts cannot be ephemerals or even annuals. Species with low DNA *C*-values which complete meiosis within 1 or 2 days are able of colonizing a wider range of habitats, larger geographical regions and wider ecological gradients.

Some authors have also found a correlation among DNA amount and plant distribution. For Knight & Ackerly (2002), mesic climates allow the largest genomes. Within the *Malva* alliance, from the five species with 1Cx-values classified as large (table 2), four are endemic to the Mediterranean region, only *L. thuringiaca* being common in Central and Eastern Europe, reaching Crimea and Central Russia. From the six species which naturally occur in the Scandinavian Peninsula and Denmark, four (*M. neglecta*, *M. parviflora*, *M. sylvestris* and *M. verticillata*) display very small 1Cx-values, while just one (*M. moschata*) is small or (*M. alcea*) medium-sized. The four species with very small genomes are annual ruderal elements associated to the activity of man, whereas the two remaining are perennials and grow in meadows and forest clearings. We argue that the fact that most northern species display very low genome sizes is related with their fast cycles and ability to success in man-disturbed habitats rather than with a latitudinal trend towards DNA reduction.

The genome size in the *Malva* alliance is therefore a character of great ecological importance, and has underwent a complex history of expansion and reduction subject to evolutionary forces which determine the type of life cycles and ecology displayed by each taxon. The long-lived Mediterranean species are inferred to have undergone genome expansion while contrastingly, the ruderal annual mallows with fast life cycles adapted to man-made ecological disruptions have diversified after genome miniaturization, and display genomes up to 5 times smaller than their closest shrubby relatives.

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Table 1. Material studied.

Taxon	Voucher	Origin
Alcea pallida	PE415	Turkey. Aydin.
Alcea rosea	PE 416	Spain. Madrid: Madrid.
Althaea armeniaca	PE 427	Index Seminum.
Althaea cannabina	PE 429	Spain. Lérida: Solsona.
Althaea hirsuta	PE 270	Italy. Sardinia: Perdasdefogu.
Althaea longiflora	PE 296	Spain. Badajoz: Magacela.
Althaea ludwigii	PE 616	Iran. Tehran.
Althaea officinalis	PE 409	Spain. Madrid: Aranjuez.
Lavatera acerifolia	PE 951	Spain. Tenerife: Los Gigantes.
Lavatera arborea	PE 252	Italy. Sardinia: Alghero.
Lavatera assurgentiflora	PE 570	United States. California.

Lavatera bryoniifolia	PE 141	Greece. Crete: Rethimnion.
Lavatera cretica	PE 599	Morocco. Rif: Sidi Yahya.
Lavatera maritima	PE 598	Morocco. Gorges du Zegzel.
Lavatera maroccana	PE 311	Spain. Sevilla: Las Cabezas de San Juan.
Lavatera mauritanica	PE 319	Portugal. Algarve. Cabo de São Vicente.
Lavatera oblongifolia	PE 144	Spain. Almería.
Lavatera olbia	PE 451	Italy. Sardinia: San Giovanni di Sinis.
Lavatera phoenicea	PE 952	Spain. Tenerife: Teno.
Lavatera punctata	PE 450	Turkey. Aydin.
Lavatera thuringiaca	PE 590	Austria. Wien.
Lavatera triloba subsp. *pallescens*	PE 564	Spain. Baleares: Isla Colom.
Lavatera triloba subsp. *triloba*	PE 606	Spain. Madrid: Arganda del Rey.
Lavatera trimestris	PE 595	Morocco. Rif: Chefchaouen.
Malope malacoides	PE 600	Morocco. Rif: Fnidek.
Malope trifida	PE 601	Morocco. Rif: Khenichet.
Malva aegyptia	PE 681	Greece. Crete: Rethimnion.
Malva alcea	PE 338	Spain. Ávila: Mijares.
Malva cretica subsp. *althaeoides*	PE 950	Spain. Cádiz: Algodonales.
Malva hispanica	PE 602	Spain. Badajoz: Guadajira.
Malva moschata	PE 593	France. Pyrenées Orientales: Lortet.
Malva neglecta	PE 795	Italy. Sardinia: Lago Cuga.
Malva nicaeensis	PE 226	Italy. Sardinia: Uri.
Malva parviflora	PE 603	Spain. Badajoz: Guadajira.
Malva sylvestris	PE 597	Morocco. Oujda.
Malva tournefortiana	PE 185	Spain. Badajoz: Talarrubias.
Malva trifida	PE 605	Spain. Madrid: San Martín de la Vega.
Malva verticillata	PE 442	Index Seminum.

Table 2. 2n, Observed chromosome numbers. **Ploid**, ploidy levels. **2C (F)**, observed mean 2C-values with Feulgen microdensitometry. **2C (FC)** observed mean 2C-values with Flow Cytometry. **Mean 2C**, mean of Feulgen and Flow measurements, when both available. **1Cx-value**, Mean 2C divided by the ploidy level. **Class**, genome size class, VS very small (0.198-0.321pg), S small (0.322-0.597), M medium (0.598-1.122), L large (1.123-1.690). **Standard**, standard organism used in Flow Cytometry measurements. *P. s.*, *Pisum sativum* 'Kleine R.' = Pisum sativum 'Kleine Rheinländerin', Z. mays, *Zea mays*, S. c., *Secale cereale*.

Taxon	2n	Ploid	2C (F)	2C (FC)	Mean 2C	1Cx	Class	Standard
Alcea pallida	42	6x		2,316	2,316	0,386	S	
Alcea rosea	42	6x		2,268	2,268	0,378	S	
Althaea armeniaca	84	12x	6,838	6,806	6,822	0,568	S	*P. s.*
Althaea cannabina	84	12x	6,510	6,597	6,554	0,546	S	*P. s.*
Althaea hirsuta	52	6x	4,847	4,413	4,630	0,772	M	*P. s.*
Althaea longiflora	22	4x	2,167	2,224	2,195	0,549	S	*P. s.*
Althaea ludwigii	44	6x	2,256	2,180	2,218	0,370	S	*P. s.*
Althaea officinalis	42	6x	3,734	3,570	3,652	0,609	M	*P. s.*
Lavatera acerifolia	44	6x		3,582	3,582	0,597	S	*P. s.*
Lavatera arborea	40	6x	1,437	1,513	1,475	0,246	VS	*Z. mays*
Lavatera assurgentiflora	84	12x	2,374		2,374	0,198	VS	
Lavatera bryoniifolia	42	6x	6,652	6,811	6,731	1,122	M	*P. s.*
Lavatera cretica	112	16x	3,659	3,586	3,623	0,226	VS	*P. s.*
Lavatera maritima	44	6x	4,290	3,998	4,144	0,691	M	*P. s.*
Lavatera maroccana	44	6x	2,113	2,156	2,134	0,356	S	*P. s.*
Lavatera mauritanica	84	12x	2,701	2,566	2,633	0,219	VS	*P. s.*
Lavatera oblongifolia	42	6x	6,529	6,013	6,271	1,045	M	*P. s.*
Lavatera olbia	42	6x	6,416	6,668	6,542	1,090	M	*P. s.*
Lavatera phoenicea	44	6x		4,061	4,061	0,677	M	*P. s.*
Lavatera punctata	42	6x	7,165	7,074	7,119	1,187	L	*P. s.*
Lavatera thuringiaca	44	6x	8,430		8,430	1,405	L	
Lavatera triloba subsp. *pallescens*	42	6x	7,675	7,447	7,561	1,260	L	*P. s.*
Lavatera triloba subsp. *triloba*	42	6x	8,016	7,890	7,953	1,325	L	*S. c.*
Lavatera trimestris	14	2x	3,257	3,504	3,380	1,690	L	*P. s.*
Malope malacoides	44	6x	2,217		2,217	0,370	S	
Malope trifida	44	6x	1,861		1,861	0,310	VS	
Malva aegyptia	42	6x	1,871	1,980	1,925	0,321	VS	*Z. mays*
Malva alcea	84	12x	10,94	10,950	10,948	0,912	M	*P. s.*
Malva cretica ssp*. althaeoides*	44	6x		2,606	2,606	0,434	S	*P. s.*
Malva hispanica	24	4x	5,763	5,759	5,761	1,440	L	*P. s.*
Malva moschata	42	6x	2,958	2,913	2,935	0,489	S	*P. s.*
Malva neglecta	42	6x	1,383	1,548	1,466	0,244	VS	*Z. mays*
Malva nicaeensis	42	6x	1,379	1,518	1,448	0,241	VS	*Z. mays*
Malva parviflora	42	6x	1,256	1,249	1,252	0,209	VS	*Z. mays*

Malva sylvestris	42	6x	1,290	1,676	1,483	0,247	VS	*Z. mays*
Malva tournefortiana	42	6x	2,992	2,901	2,946	0,491	S	*P. s.*
Malva trifida	42	6x	2,132	2,440	2,286	0,381	S	*Z. mays*
Malva verticillata	84	12x	3,688	3,545	3,617	0,301	VS	*P. s.*

5. LOW VARIABILITY IN THREE MOLECULAR MARKERS, DNA AMOUNTS AND CHROMOSOME NUMBER SUGGEST HIGH PHENOTYPIC PLASTICITY AND EXTENSIVE HYBRIDISATION WITHIN *ALCEA* L. (MALVEAE, MALVACEAE)

5.1. INTRODUCTION

Alcea is an Eastern Mediterranean - Irano-Turanian genus of biennial or perennial herbs, with a variable number of species depending on the author considered. Zohary (1963b, c) recognized 33 species native to South-Western Asia and the Eastern Mediterranean, which including the 19 former USSR endemics described previously by Iljin (1949) would make a total of 52 species. Later Riedl (1976), in her comprehensive treatment of Malvaceae for *Flora Iranica* recognized a total of 58 taxa. Pakravan (2001) recognizes in her monography 34 species for the territory of Iran. But most authors cite round numbers, of about 50 (for example Townsend, 1980, for Flora of Iraq) or 60 species (Cullen, 1966, for Flora of Turkey).

Not many attemps of infrageneric division have been done for the genus *Alcea*. Boissier (1867) in his *Flora Orientalis* first established two sections, *Apterocarpae* for species deprived of mericarp wings and *Pterocarpae* for winged-mericarp taxa. Due to the existence of polymorphic species (*A. kurdica*) with either winged or apterous mericarps this classification seems to a certain point untenable. Later Zohary (1963b, c), established informal rankless species groups on the basis of different morphological characters, namely mericarp structure, epicalyx, leaf division sequence and indumentum.

Alcea includes mostly perennial (sometimes biennial) hemicryptophytes, of simple, lobed, palmatipartite or digitate leaves, more or less covered by an indumentum of stellate and fasciculate hairs. The flowers are bisexual, showy and big (usually more than 30 mm), and appear arranged normaly in large, racemose, terminal inflorescences, though sometimes solitary and axillar. The flowers are provided with an involucrum external to the calyx which is normally referred as epicalyx, composed of (5-) 6-9 (-11) triangular segments united in their lower half. The campanulate calyx is composed of 5 fused lobes. Petals are large, obovate to obcordate, with a distinct, pubescent claw, fused in a basal ring among themselves and to the glabrous staminal column, of characteristic pentagonal section, topped by numerous stamens. The ovary is formed by numerous (18-40) subbilocular carpels, with an inner process of the pericarp (endoglossa) which delimitates a sterile upper chamber, and an one-seeded lower one. The stylar branches appear in the same number as carpels, which are laterally compressed and often presenting a more or less conspicuous dorsal wing. Fruit is a dry, undehiscent schizocarp, with mericarps separating at maturity from a central distinct conical to cylindrical carpophore. Seeds brown to black, reniform.

Due to their big, beautiful flowers, most species are ornamental, some of them (like *A. rosea*) being extensively naturalized in Europe and North America. Some species are fiber-rich, and suitable for paper production (Iljin, 1949).

As it happens with *Lavatera* and *Malva* (Escobar & al., 2007a, b), *Alcea* is a name taken by Linné from Tournefort (1700, 1706). Linné used this and other Malvaceae tournefortian names modifying substantially its meaning, keeping respectively *Alcea* for the Hollyhocks and *Althaea* for the Marshmallows. Despite both linnaean genera are easily distinguishable by epicalyx, carpel and staminal column characters, some authors have preferred to merge them within a single, expanded genus *Althaea*, like Willdenow (1800), initiating a tradition followed by De Candolle (1824), Bentham and Hooker (1862) and the great monographer of tribe Malveae Baker (1890). Despite the trials of segregating *Alcea* from *Althaea* made by Alefeld (1862) and Boissier (1867), this tradition was only broken after the Second World War by the works of Iljin (1949), Zohary (1963b, c) and Riedl (1976). Most modern floras incorporathe this vision and later phylogenetic molecular work has also added support to it (Tate & al., 2005; Escobar & al., 2007a, b).

Despite being one of the taxonomically most difficult genera of the Near East flora (Townsend, 1980), or maybe because of it, *Alcea* has deserved little attention from molecular taxonomists. The complicated political situation in some parts of the Middle East has also discouraged to a certain point studies on south western Asian taxa. Latest studies, with comprehensive species sampling and character analysis did not employ DNA techniques (Pakravan, 2001). Some protein studies with a smaller sampling exist (Pakravan, unpubl. data), revealing that SDS-PAGE electrophoresis of seed proteins yield band profiles of taxonomic interest. Only the widespread cultivated *A. rosea* has ever been included in general molecular studies of tribe *Malveae* (Tate & al., 2005) being absent from most modern approaches to *Malvaceae* (Alverson & al., 1998; La Duke & Doebley, 1995; Nyffeler & al., 2005). Outside this and to our knowledge, nobody has tried before to study any DNA marker within this genus. Therefore, a preliminary approach is urgent, to add independent, molecular support to the definition of *Alcea*, and to explore the reliability of character use in taxonomy and species grouping.

5.2. MATERIAL AND METHODS

5.2.1. Taxon Sampling

Twenty species of *Alcea* plus three outgroup species (*Althaea armeniaca*, *A. officinalis* and *Malope trifida*) have been studied (table 1). Character nomenclature and infrageneric grouping follows Zohary (1963b, c), which despite later criticism (Riedl, 1979) appears to be the most comprehensive systematic treatment available to the authors. The sampling included taxa from 6 of the 9 species groups distinguished by Zohary (1963b, c): *Aucheri*, *Remotiflora*, *Setosa*, *Kurdica*, *Rosea* and *Flavovirens* (table 2 and figs. 4.1, 4.3). No taxa from the groups *Striata* (very similar to *Remotiflora*), *Hohenackeri* and the minor (1 sp.) *Apterocarpa* could be sampled. A total of 60 sequences (21 ITS, 20 *psb*A-*trn*H, 19 *trn*L-*trn*F) belonging to 23 species have been analysed. Samples came from field recolection, and living material grown by the authors in experimental greenhouses at the Real Jardín Botánico, Madrid, and Faculty Center Botany, University of Vienna. Vouchers of all specimens used were deposited at the herbarium MA (Real Jardín Botánico, Madrid). For a complete list see table 1. All DNA sequences are available at GenBank (accessions EF679714 to EF6797772).

5.2.2 Character analysis

Four morphological, discrete qualitative characters used by the different generic treatments as group or species diagnostic have been mapped on bayesian ITS and chloroplast topologies with the program MacClade 4.0 (Maddison & Maddison, 2004). Character nomenclature and states follow Zohary, (1963b). The characters studied (see figures 1-5) are leaf indumentum (fig. 4.2, 4.4), with the states leprose (with scaly hairs), pannose (densely tomentose concealing leaf venation), phlomoid (densely tomentose not concealing leaf venation) and glabrescent; leaf sequence (figs. 1, 5.1 and 5.3), with the states *sulphurea* (homophyllous), *rufescens* (slightly heterophyllous), *kurdica* (heterophyllous) and *flavovirens* (all leaves dissected); epicalyx size with respect to the calyx (figs. 3.2, 3.4), microchitic (3-4 times shorter than the calyx), mesochitic (up to half the length of the calyx), and macrochitic (longer than three fourths of the calyx); mericarp structure (fig. 2), planocot (wingless), plagionot (wingless but canaliculate at back), plagiopterous (narrowly winged) and orthopterous (with conspicuous wings).

5.2.3 Molecular techniques

For DNA isolation DNeasy Plant Mini Kit (Qiagen) was used according to the manufacturer's recommendations. PCR products were obtained using puReTaq Ready-To-Go PCR Beads (Amersham Biosciences). 1 μl DMSO per reaction was added, and for old or difficult herbarium material 4% BSA was used. PCR programs were run in a GeneAmp PCR System 9700 (PE Applied Biosystems) and a MJ Research PTC 200 (Peltier) thermocyclers. The ITS region was amplified using the P1A and P4 primers (Fuertes, 1999), at an annealing temperature of 52ºC. For *psb*A-*trn*H region, primers used were PSB and TRN at an annealing temperature of 53ºC. The *trn*L-*trn*F region was amplified using universal primers TE and TF (Taberlet, 1991), at 50ºC annealing temperature. PCR products were checked on 1,5% D-1, low EEO agarose gel (Pronadisa), stained with ethidium bromide; and then purified with UltraClean PCR Clean-up Kit (MoBio). Cleaned PCR products were sequenced at the DNA Sequencing Service of CIB, CSIC (Madrid, Spain).

5.2.4. Data analysis

Sequences were assembled with the program BioEdit, and aligned with ClustalX followed by ocular inspection. Gap penalties were optimized to 15 for gap opening and 0,3 for gap extension.

To check for possible contaminations, the Basic Local Alignment Search Tool (BLAST search, Altschul & al., 1990) was used to search our sequences in GenBank. As ITS are a powerful tool to infer phylogeny, but due to the presence of paralogs or pseudogenes the phylogenetic analyses may be distorted (Álvarez & Wendel, 2003; Mayol & Rosselló, 2001), once the possibility of having isolated alien sequences was discarded, we checked for the preserved regions of Liu & Schardl (1994) in ITS1 and Hershkowitz & Zimmer (1996) in ITS 2, to exclude possible pseudogenes from our analyses.

The molecular data sets were analysed using PAUP*4.0b10 (Swofford, 2000). Parsimony analyses of four data sets were performed (ITS, *psb*A-*trn*H, *trn*L-*trn*F, *psb*A-*trn*H+*trn*L-*trn*F). All characters were unweighted and gaps were coded with the simple method of Simmons & Ochoterena (2003), as implemented in the IndelCoder program version provided by the package SeqState 1.25 (Müller, 2005). For each data set, heuristic searches were conducted with 1000 random stepwise addition replicates, and tree bisection-reconnection (TBR) branch swapping holding and saving 10 trees per replicate. Bootstrap support analyses (Felsenstein, 1985) were performed running 100 replicates of random sequence addition, equal weighting and TBR branch-swapping.

Bayesian analyses (Huelsenbeck et al., 2001; Larget & Simon, 1999) were implemented in MrBayes 3.1 (Huelsenbeck & Ronquist, 2001). Hierarchical likelihood ratio tests conducted in Modeltest version 3.06 (Posada & Crandall, 1998, 2001) yielded the General Time-Reversible (GTR) model (Rodríguez et al., 1990) with gamma distribution as the sequence evolution model best fitting our datasets. Four simultaneous Markov chains were run for 1,000,000 generations, with tree sampling every 100 generations. The first 2000 trees were discarded as burnin, 50% majority-rule trees are shown in figures 3.1 and 3.3.

5.2.5. Chromosome counts

Immediately after excision, root tips were treated with a saturated solution of 8-quinolinol (Sigma-Aldrich) for 2 h at room temperature and Feulgen-stained as indicated below.

5.2.6. Genome size estimation

Seeds from available species were grown in Petri dishes and fresh root tips were excised and co-fixed with a standard (see table 3) in 3:1 methanol : acetic acid as indicated below. Nested ANOVA were carried out with the program NESTAN (Applied Biostatistics, Inc., 1991), considering variation at infraspecific and specific levels.

a) Feulgen Densitometry

For Feulgen staining (Feulgen & Voit, 1924), root tips of both sample and standard (*Pisum sativum* 'Kleine Rheinländerin', 2C = 8.84, Greilhuber & Ebert, 1994) were co-fixed in freshly prepared 3:1 methanol : acetic acid, transferred to 96° ethanol, and then stored at -20°C until use. Root tips were later hydrolytically depurinized in 5M HCl at 20°C for 60 minutes, then stained in Schiff´s reagent prepared from basic fuchsin (Fluka), as described in Greilhuber & Ebert (1994). Hydrolysis was stopped by thoroughly rinsing the root tips in distilled water. Samples were then stained with Schiff´s reagent over 1.5 h in the dark at room temperature. Afterwards samples were washed with SO_2 water (for 100 ml 0,50 g $K_2S_2O_5$ and 5 ml 1N HCl in 95 ml distilled water) and then squashed in 45% acetic acid. Squashed slides were disposed over a cold plate to remove coverslips, ethanol-dehydrated and air dried, then stored in the dark until measurement.

Nuclear 2C and 4C values were estimated using the software of image analysis CIRES (Cell Image Retrieval and Evaluation System 3.1, Kontron, Munich, Germany) following Greilhuber & Ebert (1994) and Greilhuber & Temsch (2001). Measurements of nuclei IOD (integrated optical density) were performed using a monochromatic green filter under a 63x oil immersion objective.

b) Flow Cytometry

For nuclei isolation, the protocols of Baranyi & Greilhuber (1996) and Temsch (2003) were followed. Up to 25 mg of leaf tissue from sample and standard (*Pisum sativum* 'Kleine Rheinländerin', 2C = 8.84, Greilhuber & Ebert, 1994; *Secale cereale*, 2C = 15.57, Doležel, 1998; *Zea mays*, 2C = 5.46, Doležel, 1998) were co-chopped in 1.1 ml citric acid isolation buffer (pH 1.5, Galbraith & *al.*, 1983). The nuclei suspension was filtered through a 30 μm nylon mesh (Sefar AG, Rüschlikon, Switzerland) to remove cell debris, and then incubated for 30 min at 37°C with RNAse A. Samples were stained with 4 ml propidium iodide (PI) solution (pH 9.5) for 1 h at 4°C in the dark, then immediately measured with a Cell Analyzer (CAII) Partec (Münster, Germany) flow cytometer. Samples were polysaccharide-rich, making measurements difficult in many cases.

For 2C nuclear DNA content estimation, three to five individuals per species were analyzed, performing 3-5 runs per individual together with the standards (see table 3). Additional runs with standard alone were performed to align the instrument. In each run 5000 cells were analyzed. The 2C-value of each sample was calculated using the position of peaks in relative fluorescence intensity histograms with the following ratio:

$$_{s}2C = {}_{s}G_1 \times ({}_{st}G_1)^{-1} \times {}_{st}2C$$

Where $_{s}2C$ = sample 2C-value, $_{s}G_1$ = sample G_1 mean peak, $_{st}G_1$ = standard G_1 mean peak and $_{st}2C$ = standard 2C-value. Peaks with coefficient of variation higher than 3.5 were discarded.

5.3. RESULTS

5.3.1. ITS data

The ITS1 preserved domain of Liu & Schardl (1994) was found to have the sequence GGCGCGAATYGCGTCAAGAA (Y = C, T). All the six conserved regions of Hershkowitz & Zimmer (1996) are present in ITS2, starting with c1, an 11 bp region with the sequence ATCGTYGCCCC. A variable region changing from C- to G-rich towards the 3´ end is followed by the second conserved region c2 (GGGCGGAAATTGGCCTCYCG). After 10 variable bp c3 (CGCTCRYGGTTGGCCTAAA) is found, followed by a variable 6-8 bp region and TCCTC. After a short AG rich region the preserved domains c4 (YGCCRCGACAATCGGTGGGA) and c5 (YTGTGCTCGT) appear. The last conserved and shortest region (c6, 6 bp) presents the sequence GACCCT.

Maximum parsimony (MP) analyses of 760 total characters, from which 648 were constant, 68 variable parsimony-uninformative and 44 parsimony-informative, yielded 6 most parsimonious trees with a length of 123, consistency index (CI) = 1,000, retention index (RI) = 1,000 and homoplasy index (HI) = 0,000. This ITS analysis yielded mostly unresolved trees, in which the linnean vision of *Alcea* as a separated and autonomous entity, not including any species of *Althaea* is strongly supported here. Perennial *Althaea* appear to be sister-group to the whole *Alcea*. Neither of Zohary´s species groups are supported by this ITS MP data analysis (figures 3.1, 3.3). Only *A. pallida* from the *Rosea* group is basal to the remaining species with high bootstrap support. The other taxon belonging to the *Rosea* group, *A. rosea*, appears at the top of the consensus tree in a derived, also highly-supported position. Most *Flavovirens* taxa are clustered together (BS) in a derived position, arising from a polytomy where most *Koelzi* species are also found. *Aucheri* taxa appear scattered through the cladogram, being *A. aucheri* sister to all taxa but *A. pallida*.

Bayesian topologies (fig. 3.1) are compatible and slightly better-resolved than the MP ones. Neither of Zohary´s species groups studied here are fully supported, all of them appearing to be polyphyletic. *A. pallida* is basal to the whole group, being *A. aucheri* the next most basal species. Most *Kurdica* taxa cluster together including *A. sulphurea* from group *Aucheri* and *A. tabrisiana* from *Flavovirens*. *Remotiflora* is sister to a big clade containing the remaining of *Flavovirens* species, group *Setosa* and *A. rosea*, from group *Rosea*.

5.3.2 Plastid data

The *psb*A-*trn*H parsimony analysis included 569 total characters, from which 541 were constant, 21 variable characters were parsimony-uninformative and 7 were parsimony-informative. MP analyses resulted in 2 most parsimonious trees (not shown), with a length of 30, CI = 0,8750, RI = 0,9000 and HI = 0,1250. The topology of the tree is largely unresolved, with all major clades arising from a single, basal politomy.

The *trn*L-*trn*F matrix included 447 total characters, 430 constant, 11 variable parsimony-uninformative and 6 parsimony-informative. MP analyses resulted in 1 most parsimonious tree (not shown), with a length of 17, CI = 1,000, RI = 1,000 and HI = 0,000. This analysis yielded almost totally unresolved trees.

To increase the number of parsimony-informative characters, both chloroplast matrices were merged including a total of 1017 characters, from which 972 were constant, 32 variable characters were parsimony-uninformative and 13 were parsimony-informative. The MP analyses resulted in a single most parsimonious tree (figures 3.3), with a length of 47, CI= 0,9286, RI = 0,9737 and HI = 0,0714. The topology of the combined *psb*A-*trn*H + *trn*L-*trn*F tree is better-resolved as compared with the single-marker trees, though large polytomies remain. The monophylly of *Alcea* sensu Linné is also strongly supported by these data. The taxa from the *Rosea* group appear basal to the remaining of the ingroup species, relation which is well-supported by bootstrap analysis. The *Aucheri* taxa appear embedded within a larger, unresolved clade including most *Flavovirens*. Groups *Kurdica* and *Setosa* appear scattered within *Flavovirens*, though these relationships are not highly-supported by bootstrap analysis.

Bayesian analyses yielded topologies compatible with MP ones (figure 3.3), but better resolved, as in the previous section. Extensive incongruence with ITS data occurs, with *Rosea* species monophyletic and basal to the remaining, and groups *Setosa* and *Kurdica* appearing interspersed among the *Flavovirens* taxa. The *Aucheri* group is monophyletic and derived within the big clade including most of *Flavovirens* taxa.

5.3.3. Character analysis

Our character analyses (figs. 3-5) support only partially the species groups established by Zohary (1963b, c). Leaf indumentum (figs. 4.2 and 4.4) is very variable, with a marked tendency to produce more or less depilated forms. Group *Aucheri*, monophyletic in the chloroplast data analysis, displays two indument types, leprose (autapomorphy of *A. aucheri*) and pannose, both restricted to it. The phlomoid type is found interspersed in the other groups, and also in the outgroups (*Althaea officinalis*).

Leaf sequence is also variable (figs. 1, 5.1 and 5.3), with the *sulphurea* type predominating in group *Aucheri* (although some sligthly heterophyllous forms are also found here), and the *flavovirens* type restricted to group *Flavovirens*, whose monophyly is not supported neither by chloroplast nor ITS data. The *kurdica* type is the most widespread of all appearing in all groups but *Aucheri*, some forms within group *Flavovirens* being also heterophyllous.

Proportions of calyx and epicalyx (figs. 2, 3.2 and 3.4), despite useful to diagnose species do not support any grouping, being the mesochitic type the most widespread.

Mericarp structure is more informative and though many reversals are inferred (specially regarding the distinction between plagionot-plagiopterous, sometimes difficult to assess in *A. kurdica*, or plagiopterous-orthopterous), the taxa from group *Aucheri* are plagionot, the other states being found elsewhere.

5.3.4. Genome size and Chromosome counts

Genome size estimation by flow cytometry was severely obstacled by the presence of high amounts of mucillage, which made often impossible the measurements. Mucopolysaccharides are released from the cells as they are co-chopped with the standard, pipetting becomes difficult and nuclei stick together with tissue aggregates.

Feulgen-stained and flow cytometry samples yielded very similar measurements. No statistically significative variation among samples or species was found, with 2C-values measured narrowly oscillating around 2.5 pg. For further details see table 3. Chromosome counts yielded equally no variation, with all species for which it was studied sharing 2n = 6x = 42.

5.4. DISCUSSION

5.4.1. The problem of generic delimitation: *Alcea* vs. *Althaea*

Despite being clearly distinguishable genera, *Alcea* and *Althaea* have been merged up within an extended genus *Althaea* for almost 150 years. This trend started with the work of Willdenow (1800), and was continued by De Candolle (1824), Bentham and Hooker (1862) and Baker (1890). Although many authors have claimed for the maintenance of both genera as originally set by Linnaeus in 1753 (Alefeld 1862; Boissier, 1867), this tradition was only broken in relatively recent times by the Russian Iljin (1949), and continued by Zohary (1963a, b) and Riedl (1976). These three authors coincide in the fact that *Alcea* is clearly distinguishable from *Althaea* in several morphological traits. The flowers of *Alcea* display a staminal column of pentagonal section and are rarely smaller than 30 mm, contrasting with the small, relatively unconspicuous flowers of *Althaea*, which present a staminal column of circular section. Carpologically, the differences are even more striking, with all *Alcea* showing an internal expansion of the pericarp surface, the endoglossa, which divides incompletely the mericarp into an upper, sterile chamber and a lower, one-seeded chamber. Mericarps are always clearly unilocular in *Althaea*.

While *Alcea* is a clearly-defined and morphologically easily diagnosable genus, the opposite is true for *Althaea*. Within this genus it is possible to distinguish two species groups: sect. *Althaea*, comprising tall perennial herbs with relatively small epicalyces and smooth (at least in the center) mericarp surfaces. The other, sect. *Hirsutae*, with annual species of strongly acrescent epicalyces and transversely sulcate mericarps (Escobar & al., 2004). An overall morphological view, excluding the number of pieces of the epicalyx (the character used by Linné to split the *Malva*-alliance), suggests a closer relationship among these annual *Althaea* and some *Malva* species rather than with the perennial *Althaea*, as it has been marked out by some authors (Alefeld, 1862; Krebs, 1998a, b). Recent DNA data (Escobar & al., 2007a) agree with this point and confirm the polyphyly of genus *Althaea*. The perennial sect. *Althaea* is sister group to *Alcea*, while the annual representatives of sect.

Hirsutae appear to be more related with *Malva cretica* and the nothogenus *Malvalthaea* from Caucasus and Iran, which presents not only the same mericarp structure as the annual sect. *Hirsutae* and this *Malva* species, but also an unique three to five-lobed epicalyx.

5.4.2. The infrageneric classification of *Alcea*

Boissier (1867) first proposed an infrageneric classification for the genus *Alcea* into two sections: *Apterocarpae* and *Pterocarpae*. Members of sect. *Pterocarpae* are characterized by their canaliculate mericarp backs, expanded into well-defined, membranaceous wings. The *Apterocarpae* show canaliculate to flat backs lacking any wing-like expansion. But some species are so polymorphic that produce winged or almost unwinged mericarps, as it is the case of *A. kurdica*, in which the canaliculate back of the carpel may be expanded to certain degree forming a wing.

The presence-absence of wing, as the degree of wing expansion, seems to be a character of undiscusable diagnostic importance, though intermediate forms between winged and wingless sometimes appear. The ancestral state is probably the planocot carpel, as it is the form found in perennial *Althaea* and most related genera within Malveae. But early diverging lineages, as *A. pallida*, show already plagiopterous carpels. There seems to exist a trend towards wing development and orthopterous mericarps both within *Kurdica* and *Flavovirens* groups (as shown in figures 3.2, 3.4), with punctual reversals to plagiopterous carpels; while carpel wings could have been lost from twice up to four times.

The problem of establishing generic and infrageneric boundaries is not limited to *Alcea* or *Althaea* within Malvaceae. Some genera are recognized as artificial constructs since long ago and need urgent revision. This is the case not only of *Althaea*, but also of *Malva* and *Sida*, traditionally a jumble where schizocarpic Malvaceae with and without epicalyx, respectively, have been traditionally placed (Fryxell, 1997). As a result, large numbers of non-directly related species have accumulated until relatively recent times. In other cases, like in *Hibiscus*, the lack of characters makes classification attempts difficultwithout independent molecular data. As a result, large numbers of plesiotypic species accumulate within these residual genera while groups characterized by autapomorphies (*Abelmoschus*, *Fioria*) are arbitrarily segregated (Pfeil & al., 2002).

5.4.3. The problem of phenotypic plasticity

When dealing with *Alcea* most authors agree in the fact that it is a very difficult genus, even "the most unsatisfactory piece of work that he [the author] has ever done...", in words of Townsend (1980). Most taxonomic problems affecting *Alcea* arise from two basic characteristics of the genus: low number of discriminating characters and phenotypic plasticity.

The first problem to face when identifying an *Alcea* specimen is the low number of discriminating characters. Actually, only four or five characters are useful and even when dealing with clearly distinct species it is difficult to clearly split them, as diagnostic characters vary following continuous clines among closely related species.

All characters of taxonomical importance show quantitative extensive variation. Leaf indumentum (figs. 4.2, 4.4) is only stable in *A. aucheri*, because it is the only species presenting scaly trichomes. For all the remaining, even in cases such as *A. sulphurea* or *A. rhyticarpa*, of pannose indumentum concealing the leaf nerves, there are depilated foms that confound species delimitation, moreover when many herbarium vouchers lack ripe fruits. *A. sulphurea* is quite a characteristic taxon, but in the Western Iraqui Desert a clinal trend to glabrescence appears, so that some specimens are undistinguishable from *A. rufescens* (Townsend, 1980). Another example is the case of *A. kurdica* (*Kurdica* group), so variable that may be even undistinguishable from species like *A. hohenackeri* (*Hohenackeri* group, not studied here), *A. mosulensis* or *A. tholozanii*.

Another diagnostic character of big importance is stem indumentum, which can be homogeneousy composed of tiny stellate trichomes in some species (as in *A. galilaea* or *A. rufescens*) or heterogeneous in most of them. Many floras rely heavily on this character in their keys, but with severe pitfalls. Large variability is found not only among individuals of the same species, but also within a single individual along its life. Actually, some species present a tendency to depilate with aging. Moreover, there is a general, independet trend in different species to glabrescence, to the production of individuals much less pilose than their conspecifics. This has gaven rise to the establishment of binomials such as *A. glabrata* or *A. aegyptiaca*.

Leaf division (fig. 1) and leaf sequence (figs. 1, 5.1, 5.3) are also valuable as diagnosing characters. Some species are almost homophyllous, like *A. aucheri* or *A. sulphurea*, but most plants present clear differences among leaf size, degree of incision and lobe shape depending on their position on the stem. The most common type is that showing progressively lobed leaves upwards to the stem apex, as in *A. kurdica*, *A. setosa* or *A. dissecta*. It is also common that all the leaves are palmatifid to palmatipartite, very characteristic within group *Flavovirens* (as in *A. flavovirens* or *A. sachsachanica*). This character can also be tricky, as it has been used to heavily split some species groups (as *Flavovirens*), and whose constance is certainly not very reliable (Mouterde, 1966).

Relative length of calyx and epicalyx is a relatively constant character (figs. 5.2 and 5.4), but of interest only as diagnostic for some species. Most taxa display meso or macrochitic epicalyces, only in few occasions it is clearly microchitic (as in *A. wilhelminae*).

Mericarp shape (figs. 2, 3.2 and 3.4) is also of paramount importance and it may be impossible to distinguish some specific forms from clearly different species if the individuals lack ripe fruits. Nevertheless some intermediate individuals appear, as in the *A. kurdica* complex, being sometimes difficult to discriminate between plagionot and plagiopterous mericarps, or also between plagiopterous and orthopterous mericarps. Some intrageneric classifications rely heavily on this character (as Boissier's, 1867), but our data do not support a split among pterocarpous and apterocarpous taxa. Only the planocot group *Aucheri* is supported by chloroplast, not by ITS data (fig. 3).

The taxonomy of *Alcea* is very difficult, not only because of the preceding, but because of the fact that some binomials are based on fruitless vouchers. In this cases, specialist tend to do a "reasonable" assessment matching them to fruited forms, and proceed with the taxonomic process. But to which extent is this practice reasonable in a group where sibling forms between pterocarpous and apterocarpous taxa are not uncommon? Moreover, most herbarium vouchers are incomplete, normally being composed of some upper leaves and a piece of the inflorescence. The result is that most material is misidentified. The fact that flowers of some taxa change colour when drying does certainly not help identification.

5.4.4. Zohary´s morphological groups and character distribution

As the infrageneric classification of Boissier (1867) seemed untenable, Zohary (1963b, c) proposed an informal, rankless classification into what he considered to be "natural groups". He distinguished up to nine of these groups that were characterized upon the basis of four main morphological characters: mericarp structure and ornamentation, epicalyx-calyx relative length, leaf division sequence and nature of indumentum.

The first of these groups presented by Zohary is the *Aucheri* group, which includes *A. aucheri*, *A. sulphurea* and *A. rhyticarpa*, all apterocarpous, of pannose indumentum and almost entire leaves. Despite such a good morphological diagnosis, Zohary himself believed that this group was not a natural entity. Our results are ambiguous at this point, as there is no agreement between the chloroplast and ITS phylogeny, suggesting extensive hybridisation. According to chloroplast data, these three species would be closely related, occupying a derived position nested within the big clade comprising most *Flavovirens* group. But ITS data suggest a very different scenario, in which *A. aucheri* is a basal species, sister to all remaining *Alcea* (but *A. pallida*). ITS sequences of *A. sulphurea* appear to be closely related to these included in the *Kurdica* group.

The *Rosea* group is here represented by *A. rosea* and *A. pallida*. It is the most widespread group as both species, along with their hybrids have been used as ornamental garden plants for centuries. It has been considered an old-diverging lineage which gave rise to most of the genus. According to our data, the *Rosea* group would be the oldest lineage recognisable within *Alcea*. In both chloroplast and ITS datasets *A. pallida* appears to be sister taxon of all the remaining studied species, with *A. rosea* splitting apart in the ITS dataset to appear in the most derived position, linked to group *Striata*, and embedded within the taxa of group *Flavovirens*.

It is litte what we can say about group *Remotiflora*, as it was possible only to gather ITS data. The representative studied here, *A. gorganica*, appears basal to the clade including most of *Flavovirens* taxa. It is characterized by its plagionot mericarps, apterous carpels of sulcated back, contrasting with *Flavovirens*, most of whose species display well developed wings (orthopterous) or wing-like carpel lateral expansions (plagiopterous).

The *Setosa* group, represented here by *A. setosa*, presents also a different position depending on which dataset is considered. ITS data place the species deeply embedded within the tree, as sister taxon of *A. rosea* (*Rosea* group). Plastid data suggest that it is a more plesiotypic species, related to *A. rechingeri* from the *Kurdica* group.

Probably the most morphologically variable group is the *Kurdica* group, which includes the here represented *A. arbelensis*, *A. kurdica*, *A. rechingeri*, and *A. shirazana*. Our plastid data show the species of this group appearing scattered among these of group *Flavovirens*. Contrastingly, in the ITS phylogeny all but *A. arbelensis* cluster together to form a group which is sister to the clade containing *A. gorganica*, most of *Flavovirens*, *Setosa* and *A. rosea*;

including also the morphologically very diverging *A. sulphurea* (*Aucheri* group) and *A. tabrisiana*.

Flavovirens is the most diverse group comprises some very characteristic species, the fig-tree-leaved (after *A. ficifolia*) hollyhocks, typically with orthopterous to plagiopterous mericarps and sparse indumentum. This group has been heavily splitted by different authors, mainly Iljin (1949) and Riedl (1976). The species of this group appear clustered together in both ITS and chloroplast trees, but several taxa from other groups appear scattered among them, particularly the *Kurdica* species, and specially in the chloroplast phylogeny. As these species are homoploids sharing in most cases weedy habitats, hybridisation is likely to occur and could be the cause of extensive dataset incongruency.

5.4.5. Extensive hybridisation

Hybridisation is an important phenomenon in plant evolution (Grant, 1981), with reticulation playing a key role in the complexity of evolutionary patterns that are observed in nature (Rieseberg, 1997; Doyle & *al.*, 2003). Most examples of species with documented hybrid origin are allopolyploids (Ferguson & Sang, 2001). In this case, reproductive isolatiom from parental species is guaranteed by the difference in ploidy level. There are not so many examples of homoploid hybrid speciation, maybe due to the fact that reproductive isolation from parental species is not so easily reached in conditions of same ploidy level and sympatry (Buerkle & Rieseberg, 2000). Most examples of plant homoploid hybrid speciation occur at the diploid level (Rieseberg, 1997; Nieto Feliner, 2001), but there are also cases of homoploid polyploid hybrid speciation, as in *Gillia* (Grant, 1966) and *Paeonia* (Ferguson & Sang, 2001).

All *Alcea* taxa known to us share 2n = 6x = 46, whith no statistically significative DNA amount difference whenever these were studied, indicating not only homoploidy but similar genome structure, regardles of Zohary's species group (Zohary, 1963b, c). In some cases it is known that genome size may determine species compatibility among taxa belonging to the same genus which share chomosome numbers. It seems therefore very likely that most *Alcea* participate of regional hybrid swarms, where specific borders are blurred due to the widespread occurence of intermediate individuals. Moreover, all *Alcea* species are showy outbreeders flowering in late spring or early summer, with most species being related to open habitats, such as forest clearings and mainly weedy man-disturbed areas. Many of them are also cultivated for the beauty of their flowers and consequently some of the plants appearing in the nature are escapees of probable hybrid origin.

The most extended consequence of hybridisation is phylogenetic incongruence among independent data sets (Linder & Rieseberg, 2004), with the impossibility of *a priori* predictable hybrid phylogenetic patterns. Nevertheless, in particular cases it is possible to infer the position of hybrid taxa (Nieto & al., 2001). For instance, McDade (1992) studying the *Aphelandra pulcherrima* complex, found that hybrids were placed as a basal lineage of the most derived progenitor. Atchley and Fitch (1991, 1993), found in mice a tendency of hybrid strains to appear always close to one of the parentals. But if an analysis includes hybrid taxa, methods yielding branching phylogenetic patterns will always fail to infer the real phylogeny, no matter where hybrids are placed (Xu, 2000). nrDNA ITS, and the chloroplast markers *trn*L-*trn*F and *psb*A-*trn*H show very low levels of variation in our specific sampling. The number of parsimony-informative characters is much lower in the *Alcea* ITS data matrix than in the most closely-related groups (both perennial and annual *Althaea*, *Lavatera*, *Malva* and *Malope*, Escobar & al., 2007b). This is particularly critical regarding the chloroplast markers, where only 13 parsimony-informative characters out of a total of 1017 were found. This extensive lack of variation may be indicative not only of common reproductive dynamics within regional hybrid swarms, but can also be related with a relative young age of the whole genus. The plesiotypic position of *A. pallida*, and at least in chloroplast data the basal position of the whole *Rosea* group, could have interesting biogeographical consequences, placing the center of origin of the genus in the Aegean-East Mediterranean, to later colonize desert and semidesert areas as these formed in the beginning of Holocene. Other *Alcea* hotspots, as the Euxino-Hyrcanian region, the Zabros mountains and Central Asia-Afghanistan would consist of more recent colonization events.

As conclusive remarks, both plastid and ITS datasets are also highly incongruent. Some well supported points by both of them are, as has already been pointed out, the monophyly of *Alcea* with respect to *Althaea*, the position of perennial *Althaea* as sister group to *Alcea*, and the plesiotypic position of the East Mediterranean *A. pallida* within the genus. Only the *Flavovirens* group, including the fig-leaved hollyhocks, receives support from our data, and not completely. The *Rosea* group is supported only by chloroplast markers, as it is the case of the *Aucheri* group. Contrastingly, the *Kurdica* group receives support only from ITS data, and not for the whole of the species included. For the other groups, our species sampling was too reduced to make any conclusive filiation remark.

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Table 1. Material studied. **I**, ITS GenBank accession number; **P**, psbA-trnH GenBank accession number; **T**, trnL-trnF GenBank accession number.

Taxon	Voucher	I	P	T	Procedence
Alcea arbelensis	PE624	EF679716	-	-	Iran: Chahrmahal.
Alcea aucheri	PE617	EF679717	EF679735	EF679754	Iran: Shiraz.
Alcea excubita	PE417	EF679718	EF679736	EF679755	Iran: Tehran.
Alcea flavovirens	PE625	EF679719	-	-	Iran: Tehran.
Alcea glabrata	PE607	EF679721	-	-	Iran: Tehran.
Alcea gorganica	PE611	EF679720	-	-	Iran: Golestan Natural Park.
Alcea koelzi	PE609	EF679722	EF679737	EF679756	Iran: between Arak and Salafehegan.
Alcea kurdica	PE619	EF679723	EF679738	EF679757	Iran: Kermanshah.
Alcea longipedicellata	PE612	EF679724	EF679739	EF679758	Iran: Loshan.
Alcea pallida	PE140	EF679715	EF679740	EF679759	Turkey: Aydin.
Alcea rechingeri	PE621	EF679725	EF679741	EF679760	Iran: Estahbanat.
Alcea rhyticarpa	PE618	-	EF679742	EF679761	Iran: Khorassan.
Alcea rosea	PE422	EF679714	EF679744	EF679762	Spain: Madrid.
Alcea rugosa	PE420	-	EF679743	EF679763	Iran: Tehran.
Alcea sachsachanica	PE620	EF679726	EF679745	EF679764	Iran: Azerb.
Alcea setosa	PE424	EF679727	EF679746	EF679765	Iran: Shiraz.
Alcea shirazana	PE618	EF679728	EF679747	EF679766	Iran: Estahbanat.
Alcea sulphurea	PE610	EF679729	EF679748	EF679767	Iran: Tehran.
Alcea tabrisiana	PE613	EF679730	EF679749	EF679768	Azerbaijan: Ghotur.

Alcea wilhelminae	PE627	EF679731	EF679750	EF679769	Iran: Gilan.
Althaea armeniaca	PE427	EF679734	EF679753	EF679771	Ukraine: Danube Delta (Index Seminum).
Althaea officinalis	PE512	EF679733	EF679752	EF679770	Spain: Madrid.
Malope trifida	PE601	EF679732	EF679751	EF679772	Morocco: Khenichet.

Table 2. Main taxa from genus *Alcea* L. **Group**, Zohary´s rankless groups (Zohary 1963b, c). **Leaf ind.**, type of leaf indumentum. **Leaf div.**, type of leaf division sequence. **Epic.**, type of epicalyx. **Meric.**, mericarp configuration. For details see text.

Taxon	Group	Leaf Ind.	Leaf div.	Epic.	Meric.
Alcea angulata	*Aucheri*	Pannose	Sulphurea	Macrochitic	Planocot
Alcea arbelensis	*Kurdica*	Green pilose	Kurdica	Macrochitic	Plagiopterous
Alcea aucheri	*Aucheri*	Scurfy	Sulphurea	Macrochitic	Planocot
Alcea excubita	*Flavovirens*	Green pilose	Flavovirens	Mesochitic	Orthopterous
Alcea flavovirens	*Flavovirens*	Green pilose	Flavovirens	Mesochitic	Orthopterous
Alcea glabrata	*Flavovirens*	Green pilose	Flavovirens	Mesochitic	Plagiopterous
Alcea gorganica	*Remotiflora*	Green pilose	Kurdica	Macrochitic	Plagionot
Alcea koelzi	*Flavovirens*	Green pilose	Flavovirens	Macrochitic	Orthopterous
Alcea kurdica	*Kurdica*	Green pilose	Kurdica	Mesochitic	Orthopterous
Alcea longipedicellata	*Flavovirens*	Phlomoid	Flavovirens	Mesochitic	Orthopterous
Alcea nudiflora	*Hohenackeri*	Green pilose	Rufescens	Macrochitic	Plagiopterous
Alcea pallida	*Rosea*	Phlomoid	Rufescens	Macrochitic	Plagiopterous

Alcea rechingeri	*Kurdica*	Green pilose	Kurdica	Macrochitic	Plagiopterous
Alcea rhyticarpa	*Aucheri*	Pannose	Sulphurea	Mesochitic	Planocot
Alcea rosea	*Rosea*	Green pilose	Kurdica	Macrochitic	Plagiopterous
Alcea rugosa	*Flavovirens*	Phlomoid	Flavovirens	Mesochitic	Orthopterous
Alcea sachsachanica	*Flavovirens*	Green pilose	Flavovirens	Mesochitic	Orthopterous
Alcea shirazana	*Kurdica*	Green pilose	Kurdica	Mesochitic	Orthopterous
Alcea setosa	*Setosa*	Green pilose	Rufescens	Macrochitic	Planocot
Alcea sulphurea	*Aucheri*	Pannose	Sulphurea	Macrochitic	Planocot
Alcea tabrisiana	*Flavovirens*	Green pilose	Flavovirens	Mesochitic	Orthopterous
Alcea tiliacea	*Hohenackeri*	Pannose	Sulphurea	Macrochitic	Plagiopterous
Alcea wilhelminae	*Flavovirens*	Green pilose	Flavovirens	Microchitic	Orthopterous

Table 3. Mean 2C-values measured with flow cytometry (regular font) or Feulgen (bold). The standard used was *Pisum sativum* ' Kleine Rheinländerin'.

Taxon	**Voucher**	**2n**	**Ploidy**	**2*C***
Alcea arbelensis	PE624	42	6x	**2.320**
Alcea aucheri	PE617	42	6x	2.450
Alcea excubita	PE417	42	6x	**2.495**
Alcea flavovirens	PE625	42	6x	2.524
Alcea glabrata	PE607	42	6x	2.758

Alcea gorganica	PE611	42	6x	2.528
Alcea koelzi	PE609	42	6x	2.565
Alcea kurdica	PE619	42	6x	2.505
Alcea longipedicellata	PE612	42	6x	**2.491**
Alcea pallida	PE140	42	6x	2.673
Alcea rechingeri	PE621	42	6x	2.388
Alcea rhyticarpa	PE618	42	6x	2.675
Alcea rosea	PE422	42	6x	2.512
Alcea rugosa	PE420	42	6x	**2.295**
Alcea sachsachanica	PE620	42	6x	**2.523**
Alcea setosa	PE424	42	6x	2.667
Alcea shirazana	PE618	42	6x	2.446
Alcea sulcata	PE610	42	6x	**2.527**
Alcea tabrisiana	PE613	42	6x	2.604
Alcea wilhelminae	PE627	42	6x	2.595
Althaea armeniaca	PE427	84	12	6.806
Althaea officinalis	PE512	42	6x	3.652
Malope trifida	PE601	44	6x	**1.861**

6. LOW COPY NUCLEAR MARKER *CES*A1B REVEALS PREVIOUSLY UNSUSPECTED PHYLOGENETIC RELATIONSHIPS WITHIN THE *MALVA* ALLIANCE (MALVACEAE).

6.1. INTRODUCTION

The genera *Malva*, *Lavatera*, *Althaea* and *Alcea* integrate a well-defined morphological group that receives the name of *Malva* alliance (Bates 1968; Bayer and Kubitzki 2003). *Malope* is directly related to *Malva* and *Lavatera* (Escobar et al. 2007a, Fuertes et al. 2002; Tate et al. 2005), while *Kitaibela* appears to be closer to *Alcea* and the perennial *Althaea* species. The *Malva* alliance comprises perennial herbs, evergreen shrubs and annuals mainly of Mediterranean distribution, which extend northwards to Atlantic Europe and eastwards to South-Western Asia, with main centres of diversity in the Western Mediterranean Basin and the Middle East. Nevertheless, some species occur in areas remote to the preceding such as the Californian Channel Islands (*Lavatera assurgentiflora* aggregate), Australia (*L. plebeia*) and the highlands of Ethiopia (*L. abyssinica*). Of the genera involved *Alcea* is the most diverse (about 60 species, Pakravan 2001; Riedl 1976; Zohary 1963a, b; Escobar et al. 2007c), followed by *Lavatera* (about 20 species, Fernandes 1968a, b), and *Malva* (with the widest geographical range and about 12 species, Dalby 1968). Minor groups are *Althaea* (5-6 species, Tutin 1968), *Malope* (2-3 species, Webb 1968; Cullen 1966), *Kitaibela* as well as the genus *Malvalthaea* (1-2 spp, Iljin 1974; Riedl 1976).

Lavatera and *Malva* have posed a challenge to plant systematists since the times of Linnaeus, who established the classical generic limits focusing on the nature of the epicalyx: three fused bracts in *Lavatera* and two or three free ones for *Malva*. Despite extensive criticism already since Medikus (1787), this generic definition is still present in most modern floras. Two factors account for the general reluctance of most workers to accept an alternative taxonomic framework instead of the classical one. First, these alternative taxonomical approaches are often incompatible among themselves, dissuading many authors of generic syntheses of taking into consideration new proposals in the lack of independent data. Second, acritical acceptance of previous work done by authorities (Linné 1753, 1789, Baker 1890-1894) has led to a high degree of conservativeness in taxonomy. Several modern reviewers have already provided evidence on the subject (*Lavatera* by Fernandes, 1968a, b; *Althaea* by Krebs 1994 a, b), but it was not until relatively recent when molecular data were gathered by Ray (1995), in a paper showing that *Lavatera* and *Malva* as currently defined are artificial genera. Later, Escobar et al. (2007a, b) further explored this approach with an extended sampling and new markers showing that also *Althaea* was arbitrarily delimited.

Despite previous molecular work (Ray 1995, Fuertes et al. 2002, Tate et al. 2005, Escobar et al. 2007a, b) the relationships among the genera, as well as their limits – in particular regarding the lavateroid *Lavatera* – remain obscure. The lavateroid species (Ray 1995) have rapidly diversified and as a result, tree branches provided by different studied markers (ITS, *psb*A-*trn*H, *trn*L-*trn*F) are short at critical points (see Escobar & al. 2007a). This is one of the reasons why phylogenetic analyses often fail to recover the same phylogenies yielding polytomies where branching order cannot be reliably inferred. Accordingly resampling methods (bootstrap, jackknife) tend to produce low scores for these branches.

Interspecific relationships are further complicated by the presence of extensive polyploidy and hybridisation. All the taxa included in this study (except the diploid *Lavatera trimestris* and the tetraploids *Malva hispanica* and *Althaea longiflora*) are at least hexaploids with 2n = 42, 44, while some dodecaploids or even 16-ploids are also present (see figure 6). Hybrid speciation is inferred to have occurred at least three times: once in the *Malvalthaea* lineage and two more times within the malvoid group, affecting *L. mauritanica* and probably also the *L. assurgentiflora* aggregate (discussed in Escobar et al. 2007a). The hexaploid annual mallows are also reported to hybridise commonly (Nogueira et al. 1993, Sennen 1932), with some intermediate forms being relatively common in the wild.

In previous work with ITS and the chloroplast spacers *psb*A-*trn*H and *trn*L-*trn*F (Escobar et al. 2007a), the authors found extensive incongruence among the phylogenetic trees inferred from nuclear and chloroplast datasets. The very nature of ITS, subjected to concerted evolution, and the uniparental inheritance of chloroplast genome are *per se* a source of potential incongruence between the two markers. Chloroplast markers fall within a single linkage group and are therefore expected to yield a unique topology, whereas ITS, often subjected to concerted evolution, may or may not reflect the same history. Low copy nuclear genes (LCNG) may agree with either ITS or chloroplast, with both of them, or with none. In our case, the extensive and often high levels of polyploidy (up to 16x in *Lavatera cretica*), along with the occurence of hybridisation, pose additional challenges.

An appropriate approach to solve these problems is the comparison of multiple unlinked genes (Wendel and Doyle 1998). LCNG provide nowadays a wealth of independent evidence due to the recent accessibility to many genes provided by genome sequencing projects. Among the benefits of low-copy markers use in plant systematics (reviewed in Sang 2002, Small 2004, Schlüter et al. 2005) it is possible to mention the higher rate of sequence evolution relative to chloroplast genome (Gaut, 1998), which means a greater efficiency of sequencing effort. In addition, rates of evolution are variable within the same marker, with different regions evolving at different paces. Exons are likely to be conserved at first and second positions, with third positions diverging usually at similar rates than non-coding regions (Small 2004). This may be very useful in phylogenies below the familial level, due to the fact that the same marker provides information at several categories. But what makes low-copy markers especially suitable for plant phylogeny reconstruction is that they are typically biparentally inherited. This is a notable advantage over chloroplast markers, and one of the reasons of low-copy use in systematics sky-rocketing in recent times.

Despite all these desirable properties, low-copy markers also present a series of drawbacks which can be limiting. The first concern is related to their complex architecture, normally in gene families with different copies related by gene duplication, which can make orthology assesment challenging (Thornton 2000, Waters 1995). The dynamic nature of plant nuclear genome makes the assessment of orthology a lineage-specific issue, with the same marker being single-copy in some species, and a swarm of mutiple copies in others (Hughes et al. 2005).

In our case, we decided to sequence the first five exons of the cellulose synthase 1b gene (*ces*A1b) and their four spanning introns, based on the encouraging results obtained by Cronn et al. (2002) and Álvarez et al. (2005, and personal communication). The marker was inferred by the preceding authors to be single copy in diploid *Gossypium*, a fact that together with the high level of informative positions appeared promising to us. The *ces*A1b gene has been studied in a number of plants and bacteria (Doblin et al. 2000, Pear et al. 1996, Ranik et Myburg 2005, Ruotolo et al. 2006, Tiang et al. 2005, Wendel et al. 2001 among others), being part of a reduced gene family with two different members present in *Gossypium* (Cronn et al. 2002).

This paper aims to test the sequence diversity and phylogenetic utility of the low-copy *ces*A1b nuclear marker, comparing its phylogenetical signal to a molecular data set potentially subjected to concerted evolution (ITS), and to a maternally inherited chloroplast data set, with both coding (*mat*K and *ndh*F) and noncoding regions (*psb*A-*trn*H, *trn*L-*trn*F), with the ultimate expectation of clarifying the complex relationships that arise in the phylogenetic study of the *Malva* alliance.

6.2. MATERIAL AND METHODS

6.2.1 Sampling

Forty-three representatives of the *Malva* alliance have been studied (2 *Alcea*, 6 *Althaea*, 1 *Kitaibela*, 19 *Lavatera*, 2 *Malope*, 12 *Malva*, 1 *Malvalthaea*, see table 1). *Anisodontea capensis*, *Malvella sherardiana* and *Gossypium turneri* were chosen as outgroup species based on results of previous work (Fuertes et al. 2002; Tate et al. 2005, Álvarez et al. 2005). A total of 431 sequences (44 *mat*K, 43 *ndh*F, 344 *ces*A1b) belonging to 46 species have been generated and analysed along with 348 sequences (121 ITS, 115 *psb*A-*trn*H, 112 *trn*L-*trn*F) that came from previous work (Escobar et al. 2007a), building up a total of 779 sequences spanning 6767 base pairs (see appendix 1).

Samples came from field collections in the Mediterranean area (Spain, Portugal, Morocco, France, Italy), living material grown by the authors in experimental greenhouses at the Real Jardín Botánico, Madrid, and Botanischer Garten der Universität Wien (Vienna, Austria), or herbaria specimens. For some species, material from *index seminum* was cultivated and only included into the analyses when securely identified. Vouchers of all specimens used were deposited at the herbarium MA (Real Jardín Botánico, Madrid). For a complete list see appendix 1. All DNA sequences are available at GenBank (http://www.ncbi.nlm.nih.gov, accession numbers EF419430 to EF419769, and EF689380 to EF689725).

In the following text, generic abbreviations are as follows: *Althaea* = *A.*, *Kitaibela* = *K.*, *Lavatera* = *L.*, *Malva* = *M.*; *Alcea*, *Malvella*, *Malope* and *Malvalthaea* are never abbreviated. For the names of main clades we follow Ray (1995) and previous work presented by the authors (Escobar et al. 2007a).

6.2.2. DNA isolation, PCR and sequencing

Details concerning the ITS, *psb*A-*trn*H and *trn*L-*trn*F regions are provided in Escobar et al. (2007a). *mat*K and the surrounding regions of the *trn*K intron were amplified and sequenced with a set of primers designed using a *Lavatera acerifolia* sequence from Nyffeler et al. (2005) downloaded from GenBank (http://www.ncbi.nlm.nih.gov). For *ndh*F, primers were designed using a *Malva neglecta* sequence from Pfeil. et al. (2002). For amplification and sequencing of *ces*A1b the primers *ces*AF and *ces*AR of Cronn et al. (2002) and Álvarez et al. (2005) were used. Details are given in figure 1.

DNA isolation was performed using liquid nitrogen, fresh young leaf tissue following the CTAB (cetyltrimethyl ammonium bromide) protocol of Doyle and Doyle (1987), with additional wash steps using a sorbitol buffer (Tel-Zur et al. 1999; M. Barfuss, personal communication), which allowed eliminating copious polysaccharide amounts present in most members of the Malvaceae family. Total DNA was checked in 1.5 % agarose gels to test amount and quality of extracts.

50 µl PCR reactions containing ReddyMix PCR MasterMix, (Advanced Biotechnologies), 1 µl 1:10 dilluted DNA and 0.5 µl of 10µM primers were run in GeneAmp PCR System 9700 (PE Applied Biosystems) and MJ Research PTC 200 (Peltier) thermocyclers. PCR conditions are as in Escobar et al. (2007a) and Cronn et al. (2002). Ethidium bromide-stained gels were checked on 1,5% D-1, low EEO agarose gel and purified with UltraClean PCR Clean-up Kit (MoBio).

As direct sequencing of *ces*A1b was impossible due to sequence polymorphism, extensive clonig with TOPO TA cloning kit (Invitrogen) was performed following manufacturer´s recommendations. Screening via colony-PCR was performed, picking up recombinant colonies and suspending them in 50 µl distilled water, vortexing and heat-shocking for 5 min at 95ºC. Then, further amplification and sequencing were performed with the same primers as above. Usually 10-15 clones per species were sequenced, but in cases of higher polymorphism we increased these figures sequencing up to 20 clones. This number seems to be enough due to the fact that sequence polymorphism was not directly related with ploidy level, with both high and low levels of sequence variations among the hexaploid and dodecaploid taxa.

Cycle sequencing with ABI PRISM BigDye Terminator kit, (Applied Biosystems) of *mat*K, *ndh*F and cloned *ces*A1b was carried out at the Faculty

Center Botany (University of Vienna). Sequencing was performed using an 3130x Genetic Analyzer (Applied Biosystems).

6.2.3. Data analysis

Eleven molecular data sets were analysed: ITS, chloroplast non-coding *psb*A-*trn*H and *trn*L-*trn*F, chloroplast coding *mat*K and *ndh*F, nuclear low-copy *ces*A1b paralogs 1, 2 and 3. In addition, combined data sets with all non-coding chloroplast markers, all coding chloroplast markers, and all chloroplast sequences combined were also studied. Sequences were assembled with the program BioEdit version 7.0.5.2 (Hall 1999), and aligned with ClustalX (Thompson et al. 1997) followed by visual inspection.

To detect the potential presence of PCR-mediated recombinant chimaeras, the software RDP V 2.0 (Martin et. al., 2005) was used implementing the RDP, GENECONV, MaxChi and Chimaera algorithms with default parameters, following the program authors´ reccomendations.

Hierarchical likelihood ratio tests conducted in Modeltest version 3.06 (Posada and Crandall 1998, 2001) indicated the General Time-Reversible (GTR) model (Rodríguez et al. 1990) with gamma distribution as the sequence evolution model best fitting our datasets.

Parsimony analyses with PAUP*4.0b10 (Swofford 2000) of the eleven data sets were performed. All characters were unweighted in non-coding regions. Coding regions were analysed with third position downweighted. Gaps were coded with the simple method of Simmons and Ochoterena (2003), as implemented in IndelCoder provided by the software SeqState 1.25 (Müller 2005). For each data set, heuristic searches were conducted with 1000 random stepwise addition replicates, and tree bisection-reconnection (TBR) branch swapping holding and saving 10 trees per replicate.

Bayesian analyses (Huelsenbeck et al. 2001; Larget and Simon 1999) were conducted in MrBayes 3.1 (Huelsenbeck and Ronquist 2001). Partitions with third codon positions downweighted were included where coding regions were present, gaps were treated as missing data. Four simultaneous Markov chains were run for 1,000,000 generations, in all cases more than enough to allow for stabilization of likelihoods, as stationarity was normally reached around generation 100,000. Tree sampling every 100 generations was performed. The first 2500 trees (25%) were discarded as burnin.

As a measure of clade reliability, bayesian posterior probabilities were used along with bootstrap (BS) and jackknife support (JS) (Felsenstein 1985).

For both BS ad JS 1000 replicates of random sequence addition, equal weighting and TBR branch-swapping were run.

6.2.4. Statistical analyses

As the present dataset contains markers inherited in different ways (maternal for chloroplast, biparental for nuclear), and therefore potentially reflecting different evolutionary histories (chloroplast, ITS and low-copy nuclear) incongruence is likely to occur. Character congruence analyses using ILD tests (Incongruence Length Difference, Farris et al. 1994) implemented by PAUP*4.0b10 (Swofford 2000) were carried out to test for possible data incompatibilities. We used an heuristic approach performing multiple rounds of pairwise tests until all possible partition combinations were checked. Though time-consuming and despite some criticism, the ILD test has proven to be a powerful tool for incongruence detection (Dolphin et al. 2000, Darlu et Lacointre 2002, Hipp et al. 2004, Planet 2006).

When dealing with the comparison of tree topologies several alternatives are available. Until recently the most commonly used test (KH, Kishino and Hasegawa, 1989) has proven to be subjected to selection bias (Swofford et al. 1996), while the alternative SOWH test (Swofford-Olsen-Waddel-Hillis, Goldman et al. 1993) shows a tendency to overconfidence on tested hypotheses (high type I error, Planet 2006). We decided to use the non-parametric bootstrap approach of Shimodaira-Hasegawa (SH) test (Shimodaira and Hasegawa, 1989, 1998), which poses the only inconvenience of being conservative in the rejection of null hypothesis but only when numbers of tested trees are very large (Buckley 2002, Shimodaira 2002).

6.3. RESULTS

6.3.1. Sequence variation

A) ITS

The ITS dataset is the second most informative marker after *ces*A1b, with a total length of 778 characters, 29% of which were parsimony-informative (outgroup sequences included, see table 2). These ITS sequences come from previous work by Escobar et al. (2007a).

B) *ces*A1b

Most sequences grouped clearly in three paralogs, with the outgroups falling at the base of each. A small number of sequences that appeared to be intermediate among paralogs were found by RPD to be recombination artifacts ($P < 0.05$) and thus eliminated from the analysis. Sequences showing marks of pseudogenization –high non-synonymous substitution rates, premature stop codons, large deletions, or indels causing reading frame shifts– were also eliminated.

Both exons and protein were alignable with sequences from other workers, including diverse Malvaceae (several *Gossypium* from Wendel et al. 2001, *Hibiscus cannabinus*, Ruotolo et al. 2006), and diverging taxa as *Boehmeria nivea* (Urticaceae, from Tiang et al. 2005), *Eucalyptus grandis* (Myrtaceae, Ranik et Myburg 2005), *Nicotiana alata* (Solanaceae, Doblin et al. 2000) and some species of *Acacia* (Wang et al. unpublished). Intron sequence variability was high, making alignment impossible with non-Malvaceae. A 40 bp microsatellite sequence (intron four) was excluded from the analyses due to the difficulty of unambiguous alignment. The total data set included 1268 characters, 730 corresponding to introns and 538 to exons, both retaining a high number of informative sites (for details see table 2).

From the 351 sequences analysed, most (197) corresponded to paralog 1 (P1), the remaining belonging to paralogs 2 (P2, 98 sequences) and 3 (P3, 56 sequences). The degree of paralog representation in different ingroup species is variable. In most taxa, particularly among the lavateroids, only P1 was present, being also common the presence of two paralogs (figure 6).

The three paralogs differ mainly in exon sequence. There are also differences in sequence length, with P1 being the longest and P3 the shortest. Exon sequence variation among paralogs is mostly expressed in the form of synonymous changes. Changes of C<>T and A<>G are not unfrequent in all exons, normally with two paralogs P1 and P3 sharing the third codon position and P2 diverging. Exons IV and V are the most variable. Here, not only synonymous changes are found, but also indels. Exon IV has a 3 bp deletion in P2, while exon V presents a 3 bp insertion in P3. Lengh variation among paralogs is caused by intron extension. Introns are shorter in P3 as compared to P2 and above all to P1. Introns I and III are more constant in size in all three paralogs, whereas intron II is substantially reduced in P3. The structure of intron IV also differs, with P1 and P2 presenting an AT+AC microsatellite towards the

5' end which is absent from P3. This microsatellite region is longer in P1, with more final AC repetitions than in P2.

Results concerning sequence diversity and paralog number are shown in figure 6. Allelic variation is complex and clade specific. There are no general trends, but low sequence diversity in low ploidy levels and high or low diversity in higher ones. Heterozigosity does not seem to be related to floral biology, with inbreeders showing high (*Malva verticillata*) or low (*Malva parviflora*) heterozigosity levels and showy outcrossers also displaying either low levels (*Lavatera thuringiaca*) or high (*Lavatera cretica*).

C) Plastid markers

We sequenced four different chloroplast markers spanning 4954 characters (see table 2).

The longest markers were *mat*K (with 1986 characters) and *ndh*F (with 1845), the shortest *trn*L-*trn*F with only 464. The information contained in the chloroplast datasets (figure 3) was variable and comparatively low, with an 86% of constant characters in the most variable dataset (*psb*A-*trn*H) and up to a 96% in *ndh*F. The number of parsimony-informative characters was also low to very low, with approximately a 7% of informative characters in both spacers, 4.5% in *mat*K-*trn*K and just a 1.5% in *ndh*F.

6.3.2. Phylogenetic analyses

A) ITS

The ITS topology is the most resolved and well-supported of all the markers studied, remaining essentially the same irrespective to the method of inference used, whether bayesian or parsimony (for details see table 4). The branches are longer toward the tree base, resulting in a solidly-supported deep structure. Toward the distal region branches are shorter, particularly within the malvoid and lavateroid groups, leading to moderate or low support scores.

The deep structure consists of a perennial *Althaea*-*Alcea* clade sister to the *Malope*, which is sister to all *Lavatera*, *Malva* and annual *Althaea* except for *Lavatera phoenicea*, that is sister to all remaining ingroup taxa. There is a polytomy at the base of the ingroup from which several well-supported groups arise. The annual *Althaea* plus *M. cretica*, *M. aegyptia* plus *M. trifida* and the malvoids are solidly supported clades. Contrastig with it, the lavateroids are not fully supported, with the *Bismalva* and the perennial *Lavatera* clustering in well-supported clades, and the annual *Lavatera*, *L. thuringiaca* and *M. hispanica* appearing unresolved. Within the malvoids, the basal clades are well-supported, with a general loss of resolution toward the annual mallows.

B) *ces*A1b

Both parsimony and bayesian analyses of the joint matrix (351 sequences, see table 4) yielded similar tree topologies for P2 and P3, with minor changes in apical branches. Both analyses retrieve a solid three-paralog topology, as supported by bayesian posterior probability, bootstrap and jackknife scores (figures 5a, b and c). Contrastingly, the phylogenetic structure of P1 (figure 5a) is labile and some clades which appear in the parsimony topology did not appear in the bayesian one (not shown). The phylogenetic signal is stronger at both deep and terminal levels, as some intermediate nodes collapse in bootstrap and jackknife analyses. Phylogenetic relationships retrieved (except for P1) proved to be stable under different analytical conditions (bayesian or parsimony, gaps coded or treated as missing data, different codon weighting schemes).

Only seven species yielded sequences belonging to the three paralogues, most taxa being represented by sequences falling within P1, P2 or both. This fact difficults comparison among single paralog branches and reduces the phylogenetic signal for those taxa not represented in the three paralogue trees. Especifically, most lavateroids are well-represented in P1, with a reduced presence in P2 and P3, while most P2 sequences belong to malvoid taxa. P3 is best represented among taxa reconstructed as basal by the other markers, as *M. aegyptia-trifida*, *M. cretica* and *Alcea*. There are several points of agreement among paralogues. First, the basal position of perennial *Alcea*-perennial *Althaea*, which are the sister group to all remaining taxa, followed by the *Malope* clade (only in P1 and P2, see figures 5b, c). The malvoid group is also well-supported, as the *L. triloba* aggregate. But the lavateroid clade do not receive unambiguous support and collapse in both BS and JK analyses in P1 as well as in P2.

The phylogenetic signal of **P1** (figure 5a) is the least solid of the three paralogues. The clades *Alcea-Althaea* and *Malope* are reconstructed to be sister to all remaining species, but most branches at the tree core collapse forming a large polytomy from which the malvoids (scarcely supported, BS68, JK56), the perennial *Lavatera* (BS100, JK99) and *Bismalva* (BS97, JK97) arise together with the annual *Lavatera*, *A. hirsuta* and *L. thuringiaca*. This latter species is closely related to one allele from *M. alcea* (BS100, JK100), while the other is deeply embedded within *Bismalva*. One allele of *A. hirsuta* is sister to *M. cretica* (BS69, JK66).

Within **P2** (figure 5b) the malvoids are best-represented, and cluster together but with low support (BS73, JK71). *Lavatera phoenicea* appears as sister to the malvoids equally with low support scores. The alleles from *L. mauritanica* are sister either to *L. arborea* (BS85, Jk76) or to *M. parviflora-verticillata* (BS71, JK70). The lavateroids are not well-represented and fail to cluster together, falling in a polytomy at the base of the malvoid clade.

Despite the reduced number of species which are represented in the **P3** (figure 5c) subtree, this paralog displays the most solid structure, with the largest amount of basal species. The malvoids receive high support (BS99, JK98), as the ruderal mallows do, which appear solidly nested within them (BS90, JK88). The perennial *Lavatera* (the only lavateroids present) also group together and with the malvoids in a single, moderately-supported *Lavatera-Malva* clade 8BS82, JK78), to which *M. aegyptia-trifida* and *M. cretica* appear sister.

C) Plastid markers

All chloroplast analyses share a poor resolution derived from the short or very short branch lengths (figures 3 and 4). In two cases (*ndh*F, *psb*A-*trn*H) bayesian and parsimony analyses failed to retrieve compatible topologies. Despite this general lack of resolution, some taxa groups are strongly supported by bootstrap and jackknife scores, and mostly compatible with the correspondent clades retrieved from ITS and *ces*A1b. For analysis scores see table 4.

trn**L-*****trn*****F**: Basal internodes are fully resolved both in bayesian and parsimony analyses. The perennial *Alcea* plus *Althaea* are sister to *Malope*, which is sister to the remaining taxa, which arise from a large polytomy where it is possible to recognize a partial lavateroid group without *L. trimestris* and *Bismalva*, and a malvoid group without *L. maritima* and *L. acerifolia*. The annual *Althaea* appear also independently of each other, while *M. trifida* and *M. aegyptia* cluster solidly, so *Malvalthaea* and *M. cretica* do.

psb**A-*****trn*****H**: The trees arising from bayesian and parsimony analyses were not compatible and contained mostly polytomies. The perennial *Althaea* plus *Alcea* form a highly-supported clade, as also *M. aegyptia* plus *M. trifida* and the *Malope*. *Althaea hirsuta* is closely linked to both *Malvalthaea* and *M. cretica*. The *Bismalva* clade appears solidly supported, while the malvoids are not.

Some species have labile positions (*L. maritima*, *L. maroccana*, *L. trimestris*, *Althaea longiflora* and *A. ludwigii*).

matK plus partial *trn*K (fig. 3): This dataset yields comparatively long terminal branches. The deep structure of the cladogram is not well-supported but the branching order is the same as that observed in *trn*L-*trn*F, with a basal perennial *Althaea-Alcea* and a *Malope* clades sister to a polytomy where several recognizable groups receive moderate to high support. *Malva cretica* and *Althaea hirsuta* are closely linked. *Lavatera acerifolia* plus *L. maritima*, *M. trifida* plus *M. aegyptia*, the *Bismalva* and reduced malvoid and lavateroid groups receive high to moderate bootstrap and jackknife support. Some species present unstable phylogenetic positions (*L. flava*, *L. plazzae* and *L. trimestris*). Some taxa (*L. flava*, *L. triloba* ssp. *pallescens*, *L. maroccana*, *L. acerifolia*) appear at the end of comparatively long branches at random positions.

***ndh*F**: This dataset yields uncompatible trees when analysed using bayesian and parsimony. The branching order at deep levels, though not supported neither by bootstrap or jackknife analyses is the same as previously observed. Perennial *Althaea-Alcea* and *Malope* clades being sister group to a large polytomy containing most taxa. Despite this, *Bismalva* still cluster together, *M. aegyptia-trifida* appear to be moderately supported, as *L. maritima-acerifolia*.

Joint analyses (fig 4): Though all chloroplast markers are supposed to converge in the same topology, none of them yielded the same phylogenetic tree. Joint analyses of chloroplast data were performed in all possible combinations. The analyses of *mat*K plus *trn*L-*trn*F and the joint analysis of all chloroplast markers did not produce significantly different topologies, but the latter analysis yielded only 10 MPTs, contrasting with the hundreds or thousands produced by single-marker analyses (table 4).

The joint tree displays an *Alcea*-perennial *Althaea* and *Malope* clades sister to the remaining taxa, which appear as a polytomy from which the annual *Althaea* -failing to cluster together- and the *M. aegyptia-trifida* clade arise. Nested within this clade the malvoids are better resolved, but only at their basal branches, as the annual mallows form a terminal polytomy. Within the lavateroids only the *Bismalva* and the *L. agrigentina* plus *L. flava* clade are unambiguously resolved. The joint analysis increased branch lengths, and support scores for clades already retrieved by individual marker analyses, e. g. for the clades formed by *A. hirsuta* plus *Malva cretica* and *M. aegyptia* plus *M. trifida*.

6.3.3. Statistical tests

Congruence tests are normally a decisive step in phylogenetic analysis as its result may determine which datasets will be analysed together and which separately. Our results indicate that there is significant incongruence among datasets, particularly among *ces*A1b, ITS and the chloroplast markers (table 3). But surprisingly, and despite all chloroplast markers being expected to converge in the same topology, as parts of a common linkage group, the ILD test showed incongruence among different plastid markers, *ndh*F and *psb*A-*trn*H particularly affected. The interpretation of ILD test requires caution, as the results of the test may be affected by homoplasy. This is a polemic issue, as some authors claim it to be unimportant (Swofford 1991), while others suspect that in fact it could a decissive issue (Graham et al. 1998). The solution proposed by the latter authors consists of removing poorly supported branches from the analysis. This approach does not seem viable in our case, as support for chloroplast markers is generally low, particularly at critical deep branches. For Dolphin et al. (2000) some significant results could be due to the presence of unresolved trees (as it is the case of the *ndh*F and *psb*A-*trn*H, consisting of largely unresolved polytomies). Because of this, and despite significant results concerning these two markers, we decided to combine the chloroplast markers in several ways, as it is described in the next sections.

Regarding the Shimodaira-Hasegawa tests, likelihood scores were used to determine congruence among topologies in a combined dataset. The results of the one-tailed test with 1000 replicates show that the topologies differ significantly, with best likelihood scores obtained by the ITS tree, followed by *ces*A1b.

6.4. DISCUSSION

The incorporation of the low-copy nuclear marker *ces*A1b to the chloroplast and ITS datasets provides new evidence to address questions so far not explained by existing work. For instance, the lack of resolution at the base of the *Lavatera*-*Malva* clade, affecting also the basal nodes of the perennial *Lavatera* could be due to the existence of a hard polytomy. In view of these new results, the current taxonomic status of the *L. triloba* aggregate is no longer acceptable, with its geographically split taxa. New evidence for the allopolyploid hybrid speciation of *L. mauritanica* is presented, and a previously unnoticed case of hybrid speciation (*M. alcea*) is reported. Our data regarding *L. phoenicea* reopen a debate started by Webb and Berthelot (1836) about the position of the species that seemed to be clarified after the work of Fuertes et al. (2002) and Escobar et al. (2007a). Despite the presence of multiple alleles which often fail to coalesce within specific limits, *ces*A1b is highly informative, and adds new supportive evidence to the existing early branching scheme of the *Malva* alliance.

6.4.1. Is *Lavatera triloba* ssp. *pallescens* a separate species?

The taxonomic literature has since long been inconsistent with the treatment of the members of the *L. triloba* aggregate, with the taxa being split according to political borders rather than to morphology. The Iberian authors (Nogueira et al., 1993) have traditionally considered the existence of a polymorphic species, *L. triloba*, with a large, purple-flowered peninsular morphotype - ssp. *triloba* - and a thyrrenian dwarf, yellow-flowered morphotype - ssp. *pallescens* -, though some authors have considered them to be closely related species (Moris 1837). For the Italian school (Pignatti 1982), the dwarf plants that grow in Sardinia would be a part of ssp. *pallescens*, while the yellow-flowered, large plants found in Sicily and Calabria represent an independent species, *L. agrigentina*. *Lavatera triloba* ssp. *triloba* has been recorded from Sardinia, though their affinities with the Iberian populations remain unclear. The French school (Maire 1963) separates the Western North African plants, with either purple or more commonly yellow flowers and longer sepals into a different species, *L. flava*, as well as the Tunisian populations, with purple, narrower petals, into an independent species, *L. stenopetala*.

Our *ces*A1b and ITS results indicate a clear affinity of all these yellow-flowered taxa, which cluster together in a clade sister to the Iberian plants or fall in a polytomy at the base of a well supported clade containing all the Iberian representatives. The plastid data are not so informative and, despite unambiguously supporting the link among *L. agrigentina* and *L. flava*, place *L. triloba* ssp. *pallescens* at the end of a long branch and its position is phylogenetically unstable. In the *ces*A1b dataset, there are several alleles which coalesce beyond the specific limits, but at least supporting unambiguously the monophyly of the *L. triloba* aggregate.

Further studies with extensive population sampling would be needed, but up to the present date, it appears that the current taxonomical status of these entities is not coherent with their relationships. Either an extended *L. triloba* including the yellow- and purple-flowered Italian and North-African representatives, or a further splitting with *L. triloba* ssp. *pallescens* recognized as an independen taxon would be desirable.

6.4.2. Are the shrubby lavateroids directly related?

A close relationship among the shrubby lavateroids (*L. bryoniifolia*, *L. oblongifolia* and *L. olbia*) is supposed since long time ago (section *Olbia* [Medik.] DC.), but the possibility that they are a paraphyletic aggregate should be addressed. ITS suggest a close link among *L. oblongifolia*, an endemic of SE Spain, and *L. olbia*, while *L. bryoniifolia* falls in a polytomy at the base of the perennial lavatera clade. The chloroplast data set does not resolve the relationship satisfactorily, grouping *L. oblongifolia* either with the Eastern-Europaean *L. thuringiaca*, or the Eastern Mediterranean *L. bryoniifolia* with the Iberian *L. triloba*. The result of the joint analysis is a polytomy. The *ces*A1b dataset is not much more informative, as P1 places these Lavateras in a polytomy and P2 links *L. oblongifolia* to *L. bryoniifolia*, while *L. olbia* falls to a basal polytomy.

There are two perennial species though not shrubby themselves, show ambiguous affinities to the shrubby *Lavatera*. This species are *L. plazzae*, a recently discovered, morphologically diverging Sardinian endemic (Atzei, 1995) and *L. thuringiaca*, a widely-distributed European taxon of isolated position. The phylogenetic position of both species is inconsistent, as they appear linked to the shrubby representatives - always with low support scores - or form a polytomy either into a basal, perennial lavateroid clade, or within the large basal polytomy from which also the malvoids arise in some cloroplast analyses. We lack *ces*A1b data for *L. plazzae*, but in the *ces*A1b P1 dataset *L. thuringiaca* shows a highly supported relationship to the P1-b allele of *M. alcea*. This result poses the question of whether this species is involved in the formation of the high polyploid *M. alcea*.

The unstable phylogenetic position of these species, together with the low supporting scores obtained despite the sequencing effort made, suggest that these taxa are members of an early, fast diverging lineage, which in fact represents a lavateroid hard polytomy.

6.4.3. Are the lavateroids an example of hard polytomy?

The morphological affinities of most *Lavatera* and *Malva* species are more or less clear, most of them being either malvoid (with thick-walled indehiscent mericarps) or lavateroid (with more or less soft-walled, dehiscent mericarps), with few annuals being basal to the complex and thus not being in either of these two groups. These groups seem to reflect true relationships, regardless of the degree of fusion of the epicalyx bracts, the charater used by Linné (1753, 1789) to separate both genera. But with a broadened sampling the relations among the malvoids and lavateroids are no longer so simple as depicted in previous work (Ray 1995), and as a result of short branches at the base of *Lavatera-Malva* clade (see figure 2), the phylogenetic relationships become unstable. The pattern (Kim, 1997) revealed by these different markers is widespread among the Angiosperms, where at least 25 of the 45 orders of latest classifications (APG 2003) show a tendency to accumulate short branches, with unstable clade resolution and low support. Recent simulations in Lamiales (Wortley et al. 2005) suggest that only large datasets with combination of different markers may be able of resolving certain polytomies, rather than intensive taxon sampling effort.

Our present dataset presents more than 9000 characters in eight partitions, but it seems to be insufficient when addressing the question of whether the lavateroids are a monophyletic group, or a paraphyletic conglomerate of morphologically similar taxa. This is critical particularly among the annual lavateroids, which despite being morphologically very close (as for example *L. trimestris*, *L. punctata* and *L. maroccana*), often fail to cluster together, falling to a basal polytomy from which several lavateroid and the malvoid lineages arise (figure 2 and 5). *Malva hispanica* is another taxon whose position remains obscure. It is a morphologically isolated annual species endemic to the Western Mediterranean, which is either reconstructed as basal to the annual lavateroids by ITS data, or to the *Bismalva* clade by chloroplast and *ces*A1b, but in neither case with reliable support.

The case of *Bismalva* is also critical. The three species of this clade have been recognized as a clear taxon since the eighteen century (Medikus 1787), but their phylogenetic position remains unclear. They are reconstructed as basal to all remaining lavateroids, or to both malvoids and lavateroids (not shown). Although it seems possible that they diversified before both the annual and the other perennial lavateroids, there is no conclusive support for this hypothesis.

Among the factors causing this short-branched, unsupported phylogenetic pattern, fast species radiation, homoplasy, insufficient sampling (either taxon or sequence length) and character conflict due to hybrid speciation (Linder & Rieseberg 2005) are often invoked. In our case, with an specific sampling covering almost every taxon (but some remote species of very restricted area) and a large molecular dataset with more than 9000 characters belonging to eight different regions, we are likely facing a hard polytomy, resulting from a fast radiation event.

6.4.4. Incongruence among ITS and low-copy datasets: a window to unsuspected phylogenetic relationships

Our results regarding the malvoid clade are complex and may be a good example of two concerns that affect the widely-used ITS (Álvarez and Wendel, 2003) and the low-copy genes, namely concerted evolution and lineage sorting. The topology retrieved from the ITS data is solid, with high support scores particularly among the basal branches (figure 2). The chloroplast and *ces*A1b datasets yield trees with a similar structure, though branching patterns are not highly supported in the former. In each case, the resolution is lost toward the tree apex, occupied by a group of six polyploid taxa here referred as the annual mallow clade. The ploidy levels span from 6x in *M. sylvestris*, *M. nicaeensis*, *M. neglecta* and *M. parviflora* to 16x in *L. cretica*, with an intermediate 12x in *M. verticillata* (figure 6). All these species have reduced DNA amounts as compared with their closest perennial relatives, presenting 2C-values which are proportional to their ploidy levels, unlike neither of the perennial malvoids (Escobar et al. 2007b). In the case of *ces*A1b high levels of sequence polymorphism are present, with alleles coalescing beyond species level, suggesting interspecific hybridisation.

In the ITS dataset the malvoids are well-supported and consist of a basal shrubby clade, integrated by the summer-deciduous Canary Island endemic *L. acerifolia* and the Western Mediterranean *L. maritima*, which is sister to the also shrubby (though facultative annual herb) *L. arborea* and the annual *L. mauritanica*. The latter two species occur on coastal environments, *L. mauritanica* being an endemic to the South-Western Iberian Peninsula, Alborán island and North-Western Morocco. The terminal group consists of a well-supported annual mallow polytomy which encompasses a clade containing the remote and shrubby *L. assurgentiflora*, *L. plebeia* and *L. abyssinica*.

The malvoid clade retrieved from the chloroplast dataset is similar but more weakly supported, with the basal *L. maritima* - *L. acerifolia* failing to cluster together and falling to a basal extensive *Lavatera-Malva* polytomy in most analyses.

The history retrieved from the low-copy dataset is complex, with some differences regarding the two main paralogs, P1 and P2. P1 presents several alleles that coalesce at the base of the malvoid clade. The clade structure is similar, with a highly-supported terminal annual mallow polytomy, arising from a basal malvoid polytomy where the different alleles of *L. assurgentiflora* and *L. plebeia* arise together with the *L. acerifolia* - maritima clade. P2 has a more complex structure due to a gene duplication, which apparently occurred in the early history of the mallow diversification, soon after the divergence of *L. acerifolia-L. maritima*, as the clones split in two clades giving origin to polyphyletic groups containing most species.

There is a point of disagreement among *ces*A1b and ITS datasets. It is the position of *L. mauritanica*. This species is sister to *L. arborea* - with similar, unique dark eyed petals - in the ITS analysis, receiving high support scores. Though several individuals from Spain, Portugal and Morocco were sampled, they appeared to be monophyletic and clustered with *L. arborea*. In contrast, plastid data indicate a position deeply embedded within the terminal annual mallow polytomy, supported also by high scores. This fact, along with its 12-ploid genome, distribution area, and some morphological characters shared with both *L. arborea* (the limestone seashore habitat, dark-eyed petals, tendency to become perennial if the conditions of aridity allow for it) and the annual malvoids, particularly with *L. cretica* (epicalyx not surpassing the calyx, both calyx and epicalyx acrescent in fruit), support the allopolyploid origin of *L. mauritanica*.

This allopolyploid speciation event is further supported by the nuclear low-copy dataset. The homogeneization of ITS copies due to concerted evolution obscure the hybrid history of this taxon, while plastid markers reflect only the maternal lineage. In the *ces*A1b dataset the history of gene duplications and the lack of coalescence of alleles becomes an advantage for testing the hypothesis of allopolyploid origin. Within P1, two different alleles (*a* and *b*) were isolated, both nesting within the annual mallow polytomy with moderate support (BS86, JK84). This position is compatible with that obtained with plastid data, but not with the equally highly supported ITS. In P2, there are also two alleles (*c* and *d*, figure 5b), *c* being sister to L. arborea, while *d* forms a polytomy with *M. parviflora* and one allele of *M. verticillata*.

6.4.5. The unexpected relationships of *Lavatera phoenicea*

Albeit not highly supported, there is a tendency in *L. phoenicea* to appear at the base of the malvoids in some partitions of the chloroplast dataset. This relationship also appears in *ces*A1b P2, with low support (BS73, JK71). In the ITS dataset, *L. phoenicea* is sister to all remaining *Lavatera-Malva* taxa with BS100. This is another case of incongruence among the ITS dataset and the LCNG. Lineage sorting retaining a basal ITS copy in *L. phoenicea*, followed by concerted evolution may be an explanation for the pattern retrieved, which is not easy to reconcile with exiting evidence. We do not think that this hypothesis is uncompatible with previous work suggesting that *L. phoenicea* and *L. acerifolia* are the result of different colonization episodes in the Canary Islands (Fuertes et al. 2002). Actually, both species are only distant relatives, where *L. acerifolia* is morphologically very similar to the continental *L. maritima* whereas *L. phoenicea*´s morphology is unique.

This position of *L. phoenicea* is compatible with the hypothesis that a basal species complex of perennials and large shrubs existed in the Mediterranean Basin and Macaronesia prior to the formation of the Mediterranean climate. The progressive aridification, as well as the extension of agriculture could have triggered the diversification of the annual mallows, while the shrubby species retreated to milder habitats. The uncertainities at this level of the tree, which do not improve or result in higher support scores despite big sequencing effort, suggest a recent fast radiation. The remote *L. abyssinica* from Somalia, as well as the Californian and Australian shrubby malvoid Lavateras coud also be the product of long-distance dispersal having retained the woody habit, rather than this habit having appeared several times independently. The whole malvoid group displays a strong tendency to herbness, from *L. phoenicea*, a rather big shrub or even small tree, with *L. acerifolia* and *L. maritima* still being true shrubs, toward the stem structure of *L. arborea*. The latter, despite reaching up to 3 m high, presents hollow stems with spongy marrow and unlike its true shrubby relatives is able to flower already during its first year of development.

6.4.6. The unexpected relations of *Malva alcea*

Malva alcea is a morphologically well-defined species whose taxonomic position was already stablished by Medikus in 1787, and never revised in later times. *Malva alcea* presents lavateroid affinities and shares many morphological traits with the hexaploid herbs *M. moschata* and *M. tournefortiana*, integrating the *Bismalva* clade together with them. It is a 12-ploid, and unlikely its close relatives, presents very large chromosomes and a high DNA amount (2C = 10.95 pg, the largest of the *Malva* alliance, Escobar et al. 2007b), not explainable merely by chromosome doubling. In contrast, the DNA amount of *M. moschata* is 2C = 2.93 (that of *M. tournefortiana* being very similar). In previous work, Escobar et al. (2007b) interpreted this high value as a case of genome expansion following an autopolyploidization event.

Both ITS and all chloroplast datasets support the close link among the taxa integrating the *Bismalva* clade. But present data lead to reassesement of the relationships, as cloning of *ces*A1b leads to the isolation of two alleles. The majority of clones are of type *a* and fall within the *Bismalva* clade. But there appear also in minor numbers sequences of type *b*, which are very similar to the three alleles isolated from *L. thuringiaca*. After verifying the origin of the clones, the different analyses clustered unambiguously the *a* allele with *Bismalva* (BS and JK 97), and the *b* allele with *L. thuringiaca* (BS and JK 100), in what we interpret as evidence for the allopolyploid origin of *M. alcea*. This way it seems that the ITS sequences of this species underwent concerted evolution towards the maternal copy, thus deleting any clue (incongruence) that could reveal the allopolyploid origin of this plant.

Further evidence is provided by genome size data. While autopolyploidy does not explain by itself neither the large genome of *M. alcea* nor the big size of its chromosomes, the allopolyploid hypothesis is consistent with the fact that the genome sizes of *M. moschata* and *L. thuringiaca* (both 6x) sum 11.36 pg, nearly the genome size of *M. alcea*.

There is also morphological evidence linking *M. alcea* with *L. thuringiaca*. While the epicalyx pieces of both *M. moschata* and *M. tournefortiana* are narrow and linear, those of *M. alcea* are lanceolate, like *L. thuringiaca*´s. Furthermore, both *L. thuringiaca* and *M. alcea* are robust plants surpassing 1.5 m, while *M. moschata* and *M. tournefortiana* do not grow usually taller than 0.80 m.

This is an example of how the use of only a dataset subjected to concerted evolution, as well as maternally inherited markers may be misleading in assessing phylogenetical relationships. Concerted evolution towards the maternal progenitor leads to a deletion of information if only ITS and chloroplast data are taken into consideration, and therefore evidence for hybridisation is not seen, though it actually may have occurred.

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Table 1. Material studied.

Taxon	Voucher no.	Origin
Alcea rosea	PE416	Spain. Madrid: Madrid.
Althaea armeniaca	PE427	Index Seminum.
Althaea cannabina	PE429	Spain. Lérida: Solsona.
Althaea hirsuta	PE270	Italy. Sardinia: Perdasdefogu.
Althaea longiflora	PE296	Spain. Badajoz: Magacela.
Althaea ludwigii	PE616	Iran. Tehran.
Althaea officinalis	PE409	Spain. Madrid: Aranjuez.
Anisodontea malvastroides	PE067	South Africa. Cape Town.
Kitaibela vitifolia	PE678	Austria. Wien. Botanischer Garten
Lavatera acerifolia	PE951	Spain. Tenerife: Los Gigantes.
Lavatera agrigentina	PE308	Italy. Sicily: Agrigento.
Lavatera arborea	PE252	Italy. Sardinia: Alghero.
Lavatera assurgentiflora	PE570	United States. California.
Lavatera bryoniifolia	PE141	Greece. Crete: Rethimnion.
Lavatera cretica	PE599	Morocco. Rif: Sidi Yahya.
Lavatera flava	PE414	Morocco. Taourirt.
Lavatera maritima	PE598	Morocco. Gorges du Zegzel.
Lavatera maroccana	PE311	Spain. Sevilla: Las Cabezas de San Juan.
Lavatera mauritanica	PE319	Portugal. Algarve. Cabo de São Vicente.
Lavatera oblongifolia	PE144	Spain. Almería.
Lavatera olbia	PE451	Italy. Sardinia: San Giovanni di Sinis.
Lavatera phoenicea	PE952	Spain. Tenerife: Teno.

Lavatera plebeia	PE634	Australia. South Australia. Adelaide.
Lavatera punctata	PE450	Turkey. Aydin.
Lavatera thuringiaca	PE590	Austria. Wien.
Lavatera triloba subsp. *pallescens*	PE564	Spain. Baleares: Isla Colom.
Lavatera triloba subsp. *triloba*	PE606	Spain. Madrid: Arganda del Rey.
Lavatera trimestris	PE595	Morocco. Rif: Chefchaouen.
Malope malacoides	PE600	Morocco. Rif: Fnidek.
Malope trifida	PE601	Morocco. Rif: Khenichet.
Malva aegyptia	PE681	Greece. Crete: Rethimnion.
Malva alcea	PE338	Spain. Ávila: Mijares.
Malva cretica subsp. *althaeoides*	PE950	Spain. Cádiz: Algodonales.
Malva hispanica	PE602	Spain. Badajoz: Guadajira.
Malva moschata	PE593	France. Pyrenées Orientales: Lortet.
Malva neglecta	PE795	Italy. Sardinia: Lago Cuga.
Malva nicaeensis	PE226	Italy. Sardinia: Uri.
Malva parviflora	PE603	Spain. Badajoz: Guadajira.
Malva sylvestris	PE597	Morocco. Oujda.
Malva tournefortiana	PE185	Spain. Badajoz: Talarrubias.
Malva trifida	PE605	Spain. Madrid: San Martín de la Vega.
Malva verticillata	PE442	Index Seminum.

Table 3. P-values for the ILD test performed between markers.

P	ITS	*ndh*F	*mat*K	*psb*A-*trn*H	*trn*L-*trn*F	*ces* P3
ITS	—	0,940	0,010	0,020	1,000	0,010
ndhF		—	0,210	0,010	0,540	0,040
matK			—	0,010	0,180	0,010
psbA-trnH				—	0,020	0,010
trnL-trnF					—	0,020
ces P3						—
P	ITS	*ndh*F	*mat*K	*psb*A-*trn*H	*trn*L-*trn*F	*ces* P2
ITS	—	0,910	0,010	0,010	0,100	0,010
ndhF		—	0,410	0,190	1,000	0,240
matK			—	0,040	0,080	0,010

psbA-trnH				—	0,060	0,180
trnL-trnF					—	0,010
ces P2						—
P	ITS	*ndh*F	*mat*K	*psb*A-*trn*H	*trn*L-*trn*F	*ces* P1
ITS	—	0,890	0,010	0,010	1,000	0,010
ndhF		—	0,200	0,010	0,590	0,070
matK			—	0,010	0,190	0,010
psbA-trnH				—	0,010	0,010
trnL-trnF					—	0,030
ces P1						—

Table 2. Data matrices. Sequences, number of sequences for each matrix. **Characters**, number of characters of each matrix. **Constant**, number of constant characters. **Variable**, number of variable characters. **Parsimony uninf.**, number of parsimony-uninformative sites. **Parsimony-inf.,** number of parsimony-informative sites. **Downweighted**, number of downweighted sites. **Excluded**, number of excluded sites. **Indels**, number of coded indels. **Ex**, exon data matrix. **Intr**, intron data matrix. **CesP1**, *ces*A1b P1 matrix. **CesP2**, *ces*A1b P2 matrix. **CesP3**, *ces*A1b P3 matrix. **ITS**, ITS matrix. **psb**, *psb*A-*trn*H plastid matrix. **trn**, *trn*L-*trn*F plastid matrix. **matK**, *mat*K plastid matrix. **ndhF**, *ndh*F plastid matrix. **MT**, joint *mat*K pus *trn*L-*trn*F plastid matrix. **MTP**, joint *mat*K pus *trn*L-*trn*F plus *psb*A-*trn*H plastid matrix. **NMPT** joint plastid matrix.

Parsimony	Ex	Intr	CesP1	CesP2	CesP3	ITS	psb	trn	matK	ndhF	MT	MTP	NMPT
Sequences	344	344	197	98	56	92	115	112	44	43	43	43	43
Characters	538	727	1203	1074	1006	778	659	464	1986	1845	2595	3236	5076
Constant	215	168	579	555	652	501	572	414	1769	1777	2244	2840	4617
Variable	323	559	624	519	354	277	87	50	217	68	351	396	459
Parsimony-uninf.	107	86	220	189	125	52	41	15	127	39	179	198	233
Parsimony-inf.	216	473	404	330	229	225	46	35	90	29	172	198	226
downweighted	175	-	174	175	173	0	0	0	0	0	0	0	0
excluded	0	49	49	49	0	0	0	0	0	0	0	0	0
Indels	12	177	128	-	43	67	99	29	43	5	72	171	176

Table 4. Analyses performed. Trees, number of retrieved trees. **Tree length. CI**, consistency index. **HI**, homoplasy index. **RI**, retention index. **Total**, joint *ces*A1b P1, P2 and P3 matrix. **Ex**, exon data matrix. **Intr**, intron data matrix. **CesP1**, *ces*A1b P1 matrix. **CesP2**, *ces*A1b P2 matrix. **CesP3**, *ces*A1b P3 matrix. **ITS**, ITS matrix. **psb**, *psb*A-*trn*H plastid matrix. **trn**, *trn*L-*trn*F plastid matrix. **matK**, *mat*K plastid matrix. **ndhF**, *ndh*F plastid matrix. **MT**, joint *mat*K pus *trn*L-*trn*F plastid matrix. **MTP**, joint *mat*K pus *trn*L-*trn*F plus *psb*A-*trn*H plastid matrix. **NMPT** joint plastid matrix.

Parsimony	Total	Exons	Introns	CesP1	CesP2	CesP3	ITS	psb	trn	matK	ndhF	MT	MPT	MNPT
Trees	1400	5230	100	7370	5865	149	9380	400	9860	7520	9580	302	91	10
Tree length	2348,8	860	1557	1006,2	946	464	649	109	51	267	93	508	574	662
CI	0,4336	0,4115	0,4516	0,5807	0,5472	0,6466	0,5613	0,7794	0,9487	0,7029	0,5472	0,546	0,5653	0,5621
HI	0,5664	0,5885	0,5484	0,4193	0,4528	0,3534	0,4387	0,2206	0,0513	0,2971	0,4528	0,454	0,4347	0,4379
RI	0,9285	0,9226	0,9349	0,9297	0,8782	0,9073	0,9172	0,9667	0,9934	0,8686	0,8209	0,803	0,8094	0,8076

7. CONCLUSIONES.

1. El carácter utilizado para la delimitación de los géneros *Malva* y *Lavatera* por Linné (1753) -número y grado de fusión de las brácteas del epicáliz- está sujeto a homoplasia y es incongruente con otros caracteres, como la morfología del fruto, así como con datos moleculares de nrDNA ITS, los espaciadores cloroplásticos *psb*A-*trn*H y *trn*L-*trn*F, los genes cloroplásticos *mat*K y *ndh*F y el gen nuclear de bajo número de copias *ces*A1b.

2. El género *Althaea* en su circunscripción tradicional es polifilético e incluye dos linajes claramente separados, que no están directamente emparentados. Las especies perennes son el grupo hermano del género *Alcea*, mientras que las anuales están más próximas a ciertas especies de *Malva*, como *Malva cretica* o *M. aegyptia*.

3. La incongruencia entre los diferentes marcadores, el patrón de compartición de alelos de *ces*A1b y análisis de APS revelan el origen alopoliploide de los taxones *Lavatera mauritanica* y *Malva alcea*, así como el origen híbrido de *Malvalthaea transcaucasica*.

4. Se realizan los siguientes conteos cromosómicos nuevos: *Althaea longiflora* 2n = 22 (4x); *Althaea ludwigii* 2n = 44 (6x); *Lavatera assurgentiflora* 2n = 84 (12x); *Lavatera phoenicea* 2n = 44 (6x); *Malope malacoides* 2n = 44 (6x); *Malva cretica* ssp. *althaeoides* 2n = 44 (6x); *Malva trifida* 2n = 42 (6x). Adicionalmente, se realizan 31 conteos que arrojan resultados concordantes con los contenidos en la bibliografía.

5. Se presentan cantidades de DNA (medidas en pg) para 38 taxones de la alianza genérica de *Malva*, realizando la reconstrucción filogenética del carácter (en forma de 1Cx) sobre una topología bayesiana de ITS. La cantidad de DNA recontruida para los nodos ancestrales es de aproximadamente 1Cx = 0,38 pg, con una marcada tendencia al crecimiento durante la historia evolutiva del grupo. Sin embargo, el patrón recuperado es más complejo dado que existen linajes que han sufrido ampliaciones o reducciones de su genoma.

6. El tamaño del genoma en la alianza genérica de *Malva* es un carácter de gran importancia ecológica, que ha estado sujeto a una evolución compleja, con múltiples expansiones y contracciones. Las especies ruderales de ciclo rápido presentan genomas miniaturizados con respecto a especies relacionadas que habitan lejos de la influencia del hombre. Adicionalmente, el tamaño del genoma no está relacionado con el nivel de ploidía, dado que debido a fenómenos de amplificación y reducción genómicas, numerosos taxones hexaploides presentan cantidades de DNA más pequeñas que el diploide (*Lavatera trimestris*) o los tetraploides (*Malva hispanica*).

7. Se presenta el primer estudio con marcadores moleculares del género *Alcea*, que incluye unas 50 especies originarias del Este del Mediterráneo y el Suroeste de Asia. En contraste con *Althaea*, encontramos que *Alcea* es un género claramente natural en su definición clásica, hecha por Linné en el siglo XVIII. La baja variabilidad encontrada en las secuencias encontradas, así como la gran plasticidad fenotípica de las especies estudiadas, sugieren hibridación extensiva.

8. El gen *ces*A1b presenta tres parálogos (P1, P2 y P3), con representación diferencial en los grandes grupos definidos por los otros marcadores, así como gran variación alélica. La incongruencia que existe entre los tres conjuntos de datos (nuclear de bajo número de copias, ITS y cloroplasto), añade evidencia a los sucesos de especiación alopoliploide anteriormente señalados. El marcador nuclear *ces*A1b se revela como una fuente de información esencial en el estudio filogenético de la alianza genérica de *Malva*.

ITS

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                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                         10         20         30         40         50         60         70         80         90        100
ILag308          CGTAGGTGAC CTGCGGAAGG ATCATTGTCG AAACCTGCCT AGCAGAACGA CCCGCGAACG TGATATCAAA CA-CAACCAA TCGAGGGGGT -GCGGATGCA
ILtp354          CGTAGGTGAC CTGCGGAAGG ATCATTGTCG AAACCTGCCT AGCAGAACGA CCCGCGAACG CGATATCAAA CA-CAACCAA TCGAGGGGGT -GCGGATGCA
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ILtr169          CGTAGGTGAC CTGCGGAAGG ATCATTGTCG AAACCTGCCT AGCAGAACGA CCCGCGAACG CGATATCAAA CA-CAACCAA TCGAGGGGGT -GCGGATGCA
ILbr141          CGTAGGTGAC CTGCGGAAGG ATCATTGTCG AAACCTGCCC AGCAGAACGA CCCGCGAACG CGATATCAAA CA-CAACCAA TCGAGGAGGT -GCGGATGCA
ILbr552          CGTAGGTGAC CTGCGGAAGG ATCATTGTCG AAACCTGCCC AGCAGAACGA CCCGCGAACG CGATATCAAA CA-CAACCAA TCGAGGAGGT -GCGGATGCA
ILob144          CGTAGGTGAC CTGCGGAAGG ATCATTGTCG AAACCTGCCT AGCAGAACGA CCCGCGAACG CGATGTCAAA CA-CAACCAA TCGAGGAGGT -GCGGATGCA
ILol004          CGTAGGTGAC CTGCGGAAGG ATCATTGTCG AAACCTGCCT AGCAGAACGA CCCGTGAACG CGATATCAAA CA-CAACCAA TCGAGGGGGC -GCGGACGCA
ILol451          CGTAGGTGAC CTGCGGAAGG ATCATTGTCG AAACCTGCCT AGCAGAACGA CCCGTGAACG CGATATCAAA CA-CAACCaA TCGAGGGGGC -GCGGACGCA
ILpl285          CGTAGGTGAC CTGCGGAAGG ATCATTGTCG AAACCTGCCT AGCAGAACGA CCCGCGAACG CGATATCAAA CA-CAACCAG TCGAGGAGGT -GCGGATGCA
ILpu450          CGTAGGTGAC CTGCGGAAGG ATCATTGTCG AAACCTGCCT AGCAGAACGA CCCGCGAACG CGATATCAAA CA-CAACCAA TCGAGGGGGT -GCGGATGCA
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ILti595          CGTAGGTGAC CTGCGGAAGG ATCATTGTCG AAACCTGCCT AGCAGAACGA CCCGCGAACG TGATATCGAA CA-CAAACAA TCGGGGGGGT -GAGGATGCA
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ILmo346          CGTAGGTGAC CTGCGGAAGG ATCATTGTCG AAACCTGCCT AGCAGAACGA CCCGCGAACG TGATATCGAA CA-CAACCAA TCGAGGGGGT -GCGGACGCA
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ILar252          CGTAGGTGAC CTGCGGAAGG ATCATTGTCG AAACCTGCCT AGCAGAACGA CCCGCGAACG TGTTATCGAC CAA---CCGA TCGAGGGGGT -GCGGATGCA
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ILcr235     CGTAGGTGAC CTGCGGAAGG ATCATTGTCG AAACCTGCCT AGCAGAACGA CCCGCGAACG TGTTATCGAA CAA---CCGA TCGAGGGGGT -GCGGATGCA
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IMhi149     CGTAGGTGAC CTGCGGAAGG ATCATTGTCG AAACCTGCCT AGCAGAACGA CCCGCGAACG TGATGTCAAA CA-CAACCAG TCGAGGGGGT -GCGGATGCA
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IAlo596     CGTAGGTGAC CTGCGGAAGG ATCATTGTCG AAACCTGCCT AGCAGAACGA CCCGTGAACG TGATATCAAA CAA---TCGA TCGAGGGGGT -GCGGATGCA
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IAhi455     CGTAGGTGAC CTGCGGAAGG ATCATTGTCG AAACCTGCCT AGCAGAACGA CCCGTGAACG TGATATCAAA CAA---TCGA TCGAGGGGGT -GCGGATGCA
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ILfl000     TCCGTGCCCC GAGCCCCC-T CGATGCCTCG GCGTGC--CC GGCCTCACCA CACGCGCCCT C--GGGCGGG TG-CGA---T GGGTTTCGTG ACGCTCCGAG
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ILti181     CCCGTGCCCC GAACCCCC-T CGATGCCTTG GTGCGC--CC GGCCTTGCCA CATACGCCCT C--GGGCGGG TG-CGA---C GGGTCTCGTC GCGCTCCAAG
ILti233     CCCGTGCCCC GAACCCCC-T CGATGCCTTG GTGCGC--CC GGCCTTGCCA CATACGCCCT C--GGGCGGG TG-CGA---C GGGTCTCGTC GCGCTCCAAG
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ILth559     TCCGTGCCCC GAACCCCC-T CGATGCCTTG GCGTGC--CC AGCCTTGCCG CACGCGCCCT C--GGGCGGG TGTC-A---T AGGTTTCGTC ACTCTCCAAG
ILth353     TCCGTGCCCC GAACCCCC-T TGA-CCCTTG GCGTTC--CC AGCCTTGCCG CACGCGCCCT C--GGGACGG TGTCGA---C AGGTTTCGTC ACTCTCCAAG
ILmo346     TCCGTGCCCC GAACCCCC-T CGATGCCTTG GCGTGC--CC AGCCTTGCCA CGCACGCCCT C--GGGCGGG TG-CGA---C GGGTTCGGTC ACGCTCCGAG
ILmo515     TCCGTGCCCC GAACCCCC-T CGATGCCTTG GCGTGC--CC AGCCTTGCCA CGCACGCCCT C--GGGCGGG TG-CGA---C GGGTTCGGTC ACGCTCCGAG
ILma598     TCCTTGCCCC GAACCCCC-T CGACGCCTCG GCGTGC--CT AGCCTCGCCG CATCCGCCCT C--GGGCGGG TG-TGA---C GGGYTTCGTC ACGCTCCGAG
ILma329     TCCTTGCCCC GAACCCCC-T CGACGCCTCG GCGTGC--CT AGCCTCGCCG CRTCCGCCCT C--GGGCGGG TG-TGA---C GGGCTTCGTC ACGCTCCGAG
ILma200     TCCTTGCCCC GAACCCCC-T CGACGCCTCG GCGTGC--CT AGCCTCGCCG CRTCCGCCCT C--GGGCGGG TG-TGA---C GGGCTTCGTC ACGCTCCGAG
ILma404     TCCTTGCCCC GAACCCCC-T CGACGCCTCG GCGTGC--CT AGCCTCGCCG CGTCCGCCCT C--GGGCGGG TG-TGA---C GGGCTTCGTC ACGCTCCGAG
ILac135     TCCTTGCCCC GAACCCCC-T CGACGCCTCG GCGTGC--CC AGCCTCGCCG CATCCGCCCT C--GGGCGGG TG-CGA---C GGGCTTCGTC ACGCTCCGAG
ILas570     TCCTTGCCCC GAGCCCCC-T CGATGCCTCG GCGCGC--CG AGCCTTGCCG CATCCGTCCT C--GGGCGGG TG-TCC---C GGGTTTCGTC GCGCTCCGAG
ILab383     TCCTTGCCCC GAGCCCCC-T CGATGCCTCG GCGCGC--CG AGCCTTGCCG CATCCGTCCT C--GGGCGGG TG-TCC---C GGGTTTCGTC GCGCTCCGAG
ILpe634     TCCTTGCCCC GAGCCCCC-T CGATGCCTCG GCGCGC--CG AGCCTTGCCG CATCCGTCCT C--GGGCGGG TG-TCC---C GGGTTTCGTC GCGCTCCGAG
ILmu318     TCCTYGCCCC GAGCCCCC-T CGACGCCTCG GCGCGC--CG AGCCTCTCCG CATCCGTCCT C--GGGCGGG TG-TCC---C GGGTCTCGTC GTGCTCCGGG
ILmu630     TCCTTGCCCC GARCCCCC-T CGATGCCTCG GCGCGC--CA AGCCTTGCCG CATCCTCCCT C--GGGCGGG TG-CCC---T GGGTTTCGTC GCGCCCCGAG
ILar153     TCCTTGCCCC GAACCCCC-T CGATGCCTCG GCGCGC--CA AGCCTTGCCG CATCCTCCCT C--GGGCGGG TG-CCC---T GGGTTTCGTC GCGCCCCGAG
ILar252     TCCTTGCCCC GAACCCCC-T CGATGCCTCG GCGCGC--CA AGCCTTGCCG CATCCTCCCT C--GGGCGGG TG-CCC---T GGGTTTCGTC GCGCCCCGAG
ILar378     TCCTTGCCCC GAACCCCC-T CGATGCCTCG GCGCGC--CA AGCCTTGCCG CATCCTCCCT C--GGGCGGG TG-CCC---T GGGTTTCGTC GCGCCCCGAG
ILar239     TCCTTGCCCC GAACCCCC-T CGATGCCTCG GCGCGC--CA AGCCTTGCCG CATCCTCCCT C--GGGCGGG TG-CCC---T GGGTTTCGTC GCGCCCCGAG
ILcr031     TCCTTGCCCC GAGCCCCC-T CGATGCCTCG GCGCGC--CG AGCCTTGCCG CATCCGTCCT C--GGGCGGG TG-TCC---C GGGTTTCGTC GCGCTCCGAG
ILcr235     TCCTTGCCCC GAGCCCCC-T CGATGCCTCG GCGCGC--CG AGCCTTGCGG CATCCGTCCT C--GGGCGGG TG-TCC---C GGGTTTCGTC GCGCTCCGAG
ILcr599     TCCTTGCCCC GAGCCCCC-T CGATGCCTCG GCGCGC--CG AGCCTTGCCG CATCCGTCCT C--GGGCGGG TG-TCC---C GGGTTTCGTC GCGCTCCGAG
IMni032     TCCTTGCCCC GAGCCCCC-T CGATGCCTCG GCGCGC--CG AGCCTTGCCG CATCCGTCCT C--GGGCGGG TG-TCC---C GGGTTTCGTC GTGCTCCGAG
IMni097     TCCTTGCCCC GAGCCCCC-T CGATGCCTCG GCGCGC--CG AGCCTTGCCG CATCCGTCCT C--GGGCGGG TG-TCC---C GGGTTTCGTC GTGCTCCGAG
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IMni105     TCCTTGCCCC GAGCCCCC-T CGATGCCTCG GCGCGC--CG AGCCTTGCCG CATCCGTCCT C--GGGCGGG TG-TCC---C GGGTTTCGTC GYGCTCCGAG
IMni633     TCCTTGCCCC GAGCCCCC-T CGATGCCTCG GCGCGC--CG AGCCTTGCCG CATCCGTCCT C--GGGCGGG TG-TCC---C GGGTTTCGTC GTGCTCCGAG
IMni228     TCCTTGCCCC GAGCCCCC-T CGATGCCTCG GCGCGC--CG AGCCTTGCCG CATCCGTCCT C--GGGCGGG TG-TCC---C GGGTTTCGTC GYGCTCCGAG
IMne349     TCCTTGCCCC GAGCCCCC-T CGACGCCTCG GCGCGC--CG AGCCTCTCCG CATCCGTCCT C--GGGCGGG TG-TCC---C GTGTCTCGTC GTGCTCCGGG
IMne632     TCCTTGCCCC GAGCCCCC-T CGACGCCTCG GCGCGC--CG AGCCTCTCCG CATCCGTCCT C--GGGCGGG TG-TCC---C GGGTCTCGTC GTGCTCCGGG
IMsy001     TCCCTGCCCC GAGCCCCC-T CGATGCCTCG GCGCGC--CG AGCCTTGCCG CATCCGTCCT C--GGGCGGG TG-TCC---C GGGTTTCGTC GCGCTCCGAG
IMsy515     TCCTTGCCCC GAGCCCCC-T CGATGCCTCG GCGCGC--CG AGCCTTGCCG CATCCGTCCT C--GGGCGGG TG-TCC---C GGGTTTCGTC GCGCTCCGAG
IMsy635     TCCYTGCCCC GAGCCCCC-T CGATGCCTCG GCGCGC--CG AGCCTTGCCG CATCCGTCCT C--GGGCGGG TG-TCC---C GGGTTTCGTC GCGMTCCGAG
IMpa005     TCCTYGCCCC GAGCCCCC-T CGACGCCTCG GCGCGC--CG AGCCTCTCCG CATCCGTCCT C--GGGCGGG TG-TCC---C GGGTCTCGTC GTGCTCCGGG
IMpa059     TCCTTGCCCC GAGCCCCC-T CGACGCCTCG GCGCGC--CG AGCCTCTCCG CATCCGTCCT C--GGGCGGG TG-TCC---C GGGTCTCGTC GTGCTCCGGG
IMpa249     TCCTYGCCCC GAGCCCCC-T CGACGCCTCG GCGCGC--CG AGCCTCTCCG CATCCGTCCT C--GGGCGGG TG-TCC---C GGGTCTCGTC GTGCTCCGGG
IMpa296     TCCTCGCCCC GAGCCCCC-T CGACGCCTCG GCGCGC--CG AGCCTCTCCG CATCCGTCCT C--GGGCGGG TG-TCC---C GGGTCTCGTC GTGCTCCGGG
IMve442     TCCTCGCCCC GAGCCCCC-T CGACGCCTCG GCGCGC--CG AGCCTCTCCG CATCCGTCCT C--GGGCGGG TG-TCC---C GGGTCTCGTC GTGCTCCGGG
IMhi149     TCCGTGCCCC GAACCCCC-T CGATGCCTTG GCGTGC--CC TGCCTTGCCA CATACGCCCT C--GGGCGGG TG-TGA---C GGGTTTCGTC ACGCTCCAAG
IMhi602     TCCGTGCCCC GAACCCCC-T CGATGCCTTG GCGTGC--CC TGCCTTGCCA CATACGCCCT C--GGGCGGG TG-TGA---C GGGTTTCGTC ACGCTCCAAG
IMhi631     TCCGTGCCCC GAACCCCC-T CGATGCCTTG GCGTGC--CC TGCCTTGCCA CATACGCCCT C--GGGCGGG TG-TGA---C GGGTTTCGTC ACGCTCCAAG
IMal539     TCCGTGCCCC GAACCCCC-T CGATGCCTCG GCRTGC--CA GGCCCGTCCG CGTACGCCTC C--GTGCGTG CG-TGA---C GGGTTTCGTC GCGCTCCAAG
IMal440     TCCGTGCCCC GAACCCCC-T CGATGCCTCG GCGTGC--CA GGCCCGTCCG CGTACGCCTC C--GTGCGTG CG-TGA---C GGGTTTCGTC GCGCTCCAAG
IMal338     TCCGTGCCCC GAACCCCC-T CGATGCCTCG GCRTGC--CA GGCCCGTCCG CGTACGCCTC C--GTGCGTG CG-TGA---C GGGTTTCGTC GCGCTCCAAG
IMmo593     TCCGTGCCCC GAACCCCC-T CGATGCCTCG GCGTGC--CA GGCCCGTCCG CGTACGCCTC C--GTGCGTG CG-TGA---C GGGTTTCGTC GCGCTCCGAG
IMmo322     TCCGTGCCCC GAACCCCC-T CGATGCCTCG GCGTGC--CA GGCCCGTCCG CGTACGCCTC C--GTGCGTG CG-TGA---C GGGTTTCGTC GCGCTCCGAG
IMmo496     TCCGTGCCCC GAACCCCC-T CGATGCCTCG GCGTGC--CA GGCCCGTCCG CGTACGCCTC C--GTGCGTG CG-TGA---C GGGTTTCGTC GCGCTCCGAG
IMto189     TCCGTGCCCC GAACCCCC-T CGATGCCTCG GCGTGC--CA GGCCCGTCCG CGTACGCCTC C--GTGCGTG CG-TGA---C GGGTTTCGTC GCGCTCCGAG
IMto489     TCCGTGCCCC GAACCCCC-T CGATGCCTCG GCGTGC--CA GGCCCGTCCG CGTACGCCTC C--GTGCGTG CG-TGA---C GGKTTTCGTC GCGCTCCGAG
IMto479     TCCGTGCCCC GAACCCCC-T CGATGCCTCG GCGTGC--CA GGCCCGTCCG CGTACGCCTC C--GTGCGTG CG-TRA---C GGTTTTCGTC GCGCTCCAAG
IAlo362     TCCGTGCCCC GTTCCCCCCT CGATGCCGCG GCGTGC--CT GCCCTTGCCA CATCCGTCCC C--GGGCGGG TG-TGA---A GGGTTTTGTC ACGTTCCAAG
IAlo596     TCCGTGCCCC GTTCCCCCCT CGATGCCGCG GCGTGC--CT GCCCTTGCCA CATCCGTCCC C--GGGCGGG TG-TGA---A GGGTTTTGTC ACGTTCCAAG
IAlo461     TCCGTGCCCC GTTCCCCCCT CGATGCCGCG GCGTGC--CT GCCCTTGCCA CATCCGTCCC C--GGGCGGG TG-TGA---A GGGTTTTGTC ACGTTCCAAG
IAlo462     TCCGTGCCCC GTTCCCCCCT CGATGCCGCG GCGTGC--CT GCCCTTGCCA CATCCGTCCC C--GGGCGGG TG-TGA---A GGGTTTTGTC ACGTTCCAAG
IAlu459     TCCGTGCCCC GTTCCCCCCT CGATGCCTCG GTGTGC--AT TCCCCTCCCA CATCCGTCCT C--GGGCGGG TG-CGA---C GGGTTTTGTC ACATTCCAAG
IAlu460     TCCGTGCCCC GTTCCCCCCT CGATGCCTCG GTGTGC--AT TCCCCTCCCA CATCCGTCCT C--GGGCGGG TG-CGA---C GGGTTTTGTC ACATTCCAAG
IAlu616     TCCGTGCCCC GTTCCCCCCT CGATGCCTCG GTGTGC--AT TCCCCTCCCA CATCCGTCCT C--GGGCGGG TG-CGA---C GGGTTTTGTC ACATTCCAAG
IAhi455     TCCGTGCCCC GTTCCCCCCT CGATGCCGCG GCGTRC--CT GCCCTTGCCA CATCCGTCCC C--GGGCGGG TG-TGA---A GGGTTTTGTC ACKTTCCAAG
IAhi454     ACCGTGCCCC GTTCCCCCCT CGATGCCGCG GCGTGC--CT GCCCTTGCCA CATCCGTCCC C--GGGCGGG TG-TGA---A GGGTTTTGTC ACTTTCCAAG
IAhi356     ACCGTGCCCC GTTCCCCCCT CGATGCCGCG GCGTGC--CT GCCCTTGCCA CATCCGTCCC C--GGGCGGG TG-TGA---A GGGTTTTGTC ACTTTCCAAG
IAhi270     WCCGTGCCCC GTTCCCCCCT CGATGCCGCG GCGTGC--CT GCCCTTGCCA CATCCGTCCC C--GGGCGGG TG-TGA---A GGGTTTTGTC ACTTTCCAAG
IMat628       T    CC  NCT     C     GTGCC C              N  T   C          T    C  G          T      G             C   C
IMca463     TCCTTGCACC GTTCCCCCCT CGATGTCTCG GTGTGC--TT GGCCTTGCCG CATCCGTCCT C--GGGCTGA TG-CGA---A GGGTTTTGTC ACGCTCCGAG
IMca389     TCCTTGCACC GTTCCCCCCT CGATGTCTCG GTGTGC--CT GGCCTTGCCG CATCCGTCCT C--GGGCTGA CG-CGA---A GGGTTTTGTC ACGCTCCGAG
IMca390     TCCTTGCACC GTTCCCCCCT CGATGTCTCG GTGTGC--CT GGCCTTGCCG CATCCGTCCT C--GGGCTGA TG-CGA---A GGGTTTTGTC ACGCTCCGAG
IMca391     TCCTTGCACC GTTCCCCCCT CGATGTCTCG GTGTGC--CT GGCCTTGCCG CATCCGTCCT C--GGGCTGA TG-CGA---A GGGTTTTGTC ACGCTCCGAG
IMae466     TCCTTGCCCC AATCCCCC-T CGATGCCTCG GTGCGC--CC AGGCTTGCCA CATCCTCCCT C--GGGAGGG TG-TGC---C AGGTTTTGTC CTGCTCCGAG
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IMae468         TCCTTGCCCC AATCCCCC-T CGATGCCTCG GTGCGC--CC AGGCTTGCCA CATCCTCCCT C--GGGAGGG TG-TGC---C AGGTTTTGTC CTGCTCCGAG
IMae467         TCCTTGCCCC AATCCCCC-T CGATGCCTCG GTGCGC--CC AGGCTTGCCA CATCCTCCCT C--GGGAGGG TG-TGC---C AGGTTTTGTC CTGCTCCGAG
IMae465         TCCTTGCCCC AATCCCCC-T CGATGCCTCG GTGCGC--CC AGGCTTGCCA CATCCTCCCT C--GGGAGGG TG-TGC---C AGGTTTTGTC CTGCTCCGAG
IMae351         TCCTTGCCCC AATCCCCC-T -GATGCCTCG GTGCGC--CC AGGCTTGCCA CATCCTCCCT C--GGGAGGG TG-TGC---C AGGTTTTGTC CTGCTCCGAG
IMtr453         TTCTTGCCCC AATCCCCC-T CGATGCCTCG GTGCGC--CC AGGCTTGCCA CATCCTCCCT C--GGGAGGG TG-TGC---C RGGTTTTGTC CTGCTCCGAG
IMtr392         TYCTTGCCCC AATCCCCC-T CGATGCCTCG GTGCGC--CC AGGCTTGCCA CATCCTCCCT C--GGGAGGG TG-TGC---C AGGTTTTGTC CTGCTCCGAG
IMtr393         TYCTTGCCCC AATCCCCC-T CGATGCCTCG GTGCGC--CC AGGCTTGCCA CATCCTCCCT C--GGGAGGG TG-TGC---C RGGTTTTGTC CTGCTCCGAG
IMtr352         TTCTTGCCCC AATCCCCC-T CGATGCCTCG GTGCGC--CC AGGCTTGCCA CATCCTCCCT C--GGGAGGG TG-TGC---C AGGTTTTGTC CTGCTCCGAG
IMtr254         TYMTTGCCCC AATCCCCC-T CGATGCCTCG GTGCGC--CC AGGCTTGCCA CATCCTCCCT C--GGGAGGG TG-TGC---C RGGTTTTGTC CTGCTCCGAG
ILph002         TCCTTGCACC AAACCCCC-T CGATGCCTAA GTGTGC--CT AGCCTTGCCA CATTCGCCCT T--GGGCAGG TG-TGA---T AGGTTTTGTC ACACTCCAAG
ILph628         TCCTTGCACC AAACCCCC-T CGATGCCTAA GTGTGC--CT AGCCTTGCCA CATTCGCCCT T--GGGCAGG TG-TGA---T AGGTTTTGTC ACACTCCAAG
ILph629         TCCTTGCACC AAACCCCC-T CGATGCCTAA GTGTGC--CT AGCCTTGCCA CATTCGCCCT T--GGGCAGG TG-TGA---T AGGTTTTGTC ACACTCCAAG
IMtf394         TCCATGCCCC AAACTCCC-T CGATGCCTTG GTGCGC--AG AGCCCGGCCG CATCCGCCCT C--GGGCGGG TG-AGT---T GGGTTTTGTC ACACTAAAGG
IMtf550         TCCATGCCCC AAACTCCC-T CGATGCCTTG GTGCGC--AG AGCCCGGCCG CATCCGCCCT C--GGGCGGG TG-AGT---T GGGTTTTGTC ACACTAAAGG
IMtf601         TCCATGCCCC AAACTCCC-T CGATGCCTTG GTGCGC--AG AGCCCGGCCG CATCCGCCCT C--GGGCGGG TG-AGT---T GGGTTTTGTC ACACTAAAGG
IMtf070         TCCATGCCCC AAACTCCC-T CGATGCCTTG GTGCGC--AG AGCCCGGCCG CATCCGCCCT C--GGGCGGG TG-AGT---T GGGTTTTGTC ACACTAAAGG
IMtf499         TCCATGCCCC AAACTCCC-T CGATGCCTTG GTGCGC--AG AGCCCGGCCG CATCCGCCCT C--GGGCGGG TG-AGT---T GGGTTTTGTC ACACTAAAGG
IMma600         TCCATGCCCC AAACTCCC-T CGATGCCTTG GTGCGC--AG AGCCCGGCCG CATCCGCCCT C--GGGCGGG TG-AGT---T GGGTTTTGTC ACTCTATAGG
IMma415         TCCATGCCCC AAACTCCC-T CGATGCCTTG GTGTGCGCAG AGCCCGGCCG CATCCGCCCT C--TTGCGGG TG-AGT---T GGGTTTTGTC ACGCTATAGG
IAof604         TCCTTGCCCC AAACCCCC-T CGCTGCCTTG GTGTGA--TT GGATTCTCCC CACTCGCTCT T--GGGCGGG TG-AGATGTC AGGTCTTGTC GCACTC--GG
IAof330         TCCTTGCCCC AAACCCCC-T CGCTGCCTTG GTGTGA--TT GGATTCTCCC CACTCGCTCT T--GGGCGGG TG-AGATGTC AGGTCTTGTC GCACTC--GG
IAof512         TCCTTGCCCC AAACCCCC-T CGCTGCCTTG GTGTGA--TT GGATTCTCCC CACTCGCTCT T--GGGCGGG TG-AGATGTC AGGTCTTGTC GCACTC--GG
IAca594         TCCTTGCCCC AAACCCCC-T CGCTGCCTTG GTGTGA--TT GGATTCTCCC CACTCGCTCT T--GGGCGGG TG-AGATGTC AGGTCTTGTC GCACTC--GG
IAca345         TCCTTGCCCC AAACCCCC-T CGCTGCCTTG GTGTGA--TT GGATTCTCCC CACTCGCTCT T--GGGCGGG TG-AGATGTC AGGTCTTGTC GCACTC--GG
IAca471         TCCTTGCCCC AAACCCCC-T CGCTGCCTTG GTGTGA--TT GGATTCTCCC CACTCGCTCT T--GGGCGGG TG-AGATGTC AGGTCTTGTC GCACTC--GG
IAar427         TCCTTGCCCC AAACCCCC-T CGCTGCCTTG GTGTGA--TT GGATTCTCCC CACTCGCTCT T--GGGCGGG TG-AGATGTC AGGTCTTGTC GCACTC--GG
Iang615         TCTTTGCCCC AAACCCCC-T CGTTGCCTAG GTGTGC--TT GGCCTTTCCT CATTCGTTCT T--GGGCGGG TG-AGATTAY AGGTCTTGTT GCACTC--AG
Iros422         TCTTTGCCCC AAACCCCC-T CGTTGCCTAG GTGTGC--TT GGCCTTTCCC CATTCGTTCT T--GGGCGGG TG-AGATTAC AGGTCTTGTT GCACTC--AG
IAsp140         TCTTTGCCCC AAACCCCC-T CGTTGCCTAG GTGTGC--TT GGCCTTTCCT CATTCGTTCT T--GGGCGGG TG-AGATTAT AGGTCTTGTT GCACTC--AG
IMsh325         ATCTTGCCCC AAACCCTC-C CGATGCCTTG TTGTGC--TT GACCTTGCCT CATTC-CCCT A--GAGAGTA TG-ATGTGCT TGGCC---TC GCACTTCAAG


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                       210        220        230        240        250        260        270        280        290        300
ILag308         GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAAAA--TG AAA-GAGTGC G--------- ---------- ---------T GTTTCGCTGT
ILtp354         GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAAAA--TG AAA-gAGTGC G--------- ---------- ---------T GCTTCGCTGT
ILtp564         GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT ACAAAA--TG AAA-GAGTGC A--------- ---------- ---------T GTTTCGCCGT
ILfl414         GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAAAA--TG AAA-GAGTGC G--------- ---------- ---------T GTTTCGCTGT
ILfl000         GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAAAA--TG AAA-GAGTGC G--------- ---------- ---------T GTTTCGCTGT
ILtr117         GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAAAA--TG AAA-GAGTGC G--------- ---------- ---------T GCTTCGCTGT
ILtr357         GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAAAA--TG AAA-GAGTGC G--------- ---------- ---------T GCTTCGCTGT
ILtr359         GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAAAA--TG AAA-GAGTGC G--------- ---------- ---------T GCTTCGCTGT
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ILtr169       GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAAAA--TG AAA-GAGTGC G--------- ---------- ---------T GCTTCGCTGT
ILbr141       GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAAAA--TG AAG-GAGTGC A--------- ---------- ---------T GTTTCGCTGT
ILbr552       GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAAAA--TG AAG-GAGTGC A--------- ---------- ---------T GTTTCGCTGT
ILob144       GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAAAA--TG AAA-GAGTGC G--------- ---------- ---------T GTTTCGCTGT
ILol004       GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAAAAAATG AAA-GAGTGC A--------- ---------- ---------T GTTTCGCCGT
ILol451       GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAAAAAATG AAA-GAGTGC A--------- ---------- ---------T GTTTCGCCGT
ILpl285       GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAAAA--TG AAA-GAGTGC A--------- ---------- ---------T GTTTCGTCGT
ILpu450       GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAAAA--TG AAA-GAGTGC G--------- ---------- ---------T GCTTCGCTGT
ILpu348       GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT ACAAAA--TG AAA-GAGTGC A--------- ---------- ---------T GTTTCGCCGT
ILti595       GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAAAA--TG AAA-GAGTGC A--------- ---------- ---------T GTTTCGTTGT
ILti181       GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAAAA--TG AAA-GAGTGC A--------- ---------- ---------T GTTTCGTTGT
ILti233       GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAAAA--TG AAA-GAGTGC A--------- ---------- ---------T GTTTCGTTGT
ILti308       GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAAAA--TG AAA-GAGTGC A--------- ---------- ---------T GTTTCGTTGT
ILth559       GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAARAA--TG AAA-GAGTGC A--------- ---------- ---------C GTTTCGCTGT
ILth353       GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAAAA--TG AAA-GAGTGC AC-------- ---------- ---------T GTTTCGT-GT
ILmo346       GCAAAACCAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAGAA--TG AAA-GAGTGC A--------- ---------- ---------T GTTTCGCCGT
ILmo515       GCAAAACCAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAGAA--TG AAA-GAGTGC A--------- ---------- ---------T GTTTCGCCGT
ILma598       GCAAAACGAA CAACCCCCGG CGCGAACCGC GTCAAGGAAT AAAAAA--TG AAAAGAGTGC G--------- ---------- ---------T GTTTCGTTGT
ILma329       GCAAAACGAA CAACCCCCGG CGCGAACCGC GTCAAGGAAT AAAAAA--TG AAAAGAGTGC G--------- ---------- ---------T GTTTCGTTGT
ILma200       GCAAAACGAA CAACCCCCGG CGCGAACCGC GTCAAGGAAT AAAAAA--TG AAAAGAGTGC G--------- ---------- ---------T GTTTCGTTGT
ILma404       GCAAAACGAA CAACCCCCGG CGCGAACCGC GTCAAGGAAT AAAAAA--TG AAAAGAGTGC G--------- ---------- ---------T GTTTCGTTGT
ILac135       GCAAAACGAA CAACCCCCGG CGCGAACCGC GTCAAGGAAT AAAAAA--TG AAAAGAGTGC G--------- ---------- ---------T GTTTCGTTGT
ILas570       GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAAAA--TG AAAAGAGTGC G--------- ---------- ---------T GTTTCGTTGT
ILab383       GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAAAA--TG AAAAGAGTGC G--------- ---------- ---------T GTTTCGTTGT
ILpe634       GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT ACAAAA--TG AAAAGAGTGC G--------- ---------- ---------C GTTTCGTTGT
ILmu318       GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAAAA--TG AAAAGAGTGC G--------- ---------- ---------T GTTTCGTTGT
ILmu630       GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAAAA--TG AAAAGAGCGC G--------- ---------- ---------T GTTTCGTTGT
ILar153       GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAAAA--TG AAAAGAGCGC G--------- ---------- ---------T GTTTCGTTGT
ILar252       GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAAAA--TG AAAAGAGCGC G--------- ---------- ---------T GTTTCGTTGT
ILar378       GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAAAA--TG AAAAGAGCGC G--------- ---------- ---------T GTTTCGTTGT
ILar239       GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAAAA--TG AAAAGAGCGC G--------- ---------- ---------T GTTTCGTTGT
ILcr031       GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAAAA--TG AAAAGAGTGC G--------- ---------- ---------T GTTTCGTTGT
ILcr235       GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAAAA--TG AAAAGAGTGC G--------- ---------- ---------T GTTTCGTTGT
ILcr599       GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAAAA--TG AAAAGAGTGC G--------- ---------- ---------T GTTTCGTTGT
IMni032       GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAAAA--TG AAAAGAGTGC G--------- ---------- ---------T GTTTCGTTGT
IMni097       GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAAAA--TG AAAAGAGTGC G--------- ---------- ---------T GTTTCGTTGT
IMni105       GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAAAA--TG AAAAGAGTGC G--------- ---------- ---------T GTTTCGTTGT
IMni633       GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAAAA--TG AAAAGAGTGC G--------- ---------- ---------T GTTTCGTTGT
IMni228       GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAAAA--TG AAAAGAGTGC G--------- ---------- ---------T GTTTCGTTGT
IMne349       GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAAAA--TG AAAAGAGTGC G--------- ---------- ---------T GTTTCGTTGT
IMne632       GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAY AAAAAA--TG AAAAGAGTGC G--------- ---------- ---------T GTTTCGTTGT
IMsy001       GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAAAA--TG AAAAGAGTGC G--------- ---------- ---------T GTTTCGTTGT
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IMsy515      GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAAAA--TG AAAAGAGTGC G--------- ---------- ---------T GTTTCGTTGT
IMsy635      GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAAAA--TG AAAAGAGTGC G--------- ---------- ---------T GTTTCGTTGT
IMpa005      GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAAAA--TG AAAAGAGTGC G--------- ---------- ---------T GTTTCGTTGT
IMpa059      GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAAAA--TG AAAAGAGTGC G--------- ---------- ---------T GTTTCGTTGT
IMpa249      GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAAAA--TG AAAAGAGTGC G--------- ---------- ---------T GTTTCGTTGT
IMpa296      GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAAAA--TG AAAAGAGTGC G--------- ---------- ---------T GTTTCGTTGT
IMve442      GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAAAA--TG AAAAGAGTGC G--------- ---------- ---------T GTTTCGTTGT
IMhi149      GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAATA--TG AAA-GAGTGC A--------- ---------- ---------T GTTTCGTTGT
IMhi602      GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAATA--TG AAA-GAGTGC A--------- ---------- ---------T GTTTCGTTGT
IMhi631      GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAATA--TG AAA-GAGTGC A--------- ---------- ---------T GTTTCGTTGT
IMal539      GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAAAA--TG AAG-GAGTGC A--------- ---------- ---------T GTTTCGCCGT
IMal440      GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAAAA--TG AAG-GAGTGC A--------- ---------- ---------T GTTTCGCCGT
IMal338      GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAAAA--TG AAG-GAGTGC A--------- ---------- ---------T GTTTCGCCGT
IMmo593      GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAAAA--TG AAG-GAGTGC A--------- ---------- ---------T GTTTCGCCGT
IMmo322      GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAAAA--TG AAG-GAGTGC A--------- ---------- ---------T GTTTCGCCGT
IMmo496      GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAAAA--TG AAG-GAGTGC A--------- ---------- ---------T GTTTCGCCGT
IMto189      GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAAAA--TG AAG-GAGTGC AC-------- ---------- ---------T GTTTCGCCGT
IMto489      GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAAAA--TG AAG-GAGTGC A--------- ---------- ---------T GTTTCGCCGT
IMto479      GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAAAA--TG AAG-GAGTGC A--------- ---------- ---------T GTTTCGCCGT
IAlo362      GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAAAA--TG AAA-GAGTGC A--------- ---------- ---------T GTTTCTCTGT
IAlo596      GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAAAA--TG AAA-GAGTGC A--------- ---------- ---------T GTTTCTCTGT
IAlo461      GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAAAA--TG AAA-GAGTGC A--------- ---------- ---------T GTTTCTCTGT
IAlo462      GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAAAA--TG AAA-GAGTGC A--------- ---------- ---------T GTTTCTCTGT
IAlu459      GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAAAA--TG AAG-GAGTGC A--------- ---------- ---------T GTTTCGCTGT
IAlu460      GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAAAA--TG AAG-GAGTGC A--------- ---------- ---------T GTTTCGCTGT
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IMat628       C G  GA A A      CA                A----AT GAAAAA--TG AAC-RAGTGC A--------- ---------- ---------T GTTTCC-TGT
IMca463      GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAAAAAATG AAA-GGGTGC A--------- ---------- ---------T GTTTCGCTGT
IMca389      GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT CAAAAAAATG AAA-GGGTGC A--------- ---------- ---------T GTTTCGCTGT
IMca390      GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAAAAA-TG AAA-GGGTGC A--------- ---------- ---------T GTTTCGCTGT
IMca391      GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT AAAAAAA-TG AAA-GGGTGC A--------- ---------- ---------T GTTTCGCTGT
IMae466      GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT GAAAAA--TG AAC-GAGTGC A--------- ---------- ---------T GTTTC-CTGT
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IMtr352      GCAAAACGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT GAAAAA--TG AAS-GAGTGC A--------- ---------- ---------T GTTTC-CTGT
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ILph002      GCAAAACGAA CAACCCCCGG CGCGAATTGC GTCAAGGAAT AAAAAA--TG AAA-GAGTGC A--------- ---------- ---------T GTTT-ACTGT
ILph628      GCAAAACGAA CAACCCCCGG CGCGAATTGC GTCAAGGAAT AAAAAA--TG AAA-GAGTGC A--------- ---------- ---------T GTTT-ACTGT
ILph629      GCAAAACGAA CAACCCCCGG CGCGAATTGC GTCAAGGAAT AAAAAA--TG AAA-GAGTGC A--------- ---------- ---------T GTTT-ACTGT
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IMtf550      TCAAAACGAA CAACCCCCGG CGCGAATTGC GTCAAGGAAT AAAAA---TG AAA-GAGTGC ACGTTT-GCT GTCCACGTCC CGTGCGCGGT GT----CTGT
IMtf601      TCAAAACGAA CAACCCCCGG CGCGAATTGC GTCAAGGAAT AAAAA---TG AAA-GAGTGC ACGTTT-GCT GTCCACGTCC CGTGCGCGGT GT----CTGT
IMtf070      TCAAAACGAA CAACCCCCGG CGCGAATTGC GTCAAGGAAT AAAAA---TG AAA-GAGTGC ACGTTT-GCT GTCCACGTCC CGTGCGCGGT GT----CTGT
IMtf499      TCAAAACGAA CAACCCCCGG CGCGAATTGC GTCAAGGAAT AAAAA---TG AAA-GAGTGC ACGTTT-GCT GTCCACGTCC CGTGCGCGGT GT----CTGT
IMma600      TCAAA-CGAA CAACCCCCGG CGCGAATAGC GTCAAGGAAT AAAAA---TG AAA-GAGTGC ACGTTT-GCC GTCCACGTCC CGTGCGCGGT GT----CTGT
IMma415      TCAAA-CGAA CAACCCCCGG CGCGAATAGC GTCAAGGAAT AAAAA---TG AAA-GAGTGC ACGTTTTGCC GTCCACGTCC CGTGCGCGGT GC----CTGT
IAof604      GCAAAATGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT TAAAAA--TG AAAAGGGTGC GCGTCT-ACT GTCGTCGTCC CGTACGCGGT GTTT----GT
IAof330      GCAAAATGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT TAAAAA--TG AAAAGGGTGC GCG-CT-ACT GTCGTCGTCC CGTACGCGGT GTTT----GT
IAof512      GCAAAATGAA CAACCCCCGG CGCGAATCGC GTCAAGGAAT TAAAAA--TG AAAAGGGTGC GCGTCT-ACT GTCGTCGTCC CGTACGCGGT GTTT----GT
IAca594      GCAAAACGAA CAACCCCCGG CGCGAATTGC GTCAAGGAAT TAAAAA--TG AAAAGAGTGC ACGTCT-ACT GTCGTCGTCC CGTACGCGGT GTTT----GT
IAca345      GCAAAACGAA CAACCCCCGG CGCGAATTGC GTCAAGGAAT TAAAAA--TG AAAAGAGTGC ACG-CT-ACT GTCGTCGTCC CGTACGCGGT GTTT----GT
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Iang615      GTAAAATGAA CAACCCCCGG CGCGAATTGC GTCAAGGAAT TAAAAA--TG AAAAGAGTGC ACGTCT-ACT GTCATCGTCC CGTATGCGGT GTTT----GT
Iros422      GTAAAATGAA CAACCCCCGG CGCGAATTGC GTCAAGGAAT TAAAAA--TG AAAAGAGTGC ACGTCT-ACT GTCATCGTCC CGTATGCGGT GTTT----GT
IAsp140      GTAAAATGAA CAACCCCCGG CGCGAATTGC GTCAAGGAAT TAAAAA--TG AAAAGAGTGC ACG-CT-ACT GTCATCGTCC CGTATGCGGT GTTT----GT
IMsh325      GCAAAACGAA CAACCCCCGG CGCGAAAAGC GCCAAGGAAT AAAAAA---G AAAAGAGGGC ACGACC---T GTCGCCTACC CGTTCGCGGT GT----CTGT


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                    310        320        330        340        350        360        370        380        390        400
ILag308      CGCACGGCAG CG-AGGATGT T----ACTTT TGTCGTGAAA A-T--AAAAA --CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
ILtp354      CGCACGGCAG CG-AGGATGT T----ACTTT TGTCGTGAAA A-T--AAAAA --CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
ILtp564      CTCACGGCAG CG-AGGATGT C----ACTTT TGTCGTGAAA A-T--AAAAA --CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
ILfl414      CGCACGGCAG CG-AGGACGT T----ACTTT TGTCGTGAAA A-T--AAAAA --CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
ILfl000      CGCACGGCAG CG-AGGAYGT T----ACTTT TGTCGTGAAA A-Y--AAAAA --CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
ILtr117      CGCACGGCAG CG-AGGATGT T----ACTTT TGTCGTGAAA A-T--AAAAA --CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
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ILbr141      CGCACGGCGG CG-AGGATGT T----ACTTT CGTCGTGAAA A-T--AAAAA --CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
ILbr552      CGCACGGCGG CG-AGGATGT T----ACTTT CGTCGTGAAA A-T--AAAAA --CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
ILob144      CGCACGGCAG CG-AGGATGT T----ACTTT TGTCGTGAAA A-T--AAAAA --CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
ILol004      CGCACGGCAG CG-AGGATGT T----ACTTT TGTCGTGAAA A-T--AAAAA --CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
ILol451      CGCACGGCAG CG-AGGATGT T----ACTTT TGTCGTGAAA A-T--AAAAA --CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
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ILpl285       CGCACGGCGG CG-AGGATGT T----ACTTT TGTCGTGAAA A-T--AAAAA --CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
ILpu450       CGCACGGCAG CG-AGGATGT T----ACTTT TGTCGTGAAA A-T--AAAAA --CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
ILpu348       CTCACGGCAG CG-AGGATGT C----ACTTT TGTCGTGAAA A-T--AAAAA --CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
ILti595       CGCACGGCAG CG-AGGATGT C----ACTTT TGTCGTGAAA A-T--AAAAA --CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
ILti181       CGCACGGCAG CG-AGGATGT C----ACTTT TGTCGTGAAA A-T--AAAAA --CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
ILti233       CGCACGGCAG CG-AGGATGT C----ACTTT TGTCGTGAAA A-T--AAAAA --CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
ILti308       CGCACGGCAG CG-AGGATGT C----ACTTT TGTCGTGAAA A-T--AAAAA --CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
ILth559       CGCATGGCAG CG-AGGATGT C----ACTTT TGTCGTGAAA A-T--AAAAA --CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
ILth353       CGCAMGGCAG CGGAGGATGT C----ACTTT TGTCGTGAAA A-T--AAAAA --CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
ILmo346       CGCACGGCAG CG-AGGATGT C----ACTTT TGTCGTGAAA A-T--AAAAA --CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
ILmo515       CGCACGGCAG CG-AGGATGT C----ACTTT TGTCGTGAAA A-T--AAAAA --CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
ILma598       CGTCCGGCAG CG-AGGATGC T--CCACTCT AGTCGTGAAA A-T--AAAAA --CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
ILma329       CGTCCGGCAG CG-AGGATGC T--CCACTCT AGTCGTGAAA A-T--AAAAA --CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
ILma200       CGTCCGGCAG CG-AGGATGC T--CCACTCT AGTCGTGAAA A-T--AAAAA --CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
ILma404       CGTCCGGCAG CG-AGGATGC T--CCACTCT AGTCGTGAAA A-T--AAAAA --CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
ILac135       CGTCCGGCAG CG-AGGACGT C----GCTCT CGTCGTGAAA A-T--AAAAA --CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
ILas570       CGTATGGCAG CG-AGGGCGT C----GCTCT CGTCGTGAAA A-T--AAAAA A-CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
ILab383       CGTATGGCAG CG-AGGGCGT C----GCTCT CGTCGTGAAA A-T--AAAAA A-CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
ILpe634       CGTATGGCAT CG-AGGGCGT C----GCTCT CGTCGTGAAA A-T--AAAAA A-CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
ILmu318       CGTATGGCAG CG-AGGGCGT T----ACTCT CGTCGTGAAA A-TT-AAAAA --CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
ILmu630       CGTCGGGCAA CA-AACACGT C----ACTCT CGTCGTGAAA A-T--AAAAA --CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
ILar153       CGTCGGGCAA CA-AACACGT C----ACTCT CGTCGTGAAA A-T--AAAAA --CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
ILar252       CGTCGGGCAA CA-AACACGT C----ACTCT CGTCGTGAAA A-T--AAAAA --CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
ILar378       CGTCGGGCAA CA-AACACGT C----ACTCT CGTCGTGAAA A-T--AAAAA --CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
ILar239       CGTCGGGCAA CA-AACACGT C----ACTCT CGTCGTGAAA A-T--AAAAA --CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
ILcr031       CGTATGGCAG CG-AGGGCGT C----ACTCT CGTCGTGAAA A-TT-AAAAA --CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
ILcr235       CGTATGGCAG CG-AGGGCGT C----ACTCT CGTCGTGAAA A-TT-AAAAA --CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
ILcr599       CGTATGGCAG CG-AGGGCGT C----ACTCT CGTCGTGAAA A-TT-AAAAA --CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
IMni032       CGTATGGCAG CG-AGGGCGT C----ACTCT CGTCGTGAAA A-TT-AAAAA --CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
IMni097       CGTATGGCAG CG-AGGGCGT C----ACTCT CGTCGTGAAA A-TT-AAAAA --CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
IMni105       CGTATGGCAG CG-AGGGCGT C----ACTCT CGTCGTGAAA A-TT-AAAAA --CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
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IMni228       CGTATGGCAG CG-AGGGCGT C----ACTCT CGTCGTGAAA A-TT-AAAAA --CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
IMne349       CGTATGGCAG CG-AGGGCGT T----ACTCT CGTCGTGAAA A-TTTAAAA- --CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
IMne632       CGTATGGCAG CG-AGGGCGT T----ACTCT CGTCGTGAAA A-TTTAAAA- --CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
IMsy001       CGTATGGCAG CG-AGGGCGT T----ACTCT CGTCGTGAAA A-TT-AAAAA --CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
IMsy515       CGTATGGCAG CG-AGGGCGT T----ACTCT CGTCGTGAAA A-TT-AAAAA --CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
IMsy635       CGTATGGCAG CG-AGGGCGT T----ACTCT CGTCGTGAAA A-TT-AAAAA --CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
IMpa005       CGTATGGCAG C--AGGGCGT T----ACTCT CGTCGTGAAA A-TT-AAAAA --CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
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IMve442      CGTATGGCAG CG-AGGGCGT T----ACTCT CGTCGTGAAA A-TT-AAAAA --CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
IMhi149      CTCCCGGCAG CG-AGGATGT T----ACTTT TGTCGTGAAA A-T--AAAAA --CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
IMhi602      CTCMCGGCAG CG-AGGATGT T----ACTTT TGTCGTGAAA A-T--AAAAA --CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
IMhi631      CTCACGGCAG CG-AGGATGT T----ACTTT TGTCGTGAAA A-T--AAAAA --CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
IMal539      CGCACGACGG CG-AGGATGT T----ACTTT CGTCGTGAAA A-T--AAAAA --CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
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IMal338      CGCACGACGG CG-AGGATGT T----ACTTT CGTCGTGAAA A-T--AAAAA --CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
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IMmo496      CGCACGACGG CG-AGGATGT T----ACTTT CGTCGTGAAA A-T--AAAAA --CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
IMto189      CGCACGACGG CG-AGGATGT T----ACTTT CGTCGTGAAA A-T--AAAAA --CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
IMto489      CGCACGACGG CG-AGGATGT T----ACTTT CGTCGTGAAA A-T--AAAAA --CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
IMto479      CGCACGACGA CG-AGGATGT T----ACTTT CGTCGTGAAA A-T--AAAAA --CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
IAlo362      CGCCCGACAG CG-AGGATGT T----ACTTT TGTCGTGAAA A-T--AAAAA A-CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
IAlo596      CGCCCGGCAG CG-AGGATGT T----ACTTT TGTCGTGAAA A-T--AAAAA A-CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
IAlo461      CGCCCGACAG CG-AGGATGT T----ACTTT TGTCGTGAAA A-T--AAAAA A-CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
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IAhi455      CGCCCGGCAG CG-AGGATGT T----ACTTT TGTCGTGAAA A-T--AAAAA A-CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
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IAhi356      CGCCCGGCAG CG-AGGATGT T----ACTTT TGTCGTGAAA A-T--AAAAA A-CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
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IMat628      CATCTGGCAG CG-AGGATGY T----ACTTT YGTCGTGAAA A-T--AAAAA A-CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
IMca463      CGCCCGGCAG CG-AGTGTGT T----ACTTT TGTCGTGAAA A-T--AAAAA --CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
IMca389      CGCCCGGCAG CG-AGGGTGT T----ACTTT TGTCGTGAAA A-T--AAAAA --CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
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IMca391      CGCCCGGCAG CG-AGGGTGT T----ACTTT TGTCGTGAAA A-T--AAAAA --CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
IMae466      CATCTGGCAG CG-AGGATGC T----ACTTT CGTCGTGAAA A-T--AAAAA A-CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
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IMae465      CATCTGGCAG CG-AGGATGC T----ACTTT CGTCGTGAAA A-T--AAAAA A-CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
IMae351      CATCTGGCAG CG-AGGATGC T----ACTTT CGTCGTGAAA A-T--AAAAA A-CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
IMtr453      CATCTGGCAG CG-AGGATGC T----ACTTT CGTCGTGAAA A-T--AAAAA A-CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
IMtr392      CRTCTGGCAG CG-AGGATGC T----ACTTT CGTCGTGAAA A-T--AAAAA A-CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
IMtr393      CATCTGGCAG CG-AGGATGC T----ACTTT CGTCGTGAAA A-T--AAAAA A-CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
IMtr352      CRTCTGGCAG CG-AGGATGC T----ACTTT CGTCGTGAAA A-T--AAAAA A-CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
IMtr254      CRTCTGGCAG CG-AGGATGC T----ACTTT CGTCGTGAAA A-T--AAAAA A-CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
ILph002      CGCCTGGCAG TG-AGGATGT T----ACTTT TGTCGTGAAA A-T--AAAAA --CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
ILph628      CGCCTGGCAG TG-AGGATGT T----ACTTT TGTCGTGAAA A-T--AAAAA --CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
ILph629      CGCCTGGCAG TG-AGGATGT T----ACTTT TGTCGTGAAA A-T--AAAAA --CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
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IMtf394             GTGGCGGCGA CGG----TGT T----ACTTC TGTCGTGAAA AAT--AAAAA AACGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
IMtf550             GTGGCGGCGA CGG----TGT T----ACTTC TGTCGTGAAA AAT--AAAAA AACGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
IMtf601             GTGGCGGCGA CGG----TGT T----ACTTC TGTCGTGAAA AAT--AAAAA AACGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
IMtf070             GTGGCGGCGA CGG----TGT T----ACTTC TGTCGTGAAA AAT--AAAAA AACGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
IMtf499             GTGGCGGCGA CGG----TGT T----ACTTC TGTCGTGAAA AAT--AAAAA AACGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
IMma600             GTGGCGGCGA CGG----TGT T----ACTTC TGTCGTGAAA AAT--AAAAA A-CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
IMma415             GTGGCGGCGA CGG----TGT T----ACTTC TGTCGTGAAA AAT--AAAAA AACGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
IAof604             GCGGCAGTGA CGC----TGT T----ACTCT AGTCGTGAAA A-T--ACAAA A-CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
IAof330             GCGGCAGTGA CGC----TGT T----ACTCT AGTCGTGAAA A-T--ACAAA A-CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
IAof512             GCGGCAGTGA CGC----TGT T----ACTCT AGTCGTGAAA A-T--ACAAA A-CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
IAca594             GCGACAGTGA CGC----CGT T----ACTCT AGTCGTGAAA A-T--ACAAA A-CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
IAca345             GCGACAGTGA CGC----CGT T----ACTCT AGTCGTGAAA A-T--ACAAA A-CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
IAca471             GCGACAGTGA CGC----CGT T----ACTCT AGTCGTGAAA A-T--ACAAA A-CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
IAar427             GCGGCAGTGA CGC----TGT T----ACTCT AGTCGTGAAA A-T--ACAAA A-CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
Iang615             GTGGCAGTGA CGC----TGT T----ACTTT TGTCGTGAAA --T--ACAAA A-CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
Iros422             GTGGCAGTGA CGC----TGT T----ACTTT TGTCGTGAAA --T--ACAAA A-CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
IAsp140             GTGGCAGTGA CGC----TGT T----ACTTT TGTCGTGAAA --T--ACAAA A-CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA
IMsh325             GCGGCAGTGT CGT----TGT C----ACTTT TGTCGTAAAA --TT-ACAAA A-CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA


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                           410        420        430        440        450        460        470        480        490        500
ILag308             GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
ILtp354             GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
ILtp564             GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
ILfl414             GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
ILfl000             GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
ILtr117             GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
ILtr357             GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
ILtr359             GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
ILtr169             GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
ILbr141             GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
ILbr552             GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
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ILol004             GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
ILol451             GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
ILpl285             GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
ILpu450             GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
ILpu348             GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
ILti595             GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
ILti181             GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
ILti233             GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
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ILti308     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
ILth559     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
ILth353     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCKAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
ILmo346     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
ILmo515     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
ILma598     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
ILma329     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
ILma200     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
ILma404     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
ILac135     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
ILas570     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
ILab383     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
ILpe634     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
ILmu318     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
ILmu630     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
ILar153     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
ILar252     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
ILar378     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
ILar239     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
ILcr031     -CGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
ILcr235     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
ILcr599     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
IMni032     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
IMni097     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
IMni105     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
IMni633     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
IMni228     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
IMne349     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
IMne632     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
IMsy001     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
IMsy515     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
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IMpa005     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
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IMpa249     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
IMpa296     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
IMve442     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
IMhi149     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
IMhi602     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
IMhi631     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
IMal539     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
IMal440     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
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IMal338     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
IMmo593     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
IMmo322     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
IMmo496     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
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IMto479     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
IAlo362     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGTCGAGGG CACGTCTGCC
IAlo596     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGTCGAGGG CACGTCTGCC
IAlo461     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGTCGAGGG CACGTCTGCC
IAlo462     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGTCGAGGG CACGTCTGCC
IAlu459     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
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IAlu616     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
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IMat628     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
IMca463     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
IMca389     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
IMca390     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
IMca391     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
IMae466     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
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ILph629     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCTTT AGGCCGAGGG CACGTCTGCC
IMtf394     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCATT AGGCCGAGGG CACGTCTGCC
IMtf550     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCATT AGGCCGAGGG CACGTCTGCC
IMtf601     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCATT AGGCCGAGGG CACGTCTGCC
IMtf070     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCATT AGGCCGAGGG CACGTCTGCC
IMtf499     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCATT AGGCCGAGGG CACGTCTGCC
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IMma415     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCATT AGGCCGAGGG CACGTCTGCC
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IAof330     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CGAAGCCATT AGGCCGAGGG CACGTCTGCC
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IAca594     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CGAAGCCATT AGGCCGAGGG CACGTCTGCC
IAca345     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CGAAGCCATT AGGCCGAGGG CACGTCTGCC
IAca471     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CGAAGCCATT AGGCCGAGGG CACGTCTGCC
IAar427     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CGAAGCCATT AGGCCGAGGG CACGTCTGCC
Iang615     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCATT AGGCCGAGGG CACGTCTGCC
Iros422     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCATT AGGCCGAGGG CACGTCTGCC
IAsp140     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCATT AGGCCGAGGG CACGTCTGCC
IMsh325     GCGAAATGCG ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCACT AGGCCGAGGG CACGTCTGCC


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                   510        520        530        540        550        560        570        580        590        600
ILag308     TGGGTGTCAC GCGTCGTTGC CCCCATCAAA CCCCGAGCCC TC--GGGCCT CGATTGATGC GCGGGCGGAA ATTGGCCTCC CGTGCGCTCA CCGCTCGCGG
ILtp354     TGGGTGTCAC GCATCGTTGC CCCCATCAAA CCCCGAGCCC TC--GGGCCT CGATTGATGC GCGGGCGGAA ATTGGCCTCC CGTGCGCTCA CCGCTCGCGG
ILtp564     TGGGTGTCAC GCATCGTCGC CCCCATCAAA CCCCGAGCCC TC--GGGGTA CGATTGATGT GCGGGCGGAA ATTGGCCTCC CGTGCGCTCA CCGCTCGCGG
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IAlo596	TGGGTGTCAC	GCATCGTTGC	CCCCATCAAA	CCCTGAGCCC	TC--GGGCTA	GGAATGATGT	GCGGGCGGAA	ATTGGCCTCC	CGTGCGCTCA	CCGCTCGCGG
IAlo461	TGGGTGTCAC	GCATCGTTGC	CCCCATCAAA	CCCTGAGCCC	TC--GGGCTA	GGAATGATGT	GCGGGCGGAA	ATTGGCCTCC	CGTGCGCTCA	CCGCTCGCGG
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IAhi455	TGGGTGTCAC	GCATCGTTGC	CCCCATCAAA	CCCTGAGCCC	TC--GGGCTA	GGAATGATGT	GCGGGCGGAA	ATTGGCCTCC	CGTGCGCTCA	CCGCTCGCGG
IAhi454	TGGGTGTCAC	GCATCGTTGC	CCCCATCAAA	CCCTGAGCCM	TC--GGGCTA	GGAATGATGT	GCGGGCGGAA	ATTGGCCTCC	CGTGCGCTCA	CCGCTCGCGG
IAhi356	TGGGTGTCAC	GCATCGTTGC	CCCCATCAAA	CCCTGAGCCC	TC--GGGCTA	GGAATGATGT	GCGGGCGGAA	ATTGGCCTCC	CGTGCGCTCA	CCGCTCGCGG
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IMat628	TGGGTGTCAC	GCATCGTTGC	CCCCATCAAA	CATCGAGCCC	TY--GGGCYA	CGATTGATGC	GCGGGCGGAA	ATTGGCCTCC	CGTGCGCTCA	CCGCTCGCGG
IMca463	TGGGTGTCAC	GCATCGTTGC	CCCCATCAAA	CCACCAGCCC	TC--GGGCTA	GGATTGATGY	GTGGGCGGAA	ATTGGCCTCC	CGTGCGCTCA	CCGCTCGCGG
IMca389	TGGGTGTCAC	GCATCGTTGC	CCCCATCAAA	CCACTAGCCC	TC--GGGCTA	GGATTGATGC	GTGGGCGGAA	ATTGGCCTCC	CGTGCGCTCA	CCGCTCGCGG
IMca390	TGGGTGTCAC	GCATCGTTGC	CCCCATCAAA	CCACTAGCCC	TC--GGGCTA	GGATTGATGT	GTGGGCGGAA	ATTGGCCTCC	CGTGCGCTMA	CCGCTCGCGG
IMca391	TGGGTGTCAC	GCATCGTTGC	CCCCATCAAA	CCACTAGCCC	TC--GGGCTA	GGATTGATGT	GTGGGCGGAA	ATTGGCCTCC	CGTGCGCTCA	CCGCTCGCGG
IMae466	TGGGTGTCAC	GCATCGTTGC	CCCCATCAAA	CGTCGAGCCC	TC--GGGCCA	CGGTTGATGC	GCGGGCGGAA	ATTGGCCTCC	CGTGCGCTCA	CCGCTCGCGG
IMae468	TGGGTGTCAC	GCATCGTTGC	CCCCATCAAA	CATCGAGCCC	TC--GGGCCA	CGGTTGATGC	GCGGGCGGAA	ATTGGCCTCC	CGTGCGCTCA	CCGCTCGCGG
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ILph628	TGGGTGTCAC	GCATCGTTGC	CCCCATCAAA	CCCTGAGCCC	TT--GGGCTA	CGGTTGATGT	GTGGGCGGAA	ATTGGCCTCC	CGTGCGCTCA	CCGCTCGCGG
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                     610        620        630        640        650        660        670        680        690        700
ILag308       TTGGTCTAAA -TTC-GAGTC CTCGGCGATG AAGTGCC-GC GACGATCGGT GGGAATGCTT TT----GGCT GCCTCGTACG GAGTCGCGCG CGCACGTTGA
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ILth353       TTGGTCTAAA -TTC-GAGTC CTCGGCGATG AGGTGCC-GC GACTATCGGT GGGAATGCTT TT----GGCT GCCTCGTTCG GAGTCGCGCG CGCTCGTTGA
ILmo346       TTGGTCTAAA -TTC-GAGTC CTCGGCGATG AAGCGCC-GC GAC-ATCGGT GGGAATGCTT TT----TGCT GCCTCGTTCG GAGTCGCTCG CGCTC-TTGA
ILmo515       TTGGTCTAAA -TTC-GAGTC CTCGGCGATG AAGCGCC-GC GACGATCGGT GGGAATGCTT TT----TGCT GCCTCGTTCG GAGTCGCTCG CGCTCGTTGA
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ILma200       TTGGTCTAAA -TTC-GAGTC CTCGGCGATG AAGCGCC-GC GACGATCGGT GGGAATGCTT TT----GGCT GCCTCGTTCG GAGTCGCGCG CGCTCGTCGA
ILma404       TTGGTCTAAA -TTC-GAGTC CTCGGCGATG AAGCGCC-GC GACGATCGGT GGGAATGCTT TT----GGCT GCCTCGTTCG GAGTCGCGCG CGCTCGTCGA
ILac135       TTGGTCTAAA -TTC-GAGTC CTCGGCGATG AAGCGCC-GC GACGATCGGT GGGAATGCCT TT----GGCT GCCTCGTTCG GAGTCGCGCG CGCTCGTCGA
ILas570       TTGGTCTAAA -TTC-TAGTC CTCGGCGATG GAGCGCC-GC GACGATCGGT GGGAACGCCT TT----GGCT GCCTCGTTCG GAGTCGCGCG CGTTCGTCGA
ILab383       TTGGTCTAAA -TTC-GAGTC CTCGGCGATG GAGCGCC-GC GACAATCGGT GGGAACGCCT TT----GGCT GCCTCGTTCG GAGTCGCGCG CGTTCGTCGA
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ILar153        TTGGTCTAAA -TTC-RAGTC CTCGGCGATG AAGCGCC-GC GACGATCGGT GGGAACGCCT TT----GGCT GCCTCGTTCG GAGTCGCGCG CGCTCGTCGA
ILar252        TTGGTCTAAA -TTC-RAGTC YTCGGYGATG AAGCGCC-GC GACGATCGGT GGGAACGCCT TT----GGCT GCCTCGTTCG GAGTCGCGCG CGCTCGTCGA
ILar378        TTGGTCTAAA -TTC-GAGTC CTCGGCGATG AAGCGCC-GC GACGATCGGT GGGAACGCCT TT----GGCT GCCTCGTTCG GAGTCGCGCG CGCTCGTCGA
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IAlo596        TTGGTCTAAA -TTC-GAGTA CTCGGCGATG AAGTGCC-GC GACAATCGGT GGGAATGCTT TT----AGCT GCCTCTTTCG AAGTCGCGCG TGCTCGTCGA
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IAca345       CTGGCCTAAA ATGC--AGTC CTCGGCGATG AATTGCC-GC GACAATCGGT GGGAATGCTT T-G---AGCT GCCTCGTTAG TTGTCGTGTG TGCTCGTTGA
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Iros422       TTGGCCTAAA ATTT--GGTC CTCGGCGATG AATTGCC-GC GACAATCGGT GGGAATGCTT --AATAAGCT GCCTCGTTAG TTATCGTGTG TGCTCGTTGA
IAsp140       TTGGCCTAAA ATTT--GGTC CTCGGCGATG AATTGCC-GC GACAATCGGT GGGAATGCTT --AATAAGCT GCCTCGTTAG TTATCGTGTG TGCTCGTTGA
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IMal440      TCGGGACGCT CTTGA-CCCT T-TCGGCATC GCAACGTCGA TGCTCGCATC GCGACCCCAG GTCAGGCGGG ATT-----
IMal338      TCGGGACGCT CTTGA-CCCT T-TCGGCATC GCAACGTCGA TGCTCGCATC GCGACCCCAG GTCAGGCGGG ATTACCCG
IMmo593      TCGGGACGCT CTTGA-CCCT T-TCGGCATC GCAACGTCGA TGCTCGCATC GCGACCCCAG GTCAGGCGGG ATTACCCG
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IMmo496      TCGGGACGCT CTTGA-CCCT T-TCGGCATC GCAACGTCGA TGCTCGCATC GCGACCCCAG GTCAGGCGGG ATTACCCG
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PAlu616        TTTGGTTTTA GTGTATACGA GTTTTTGAAA ATAAAGGAGC AATAACCAAT TTCTTGTTCT ATCAAGAGTG TTGGTATTGC TCCTTTATTT AGATTTAGTA
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PLph628        TTTGGTTTTA GTGTATACGA GTTTTTGAAA ATAAAGGAGC AATAACCAAT TTCTTGTTCT ATCAAGAGTG TTGGTATTGC TCCTTTATTT AGATTTAGTA
PLph629        TTTGGTTTTA GTGTATACGA GTTTTTGAAA ATAAAGGAGC AATAACCAAT TTCTTGTTCT ATCAAGAGTG TTGGTATTGC TCCTTTATTT AGATTTAGTA
PMtf394        TTTGGTTTTA GTGTATACGA GTTTTTGAAA ATAAAGGAGC AATACCAACA TTCTTGATAA AACAAGAAAT TGTTTATTGC TCCTTTATTT ATATTTAGTA
PMtf070        TTTGGTTTTA GTGTATACGA GTTTTTGAAA ATAAAGGAGC AATACCAACA TTCTTGATAA AACAAGAAAT TGTTTATTGC TCCTTTATTT ATATTTAGTA
PMtf499        TTTGGTTTTA GTGTATACGA GTTTTTGAAA ATAAAGGAGC AATACCAACA TTCTTGATAA AACAAGAAAT TGTTTATTGC TCCTTTATTT ATATTTAGTA
PMma415        TTTGGTTTTA GTGTATACGA GTTTTTGAAA ATAAAGGAGC AATACCAACA TTCTTGATAA AACAAGAAAT TGTTTATTGC TCCTTTATTT ATATTTAGTA
PMma279        TTTGGTTTTA GTGTATACGA GTTTTTGAAA ATAAAGGAGC AATACCAACA TTCTTGATAA AACAAGAAAT TGTTTATTGC TCCTTTATTT ATATTTAGTA
PAof604        TTTGGTTTTA GTGTATACGA GTTTTTGAAA ATAAAGGAGC GATACCAACA CTCTTGATAG AACAAGAAAT TGGTTATTGC TCCTTTATTT AGATTTAGTA
PAof511        TTTGGTTTTA GTGTATACGA GTTTTTGAAA ATAAAGGAGC GATACCAACA CTCTTGATAG AACAAGAAAT TGGTTATTGC TCCTTTATTT AGATTTAGTA
PAof512        TTTGGTTTTA GTGTATACGA GTTTTTGAAA ATAAAGGAGC GATACCAACA CTCTTGATAG AACAAGAAAT TGGTTATTGC TCCTTTATTT AGATTTAGTA
PAof513        TTTGGTTTTA GTGTATACGA GTTTTTGAAA ATAAAGGAGC GATACCAACA CTCTTGATAG AACAAGAAAT TGGTTATTGC TCCTTTATTT AGATTTAGTA
PAof330        TTTGGTTTTA GTGTATACGA GTTTTTGAAA ATAAAGGAGC GATACCAACA CTCTTGATAG AACAAGAAAT TGGTTATTGC TCCTTTATTT AGATTTAGTA
PAca345        TTTGGTTTTA GTGTATACGA GTTTTTGAAA ATAAAGGAGC GATACCAACA CTCTTGATAG AACAAGAAAT TGGTTATTGC TCCTTTATTT AGATTTAGTA
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Pros422        TTTGGTTTTA GTGTATACGA GTTTTTGAAA ATAAAGGAGC AATACCAACA CTCTTGATAG AACAAGAAAT TGGTTATTGC TCCTTTATTT AGATTTAGTA
PMsh0325       TTTGGTTTTA GTGTATACGA GTTTTTGAAA ATAAAGGAGC AATAACCAAT TTCTTGTTCT ATCAAGAGTG TTGGTATTGC TCCTTTATTT AGTATTTATT


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                      110        120        130        140        150        160        170        180        190        200
PLpl285        GTCTTTTTTT GCGTTACACT TTTTTTTCTT TACATTTACA TAAGTTTGTT TTTTCTTTAC TTTAACTTTT TTATTTTACC TTATTTATTT CTGATTATCA
PLbr141        GTCTTTTTTT GCGTTACACT TTTTTTTCTT TACATTTACA TAAGTTTACA TAAGTTTGTT TTTTCTTTAC TTTAACTTTT TTATTTTACC TTATTTATTT
PLfl414        GTCTTTTTTT GCGTTACACT TTTTTTTCTT TACATTTACA TAAGTTTGTT TTTTCTTTAC TTTAACTTTT TTATTTTACC TTATTTATTT CTGATTATCA
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PLfl000      GTCTTTTTTT GCGTTACACT TTTTTTTCTT TACATTTACA TAAGTTTGTT TTTTCTTTAC TTTAACTTTT TTATTTTACC TTATTGATTT CTGATTATCA
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PLtp564      GTCTTTTTTT GCGTTACACT TTTTTTTCTT TACATTTACA TAAGTTTGTT TTTTCTTTAC TTTAACTTTT TTATTTTACC TTATTTATTT CTGATTATCA
PLtp354      GTCGTTTTTT GCGTTACACT TTTTTTTCTT TACATTTACA TAAGTTTGTT TTTTCTTTAC TTTAACTTTT TTATTTTACC TTATTTATTT CTGATTATCA
PLtr117      GTCTTTTTTT GCGTTACACT TTTTTTTCTT TACATTTACA TAAGTTTGTT TTTTCTTTAC TTTAACTTTT TTATTTTACC TTATTTATTT CTGATTATCA
PLtr357      GTCTTTTTTT GCGTTACACT TTTTTTTCTT TACATTTACA TAAGTTTGTT TTTTCTTTAC TTTAACTTTT TTATTTTACC TTATTTATTT CTGATTATCA
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PLob144      GTCTTTTTTT GCGTTACACT TTTTTTTCTT TACATTTACA TAAGTTTGTT TTTTCTTTAC TTTAACTTTT TTATTTTACC TTTTACCTTA TTTATTTCTG
PLol004      GTCTTTTTTT GCGTTACACT TTTTTTTCTT TACATTTACA TAAGTTTGTT TTTTCTTTAC TTTAACTTTT TTATTTTACC TTATTTATTT CTGATTATCA
PLol451      GTCTTTTTTT GCGTTACACT TTTTTTTCTT TACATTTACA TAAGTTTGTT TTTTCTTTAC TTTAACTTTT TTATTTTACC TTATTTATTT CTGATTATCA
PLmo346      GTCTTTTTTT GCGTTACACT TTTTTTTCTT TACATTTACA TAAGTTTGTT TTTTCTTTAC TTTAACTTTT TTATTTTACC TTATTTATTT CTGATTATCA
PLmo515      GTCTTTTTTT GCGTTACACT TTTTTTTCTT TACATTTACA TAAGTTTGTT TTTTCTTTAC TTTAACTTTT TTATTTTACC TTATTTATTT CTGATTATCA
PLpu450      GTCGTTTTTT GCGTTACACT TTTTTTTCTT TACATTTACA TAAGTTTGTT TTTTCTTTAC TTTAACTTTT TTATTTTACC TTATTTATTT CTGATTATCA
PLpu348      GTCTTTTTTT GCGTTACACT TTTTTTTCTT TACATTTACA TAAGTTTGTT TTTTCTTTAC TTTAACTTTT TTATTTTACC TTATTTATTT CTGATTATCA
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PLti308      GTCTTTTTTT GCGTTACACT TTTTTTTCTT TACATTTACA TAAGTTTGTT TTTTCTTTAC TTTAACTTTT TTATTTTACC TTATTTATTT CTGATTATCA
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PLma405      GTCTTTTTTT GCGTTACACT TTTTTTTCTT TACATTTACA TAAGTTTGTT TTTTCTTTAC TTTAACTTTT TTATTTTACC TTATTTATTT CTGATTATCA
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PLab383      TAGATTTAGT AGTCTTTTTT TGCGTTACAC CTTTTTTTTC TTTACATTTA CATAAGTTTG TTTTTTCTTT ACTTTAACTT TTTTATTTTA CCTTATTTAT
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PLcr076      GTCTTTTTTT GCGTTACACC TTTTTTTTCT TTACATTTAC ATAAGTTTGT TTTTTCTTTA CTTTAACTTT TTTATTTTAC CTTATTTATT TCTGATTATC
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PLcr235      GTCTTTTTTT GCGTTACACC TTTTTTTTCT TTACATTTAC ATAAGTTTGT TTTTTCTTTA CTTTAACTTT TTTATTTTAC CTTATTTATT TCTGATTATC
PLcr599      GTCTTTTTTT GCGTTACACC TTTTTTTTCT TTACATTTAC ATAAGTTTGT TTTTTCTTTA CTTTAACTTT TTTATTTTAC CTTATTTATT TCTGATTATC
PMni032      GTCTTTTTTT GCGTTACACT TTTTTTTCTT TACATTTACA TAAGTTTGTT GTTTCTTTAC TTTAACTTTT TTATTTTACC TTATTTATTT CTGATTATCA
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PMni228	GTCTTTTTTT	GCGTTACACC	TTTTTTTTCT	TTACATTTAC	ATAAGTTTGT	TTTTTCTTTA	CTTTAACTTT	TTTATTTTAC	CTTATTTATT	TCTGATTATC
PMne349	GTCTTTTTTT	GCGTTACACC	TTTTTTTTCT	TTACATTTAC	ATAAGTTTGT	TTTTTCTTTA	CTTTAACTTT	TTTATTTTAC	CTTATTTATT	TCTGATTATC
PMne632	GTCTTTTTTT	GCGTTACACC	TTTTTTTTCT	TTACATTTAC	ATAAGTTTGT	TTTTTCTTTA	CTTTAACTTT	TTTATTTTAC	CTTATTTATT	TCTGATTATC
PMsy001	GTCTTTTTTT	GCGTTACACC	TTTTTTTTCT	TTACATTTAC	ATAAGTTTGT	TTTTTCTTTA	CTTTAACTTT	TTTATTTTAC	CTTATTTATT	TCTGATTATC
PMsy635	GTCTTTTTTT	GCGTTACACC	TTTTTTTTCT	TTACATTTAC	ATAAGTTTGT	TTTTTCTTTA	CTTTAACTTT	TTTATTTTAC	CTTATTTATT	TCTGATTATC
PMpa059	GTCTTTTTTT	GCGTTACACC	TTTTTTTTCT	TTACATTTAC	ATAAGTTTGT	TTTTTCTTTA	CTTTAACTTT	TTTATTTTAC	CTTATTTATT	TCTGATTATC
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PMpa249	GTCTTTTTTT	GCGTTACACC	TTTTTTTTCT	TTACATTTAC	ATAAGTTTGT	TTTTTCTTTA	CTTTAACTTT	TTTATTTTAC	CTTATTTATT	TCTGATTATC
PMpa005	GTCTTTTTTT	GCGTTACACC	TTTTTTTTCT	TTACATTTAC	ATAAGTTTGT	TTTTTCTTTA	CTTTAACTTT	TTTATTTTAC	CTTATTTATT	TCTGATTATC
PMve442	GTCTTTTTTT	GCGTTACACC	TTTTTTTTCT	TTACATTTAC	ATAAGTTTGT	TTTTTCTTTA	CTTTAACTTT	TTTATTTTAC	CTTATTTATT	TCTGATTATC
PMhi149	GTCTTTTTTT	GCGTTACACT	TTTTTTTTCT	TTACATTTAC	ATAAGTTTGT	TTTTTCTTTA	CTTTAACTTT	TTTATTTTAC	CTTATTTATT	TCTGATTATC
PMhi602	GTCTTTTTTT	GCGTTACACT	TTTTTTTTCT	TTACATTTAC	ATAAGTTTGT	TTTTTCTTTA	CTTTAACTTT	TTTATTTTAC	CTTATTTATT	TCTGATTATC
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PMal338	GTCTTTTTTT	GCGTTACACT	TTTTTTTTCT	TTACATTTAC	ATAAGTTTGT	TTTTTCTTTA	CTTTAACTTT	TTTATTTGAC	CTTATTTATT	TCTGATTATC
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PMal539	GTCTTTTTTT	GCGTTACACT	TTTTTTTTTC	TTTACATTTA	CATAAGTTTG	TTTTTTCTTT	ACTTTAACTT	TTTTATTTGA	CCTTATTTAT	TTCTGATTAT
PMto189	GTCTTTTTTT	GCGTTACACT	TTTTTTTTCT	TTACATTTAC	ATAAGTTTGT	TTTTTCTTTA	CTTTAACTTT	TTTATTTGAC	CTTATTTATT	TCTGATTATC
PMto489	GTCTTTTTTT	GCGTTACACT	TTTTTTTTCT	TTACATTTAC	ATAAGTTTGT	TTTTTCTTTA	CTTTAACTTT	TTTATTTGAC	CTTATTTATT	TCTGATTATC
PMto479	GTCTTTTTTT	GCGTTACACT	TTTTTTTTCT	TTACATTTAC	ATAAGTTTGT	TTTTTCTTTA	CTTTAACTTT	TTTATTTGAC	CTTATTTATT	TCTGATTATC
PMmo496	GTCTTTTTTT	GCGTTACACT	TTTTTTTTTC	TTTACATTTA	CATAAGTTTG	TTTTTTCTTT	ACTTTAACTT	TTTTATTTGA	CCTTATTTAT	TTCTGATTAT
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PMmo493	GTCTTTTTTT	GCGTTACACT	TTTTTTTTTC	TTTACATTTA	CATAAGTTTG	TTTTTTCTTT	ACTTTAACTT	TTTTATTTGA	CCTTATTTAT	TTCTGATTAT
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PAhi270	GTCTTTTTTT	GCGTTACACT	TTTTTTTCTT	TACATTTACA	TAAGTTTGTT	TTTTCTTTAC	TTTAACTTTT	TTATTTTACC	TTATTTATTT	CTGATTATCA
PAhi454	GTCTTTTTTT	GCGTTACACT	TTTTTTTCTT	TACATTTACA	TAAGTTTGTT	TTTTCTTTAC	TTTAACTTTT	TTATTTTACC	TTATTTATTT	CTGATTATCA
PAhi455	GTCTTTTTTT	GCGTTACACT	TTTTTTTCTT	TACATTTACA	TAAGTTTGTT	TTTTCTTTAC	TTTAACTTTT	TTATTTTACC	TTATTTATTT	CTGATTATCA
PAhi456	GTCTTTTTTT	GCGTTACACT	TTTTTTTCTT	TACATTTACA	TAAGTTTGTT	TTTTCTTTAC	TTTAACTTTT	TTATTTTACC	TTATTTATTT	CTGATTATCA
PAhi458	GTCTTTTTTT	GCGTTACACT	TTTTTTTCTT	TACATTTACA	TAAGTTTGTT	TTTTCTTTAC	TTTAACTTTT	TTATTTTACC	TTATTTATTT	CTGATTATCA
PAhi356	GTCTTTTTTT	GCGTTACACT	TTTTTTTCTT	TACATTTACA	TAAGTTTGTT	TTTTCTTTAC	TTTAACTTTT	TTATTTTACC	TTATTTATTT	CTGATTATCA
PMca389	GTCTTTTTTT	GCGTTACACT	TTTTTTTCTT	TACATTTACA	TAAGTTTGTT	TTTTCTTTAC	TTTAACTTTT	TTATTTTACC	TTATTTATTT	CTGATTATCA
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PAca345         GTCTTTTTTT CGTTACACTT TTTTTTCTTT ACATTTACAT AAGTTTGTTT TTTCTTTACT TTAACTTTTT TATTTTACCT TATTTATTTC TGATTATCAT
PAca594         GTCTTTTTTT CGTTACACTT TTTTTTCTTT ACATTTACAT AAGTTTGTTT TTTCTTTACT TTAACTTTTT TATTTTACCT TATTTATTTC TGATTATCAT
PAca471         GTCTTTTTTT GCGTTACACT TTTTTTTCTT TACATTTACA TAAGTTTGTT TTTTCTTTAC TTTAACTTTT TTATTTTACC TTATTTATTT CTGATTATCA
PAar427         GTCTTTTTTT CGTTACACTT TTTTTTCTTT ACATTTACAT AAGTTTGTTT TTTCTTTACT TTAACTTTTT TATTTTACCT TATTTATTTC TGATTATCAT
PAsp140         GTCTTTTTTT CGTTACACTT TTTTTTCTTT ACATTTACAT AAGTTTGTTT TTTCTTTACT TTAACTTTTT TATTTTACCT TATTTATTTC TGATTATCAT
Pros422         GTCTTTTTTT CGTTACACTT TTTTTTCTTT ACATTTACAT AAGTTTGTTT TTTCTTTACT TTAACTTTTT TATTTTACCT TATTTATTTC TGATTATCAT
PMsh0325        TAGATTTAGT AGTCTTTCTT TTCTTTACAT AAGTTTGTTT TTTCTTTACT TTAACTTTTT TATTTTACCC TATTTATTTC TTATTACCAT AAGTGATTTC


                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                       210        220        230        240        250        260        270        280        290        300
PLpl285         TAAGAAATCA AAAAAAGGAT TTTTTAATGA GTTTGATTTC ATTTTATTGG ATTTGACTTA GTATTATACG TTCGTTATGT AATAATATAT TATATATTAA
PLbr141         CTGATTATCA TAAGAAATCA AAGAAAGGAT TTTTTAATGA GTTTGATTTC ATTTTATTGG ATTTGACTTA GTATTATACG TTCGTTATGT AATAATATAT
PLfl414         TAAGAAATCA AAAAAAGGAT TTTTTAATGA GTTTGATTTC ATTTTATTGG ATTTGACTTA GTATTATACG TTCGTTATGT AATAATATAT TATATATTAA
PLfl000         TAAGAAATCA AAAAAAGGAT TTTTTAATGA GTTTGATTTC ATTTTATTGG ATTTGACTTA GTATTATACG TTCGTTATGT AATAATATAT TATATATTAA
PLag308         TAAGAAATCA AAAAAAGGAT TTTTTAATGA GTTTGATTTC ATTTTATTGG ATTTGACTTA GTATTATACG TTCGTTATGT AATAATATAT TATATATTAA
PLtp564         TAAGAATTCA AAAAAAGGAT TTTTGAATGA GTTTGATTTC ATTTTATTGG ATTTGACTTA GTATTATACG TTCGTTATGT AATAATATAT TATATATTAA
PLtp354         TAAGAAATCA AAAAAAGGAT TTTTTAATGA GTTTGATTTC ATTTTATTGG ATTTGACTTA GTATTATACG TTCGTTATGT AATAATATAT TATATATTAA
PLtr117         TAAGAAATCA AAGAAAGGAT TTTTTAATGA GTTTGATTTC ATTTTATTGG ATTTGACTTA GTATTATACG TTCGTTATGT AATAATATAT TATATATTAA
PLtr357         TAAGAAATCA AAGAAAGGAT TTTTTAATGA GTTTGATTTC ATTTTATTGG ATTTGACTTA GTATTATACG TTCGTTATGT AATAATATAT TATATATTAA
PLtr359         TAAGAAATCA AAAAAAGGAT TTTTTAATGA GTTTGATTTC ATTTTATTGG ATTTGACTTA GTATTATACG TTCGTTATGT AATAATATAT TATATATTAA
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PLtr169      TAAGAAATCA AAAAAAGGAT TTTTTAATGA GTTTGATTTC ATTTTATTGG ATTTGACTTA GTATTATACG TTCGTTATGT AATAATATAT TATATATTAA
PLob144      ATTATCATAA GAAATCAAAA AAAGGATTTT TTAATGAGTT TGATTTCATT TTATTGGATT TGACTTAGTA TTATACGTTC GTTATGTAAT AATATATTAT
PLol004      TAAGAAATCA AAAAAAGGAT TTTTTAATGA GTTTGATTTC ATTTTATTGG ATTTGACTTA GTATTATACG TTCGTTATGT AATAATATAT TATATATTAA
PLol451      TAAGAAATCA AAAAAAGGAT TTTTTAATGA GTTTGATTTC ATTTTATTGG ATTTGACTTA GTATTATACG TTCGTTATGT AATAATATAT TATATATTAA
PLmo346      TAAGAAATAA AAAAAGGATT TTTTAATGAG TTTGATTTCA TTTTATTGGA TTTGACTTAG TATTATACGT TCGTTATGTA ATAATATATT ATATATTAAC
PLmo515      TAAGAAATAA AAAAAGGATT TTTTAATGAG TTTGATTTCA TTTTATTGGA TTTGACTTAG TATTATACGT TCGTTATGTA ATAATATATT ATATATTAAC
PLpu450      TAAGAAATCA AAAAAAGGAT TTTTTAATGA GTTTGATTTC ATTTTATTGG ATTTGACTTA GTATTATACG TTCGTTATGT AATAATATAT TATATATTAA
PLpu348      TAAGAATTCA AAAAAAGGAT TTTTGAATGA GTTTGATTTC ATTTTATTGG ATTTGACTTA GTATTATACG TTCGTTATGT AATAATATAT TATATATTAA
PLth353      TAAGAAATCA AAGAAAGGAT TTTTTAATGA GTTTGATTTC ATTTTATTGG ATTTGACTTA GTATTATACG TTCGTTATGT AATAATATAT TATATATTAA
PLti308      TAAGAAATCA AAAAAAGGAT TTTTTAATGA GTTTGATTTC ATTTTATTGG ATTTGACTTA GTATTATACG TTCGTTATGT AATAATATAT TATATATTAA
PLti181      TAAGAAATCA AAAAAAGGAT TTTTTAATGA GTTTGATTTC ATTTTATTGG ATTTGACTTA GTATTATACG TTCGTTATGT AATAATATAT TATATATTAA
PLti233      TAAGAAATCA AAAAAAGGAT TTTTTAATGA GTTTGATTTC ATTTTATTGG ATTTGACTTA GTATTATACG TTCGTTATGT AATAATATAT TATATATTAA
PLti595      TAAGAAATCA AAAAAAGGAT TTTTTAATGA GTTTGATTTC ATTTTATTGG ATTTGACTTA GTATTATACG TTCGTTATGT AATAATATAT TATATATTAA
PLma329      TAAGAAATCA AAAAAAGGAT TTTTTAATGA GTTTGATTTC ATTTTATTGG ATTTGACTTA GTATTATACG TTCGTTATGT AATAATATAA TATATTATAT
PLma200      TAAGAAATCA AAGAAAGGAT TTTTTAATGA GTTTGATTTC ATTTTATTGG ATTTGACTTA GTATTATACG TTCGTTATGT AATAATATAT TATATATTAA
PLma404      TAAGAAATCA AAAAAAGGAT TTTTTAATGA GTTTGATTTC ATTTTATTGG ATTTGACTTA GTATTATACG TTCGTTATGT AATAATATAA TATATTATAT
PLma405      TAAGAAATCA AAAAAAGGAT TTTTTAATGA GTTTGATTTC ATTTTATTGG ATTTGACTTA GTATTATACG TTCGTTATGT AATAATATAA TATATTATAT
PLma598      TAAGAAATCA AAAAAAGGAT TTTTTAATGA GTTTGATTTC ATTTTATTGG ATTTGACTTA GTATTATACG TTCGTTATGT AATAATATAA TATATTATAT
PLac134      TATTTATTTC TGATTATCAT AAGAAATAAA AAAAAGGATT TTTTAATGAG TTTGATTTCA TTTTATTGGA TTTGACTTAG TATTATACGT TCGTTATGTA
PLas570      ATAAGAAAAA AAAAAGATTT TTTAATGAGT TTGATTTCAT TTTATTGGAT TTGACTTAGT ATTATACGTT CGTTATGTAA TAATATATTA TATATTAACG
PLab383      TTCTGATTAT CATAAGAAAA AAAAAAAAGA TTTTTTAATG AGTTTGATTT CATTTTATTG GATTTGACTT AGTATTATAC GTTCGTTATG TAATAATATA
PLpe634      ATAAGAAAAA AAAAAAAGAT TTTTTAAGGA GTTTGATTTC ATTTTATTGG ATTTGACTTA GTATTATACG TTCGTTATGT AATAATATAT TATATATTAA
PLmu137      ATAAGAAAAA AAAAGATTTT TTAATGAGTT TGATTTCATT TTATTGGATT TGACTTAGTA TTATACGTTC GTTATGTAAT AATATATTAT ATATTAACGA
PLmu319      ATAAGAAAAA AAAAGATTTT TTAATGAGTT TGATTTCATT TTATTGGATT TGACTTAGTA TTATACGTTC GTTATGTAAT AATATATTAT ATATTAACGA
PLmu318      ATAAGAAAAA AAAAGATTTT TTAATGAGTT TGATTTCATT TTATTGGATT TGACTTAGTA TTATACGTTC GTTATGTAAT AATATATTAT ATATTAACGA
PLmu630      ATAAGAAAAA AAAAGATTTT TTAATGAGTT TGATTTCATT TTATTGGATT TGACTTAGTA TTATACGTTC GTTATGTAAT AATATATTAT ATATTAACGA
PLar153      ATAAGAAAAA AAAAAAGATT TTTTAATGAG TTTGATTTCA TTTTATTGGA TTTGACTTAG TATTATACGT TCGTTATGTA ATAATATATT ATATATTAAC
PLar239      ATAAGAAAAA AAAAAAGATT TTTTAATGAG TTTGATTTCA TTTTATTGGA TTTGACTTAG TATTATACGT TCGTTATGTA ATAATATATT ATATATTAAC
PLar252      ATAAGAAAAA AAAAAAGATT TTTTAATGAG TTTGATTTCA TTTTATTGGA TTTGACTTAG TATTATACGT TCGTTATGTA ATAATATATT ATATATTAAC
PLcr076      ATATTATCAT AAGAAAAAAA AAGATTTTTT AATGAGTTTG ATTTCATTTT ATTGGATTTG ACTTAGTATT ATACGTTCGT TATGTAATAA TATATTATAT
PLcr031      ATATTATCAT AAGAAAAAAA AAGATTTTTT AATGAGTTTG ATTTCATTTT ATTGGATTTG ACTTAGTATT ATACGTTCGT TATGTAATAA TATATTATAT
PLcr235      ATATTATCAT AAGAAAAAAA AAGATTTTTT AATGAGTTTG ATTTCATTTT ATTGGATTTG ACTTAGTATT ATACGTTCGT TATGTAATAA TATATTATAT
PLcr599      ATATTATCAT AAGAAAAAAA AAGATTTTTT AATGAGTTTG ATTTCATTTT ATTGGATTTG ACTTAGTATT ATACGTTCGT TATGTAATAA TATATTATAT
PMni032      TATTTATTTC TGATTATCAT AAGAAATAAA AAAAAGGATT TTTTAATGAG TTTGATTTCA TTTTATTGGA TTTGACTTAG TATTATACGT TCGTTATGTA
PMni097      ATAAGAAAAA AAAAAGATTT TTTAATGAGT TTGATTTCAT TTTATTGGAT TTGACTTAGT ATTATACGTT CGTTATGTAA TAATATATTA TATATTAACG
PMni105      ATAAGAAAAA AAAAAGATTT TTTAATGAGT TTGATTTCAT TTTATTGGAT TTGACTTAGT ATTATACGTT CGTTATGTAA TAATATATTA TATATTAACG
PMni633      ATAAGAAAAA AAAAAAGATT TTTTAATGAG TTTGATTTCA TTTTATTGGA TTTGACTTAG TATTATACGT TCGTTATGTA ATAATATATT ATATATTAAC
PMni228      ATAAGAAAAA AAAAGATTTT TTAATGAGTT TGATTTCATT TTATTGGATT TGACTTAGTA TTATACGTTC GTTATGTAAT AATATATTAT ATATTAACGA
PMne349      ATAAGAAAAA AAAAAAAGAT TTTTTAATGA GTTTGATTTC ATTTTATTGG ATTTGACTTA GTATTATACG TTCGTTATGT AATAATATAT TATATATTAA
PMne632      ATAAGAAAAA AAAAAGATTT TTTAATGAGT TTGATTTCAT TTTATTGGAT TTGACTTAGT ATTATACGTT CGTTATGTAA TAATATATTA TATATTAACG
PMsy001      ATAAGAAAAA AAAAAAGATT TTTTAATGAG TTTGATTTCA TTTTATTGGA TTTGACTTAG TATTATACGT TCGTTATGTA ATAATATATT ATATATTAAC
PMsy635      ATAAGAAAAA AAAAGATTTT TTAATGAGTT TGATTTCATT TTATTGGATT TGACTTAGTA TTATACGTTC GTTATGTAAT AATATATTAT ATATTAACGA
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PMpa059       ATAAGAAAAA AAAAGATTTT TTAATGAGTT TGATTTCATT TTATTGGATT TGACTTAGTA TTATACGTTC GTTATGTAAT AATATATTAT ATATTAACGA
PMpa296       ATAAGAAAAA AAAAGATTTT TTAATGAGTT TGATTTCATT TTATTGGATT TGACTTAGTA TTATACGTTC GTTATGTAAT AATATATTAT ATATTAACGA
PMpa249       ATAAGAAAAA AAAAGATTTT TTAATGAGTT TGATTTCATT TTATTGGATT TGACTTAGTA TTATACGTTC GTTATGTAAT AATATATTAT ATATTAACGA
PMpa005       ATAAGAAAAA AAAAGATTTT TTAATGAGTT TGATTTCATT TTATTGGATT TGACTTAGTA TTATACGTTC GTTATGTAAT AATATATTAT ATATTAACGA
PMve442       ATAAGAAAAA AAAGATTTTT TAATGAGTTT GATTTCATTT TATTGGATTT GACTTAGTAT TATACGTTCG TTATGTAATA ATATATTATA TATTAACGAA
PMhi149       ATAAGAAATA AAAAAAAGGA TTTTTTAATG AGTTTGATTT CATTTTATTG GATTTGACTT AGTATTATAC GTTCGTTATG TAATAATATA TTAACGAATT
PMhi602       ATAAGAAATA AAAAAAAGGA TTTTTTAATG AGTTTGATTT CATTTTATTG GATTTGACTT AGTATTATAC GTTCGTTATG TAATAATATA TTAACGAATT
PMhi631       ATAAGAAATA AAAAAAAGGA TTTTTTAATG AGTTTGATTT CATTTTATTG GATTTGACTT AGTATTATAC GTTCGTTATG TAATAATATA TTAACGAATT
PMal338       ATAAGAAATC AAAAAAAGGA TTTTTTAATG AGTTTGATTT CATTTTATTG GATTTGACTT AGTATTATAC GTTCGTTATG TAATAATATA TTATATATTA
PMal440       TAAGAAATCA AAAAAAGGAT TTTTTAATGA GTTTGATTTC ATTTTATTGG ATTTGACTTA GTATTATACG TTCGTTATGT AATAATATAT TATATATTAA
PMal539       CATAAGAAAT CAAAAAAAGG ATTTTTTAAT GAGTTTGATT TCATTTTATT GGATTTGACT TAGTATTATA CGTTCGTTAT GTAATAATAT ATTATATATT
PMto189       ATAAGAAATC AAAAAAAGGA TTTTTTAATG AGTTTGATTT CATTTTATTG GATTTGACTT AGTATTATAC GTTCGTTATG TAATAATATA TTATATATTA
PMto489       ATAAGAAATC AAAAAAAGGA TTTTTTAATG AGTTTGATTT CATTTTATTG GATTTGACTT AGTATTATAC GTTCGTTATG TAATAATATA TTATATATTA
PMto479       ATAAGAAATC AAAAAAAGGA TTTTTTAATG AGTTTGATTT CATTTTATTG GATTTGACTT AGTATTATAC GTTCGTTATG TAATAATATA TTATATTAAA
PMmo496       CATAAGAAAT CAAAAAAAGG ATTTTTTAAT GAGTTTGATT TCATTTTATT GGATTTGACT TAGTATTATA CGTTCGTTAT GTAATAATAT ATTATATATT
PMmo332       CATAAGAAAT CAAAAAAAGG ATTTTTTAAT GAGTTTGATT TCATTTTATT GGATTTGACT TAGTATTATA CGTTCGTTAT GTAATAATAT ATTATATATT
PMmo493       CATAAGAAAT CAAAAAAAGG ATTTTTTAAT GAGTTTGATT TCATTTTATT GGATTTGACT TAGTATTATA CGTTCGTTAT GTAATAATAT ATTATATATT
PMmo494       CATAAGAAAT CAAAAAAAGG ATTTTTTAAT GAGTTTGATT TCATTTTATT GGATTTGACT TAGTATTATA CGTTCGTTAT GTAATAATAT ATTATATATT
PMmo499       CATAAGAAAT CAAAAAAAGG ATTTTTTAAT GAGTTTGATT TCATTTTATT GGATTTGACT TAGTATTATA CGTTCGTTAT GTAATAATAT ATTATATATT
PAhi270       TAAGATTATC ATAAGAAATC AAAAAAAGGA TTTTTAATGA GTTTGATTTC ATTTTATTGG ATTTGATTTA GTATTATACG TTTGGTTTCG TTATGTAATA
PAhi454       TAAGATTATC ATAAGAAATC AAAAAAAGGA TTTTTAATGA GTTTGATTTC ATTTTATTGG ATTTGATTTA GTATTATACG TTTGGTTTCG TTATGTAATA
PAhi455       TAAGATTATC ATAAGAAATC AAAAAAAGGA TTTTTAATGA GTTTGATTTC ATTTTATTGG ATTTGATTTA GTATTATACG TTTGGTTTCG TTATGTAATA
PAhi456       TAAGATTATC ATAAGAAATC AAAAAAAGGA TTTTTAATGA GTTTGATTTC ATTTTATTGG ATTTGATTTA GTATTATACG TTTGGTTTCG TTATGTAATA
PAhi458       TAAGATTATC ATAAGAAATC AAAAAAAGGA TTTTTAATGA GTTTGATTTC ATTTTATTGG ATTTGATTTA GTATTATACG TTTGGTTTCG TTATGTAATA
PAhi356       TAAGAAATCA AAGAAAGGAT TTTTTAATGA GTTTGATTTC ATTTTATTGG ATTTGACTTA GTATTATACG TTCGTTATGT AATAATATAT TATATATTAA
PMca389       TAAGATTATC ATAAGAAATC AAAAAAAGGA TTTTTAATGA GTTTGATTTC ATTTTATTGG ATTTGATTTA GTATTATACG TTTGGTTTCG TTATGTAATA
PMca391       TAAGATTATC ATAAGAAATC AAAAAAAGGA TTTTTAATGA GTTTGATTTC ATTTTATTGG ATTTGATTTA GTATTATACG TTTGGTTTCG TTATGTAATA
PMca463       TAAGATTATC ATAAGAAATC AAAAAAAGGA TTTTTAATGA GTTTGATTTC ATTTTATTGG ATTTGATTTA GTATTATACG TTTGGTTTCG TTATGTAATA
PMca350       TAAGATTATC ATAAGAAATC AAAAAAAGGA TTTTTAATGA GTTTGATTTC ATTTTATTGG ATTTGATTTA GTATTAATAC GTTTGGTTTC GTTATGTAAT
PMae465       TAAGAAATCA AAAAAAGGAT TTTTTAATGA GTTTGATTTC ATTTTATTGG ATTTGACTTA GTATTATACG TTCGTTATGT AAGAATATAT TATATATTAA
PMae468       TAAGAAATCA AAAAAAGGAT TTTTTAATGA GTTTGATTTC ATTTTATTGG ATTTGACTTA GTATTATACG TTCGTTATGT AAGAATATAT TATATATTAA
PMae351       TAAGAAATCA AAAAAAGGAT TTTTTAATGA GTTTGATTTC ATTTTATTGG ATTTGACTTA GTATTATACG TTCGTTATGT AAGAATATAT TATATATTAA
PMtr392       TAAGAAATCA AAAAAAGGAT TTTTTAATGA GTTTGATTTC ATTTTATTGG ATTTGACTTA GTATTATACG TTCGTTATGT AAGAATATAT TATATATTAA
PMtr352       TAAGAAATCA AAAAAAGGAT TTTTTAATGA GTTTGATTTC ATTTTATTGG ATTTGACTTA GTATTATACG TTCGTTATGT AAGAATATAT TATATATTAA
PMtr393       TAAGAAATCA AAAAAAGGAT TTTTTAATGA GTTTGATTTC ATTTTATTGG ATTTGACTTA GTATTATACG TTCGTTATGT AAGAATATAT TATATATTAA
PMtr254       TAAGAAATCA AAAAAAGGAT TTTTTAATGA GTTTGATTTC ATTTTATTGG ATTTGACTTA GTATTATACG TTCGTTATGT AAGAATATAT TATATATTAA
PMat628       TAAGATTATC ATAAGAAATC AAAAAAAGGA TTTTTAATGA GTTTGATTTC ATTTTATTGG ATTTGATTTA GTATTATACG TTTGGTTTCG TTATGTAATA
PAlo461       TAAGAAATCA AAAAAAACGA ATTTTTTTAA AATAAAAAAA AAACGAATGA TGAATGATAG AAATTGAGAT ATTTGAAATA TTTAAACAAT AAAAAAAAAT
PAlo462       TAAGAAATCA AAAAAAACGA ATTTTTTTAA AATAAAAAAA AAACGAATGA TGAATGATAG AAATTGAGAT ATTTGAAATA TTTAAACAAT AAAAAAAAAT
PAlo596       TAAGAAATCA AAAAAAACGA ATTTTTTTAA AATAAAAAAA AAACGAATGA TGAATGATAG AAATTGAGAT ATTTGAAATA TTTAAACAAT AAAAAAAAAT
PAlu459       TAAGAAATCA AAAAAGGATT TTTTAATGAG TTTGATTTCA TTTTATTGGA TTTGATTTAG TATTATACGT TGGTTTCGT TATGTAATAA TATATTATAT
PAlu460       TAAGAAATCA AAAAAGGATT TTTTAATGAG TTTGATTTCA TTTTATTGGA TTTGATTTAG TATTATACGT TTGGTTTCGT TATGTAATAA TATATTATAT
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PAlu616       TAAGAAATCA AAAAAGGATT TTTTAATGAG TTTGATTTCA TTTTATTGGA TTTGATTTAG TATTATACGT TTGGTTTCGT TATGTAATAA TATATTATAT
PLph002       ATAAGAAATA AAAAATTTTT TAATGAGTTT GATTTCATTT TATTGGATTT GACTTAGTAT TATACGTTCG TTATGTAATA ATATTATATA TTAACGAATT
PLph628       ATAAGAAATA AAAAATTTTT TAATGAGTTT GATTTCATTT TATTGGATTT GACTTAGTAT TATACGTTCG TTATGTAATA ATATTATATA TTAACGAATT
PLph629       ATAAGAAATA AAAAATTTTT TAATGAGTTT GATTTCATTT TATTGGATTT GACTTAGTAT TATACGTTCG TTATGTAATA ATATTATATA TTAACGAATT
PMtf394       AAGAAATCAA ATAAAAAAGG ATTTTTTAAT GAGTTTGATT TCATTTTATT GGATTTGACT TAGTATTATA CGTTCGTTAT GTAATAATAT ATTATATATT
PMtf070       AAGAAATCAA ATAAAAAAGG ATTTTTTAAT GAGTTTGATT TCATTTTATT GGATTTGACT TAGTATTATA CGTTCGTTAT GTAATAATAT ATTATATATT
PMtf499       AAGAAATCAA ATAAAAAAGG ATTTTTTAAT GAGTTTGATT TCATTTTATT GGATTTGACT TAGTATTATA CGTTCGTTAT GTAATAATAT ATTATATATT
PMma415       AAGAAATCAA ATAAAAAAGG ATTTTTTAAT GAGTTTGATT TCATTTTATT GGATTTGACT TAGTATTATA CGTTCGTTAT GTAATAATAT ATTATATATT
PMma279       AAGAAATCAA ATAAAAAAGG ATTTTTTAAT GAGTTTGATT TCATTTTATT GGATTTGACT TAGTATTATA CGTTCGTTAT GTAATAATAT ATTATATATT
PAof604       AAGAAATAAA AAAAAGGATT TTTTAATGAG TTTGATTTCG TTTTATTGGA TTTGACTTAG TATTATACGT TCGTTATGTA ATAATATATT ATATATTAAC
PAof511       AAGAAATAAA AAAAAGGATT TTTTAATGAG TTTGATTTCG TTTTATTGGA TTTGACTTAG TATTATACGT TCGTTATGTA ATAATATATT ATATATTAAC
PAof512       AAGAAATAAA AAAAAGGATT TTTTAATGAG TTTGATTTCG TTTTATTGGA TTTGACTTAG TATTATACGT TCGTTATGTA ATAATATATT ATATATTAAC
PAof513       AAGAAATAAA AAAAAGGATT TTTTAATGAG TTTGATTTCG TTTTATTGGA TTTGACTTAG TATTATACGT TCGTTATGTA ATAATATATT ATATATTAAC
PAof330       AAGAAATAAA AAAAAGGATT TTTTAATGAG TTTGATTTCG TTTTATTGGA TTTGACTTAG TATTATACGT TCGTTATGTA ATAATATATT ATATATTAAC
PAca345       AAGAAATAAA AAAAAGGATT TTTTAATGAG TTTGATTTCG TTTTATTGGA TTTGACTTAG TATTATACGT TCGTTATGTA ATAATATATT ATATATTAAC
PAca594       AAGAAATAAA AAAAAGGATT TTTTAATGAG TTTGATTTCG TTTTATTGGA TTTGACTTAG TATTATACGT TCGTTATGTA ATAATATATT ATATATTAAC
PAca471       TAAGATTATC ATAAGAAATC AAAAAAAGGA TTTTTAATGA GTTTGATTTC ATTTTATTGG ATTTGATTTA GTATTATACG TTTGGTTTCG TTATGTAATA
PAar427       AAGAAATAAA AAAAAGGATT TTTTAATGAG TTTGATTTCG TTTTATTGGA TTTGACTTAG TATTATACGT TCGTTATGTA ATAATATATT ATATATTAAC
PAsp140       AAGAAATAAA AAAAAAGGAT TTTTTAATGA GTTTGATTTC ATTTTATTGG ATTTGACTTA GTATTATACG TTCGTTATGT AATAATATAT TATATATTAA
Pros422       AAGAAATAAA AAAAAAGGAT TTTTTAATGA GTTTGATTTC ATTTTATTGG ATTTGACTTA GTATTATACG TTCGTTATGT AATAATATAT TATATATTAA
PMsh0325      TTATGTTAAT AAGAAATCAA AAAAAGGATT TTTAATGAGT TTGATTTCGT TTTATTGGAT TTGACTTAGT ATTATGCGTT CGTTATGTAC TAATATAATT


              ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     310        320        330        340        350        360        370        380        390        400
PLpl285       CATTAACGAA TTTTTTTTTA ATAAAAAAAA AAGTAAAAAA GTTCTTACCA ATCTTTTGTT TGGAATTTTC TATATATCTT ATCTCAGAAA TACGAGAAAA
PLbr141       TATATATTAA CATTAACGAA TTTTTTTTTT AATAAAAAAA AAAGTAAAAA AGTTCTTACC AATCTTTTGT TTGGAATTTT CTATATATCT TATCTCAGAA
PLfl414       CATTAACGAA TTTTTTTTTA ATAAAAAAAA AAGTAAAAAA GTTCTTACCA ATCTTTTGTT TGGAATTTTC TATATATCTT ATCTCAGAAA TACGAGAAAA
PLfl000       CATTAACGAA TTTTTTTTTT TATAAAAAAA AAAGTAAAAA AGTTCTTACC AATCTTTTGT TTGGAATTTT CTATATATCT TATCTCAGAA ATACGAGAAA
PLag308       CATTAACGAA TTTTTTTTTT AATAAAAAAA AAAGTAAAAA AGTTCTTACC AATCTTTTGT TTGGAATTTT CTATATATCT TATCTCAGAA ATACGAGAAA
PLtp564       CGAATTTTTT TTTTAATAAA AAAAAAGTAA AAAAGTTCTT ACCAATCTTT TGTTTGGAAT TTTCTATATA TCTTATCTCA GAAATACGAG AAAAAAAACG
PLtp354       CATTAACGAA TTTTTTTTTT AATAAAAAAA AAGTAAAAAA GTTCTTACCA ATCTTTTGTT TGGAATTTTC TATATATCTT ATCTCAGAAA TACGAGAAAA
PLtr117       CATTAACGAA TTTTTTTTTT AATAAAAAAA AAAGTAAAAA AGTTCTTACC AATCTTTTGT TTGGAATTTT CTATATATCT TATCTCAGAA ATACGAGAAA
PLtr357       CATTAACGAA TTTTTTTTTT AATAAAAAAA AAGTAAAAAA GTTCTTACCA ATCTTTTGTT TGGAATTTTC TATATATCTT ATCTCAGAAA TACGAGAAAA
PLtr359       CATTAACGAA TTTTTTTTTT AATAAAAAAA AAGTAAAAAA GTTCTTACCA ATCTTTTGTT TGGAATTTTC TATATATCTT ATCTCAGAAA TACGAGAAAA
PLtr169       CATTAACGAA TTTTTTTTTT AATAAAAAAA AAAGTAAAAA AGTTCTTACC AATCTTTTGT TTGGAATTTT CTATATATCT TATCTCAGAA ATACGAGAAA
PLob144       ATATTAACAT TAACGAATTT TTTTTTTTAT AAAAAAAAAA GTAAAAAAGT TCTTACCAAT CTTTTGTTTG GAATTTTCTA TATATCTTAT CTCAGAAATA
PLol004       CATTAACGAA TTTTTTTTTT AATAAAAAAA AAAGTAAAAA AGTTCTTACC AATCTTTTGT TTGGAATTTT CTATATATCT TATCTCAGAA ATACGAGAAA
PLol451       CATTAACGAA TTTTTTTTTT AATAAAAAAA AAAGTAAAAA AGTTCTTACC AATCTTTTGT TTGGAATTTT CTATATATCT TATCTCAGAA ATACGAGAAA
PLmo346       GAATTTTTTT TAATAAAAAA AAAGTAAAAA AGTTCTTACC AATCTTTTGT TTGGAATTTT CTATATATCT TATCTCAGAA ATACGAGAAA AAAAAAAAAC
PLmo515       GAATTTTTTT TAATAAAAAA AAAGTAAAAA AGTTCTTACC AATCTTTTGT TTGGAATTTT CTATATATCT TATCTCAGAA ATACGAGAAA AAAAAAAAAC
PLpu450       CATTAACGAA TTTTTTTTTT AATAAAAAAA AAGTAAAAAA GTTCTTACCA ATCTTTTGTT TGGAATTTTC TATATATCTT ATCTCAGAAA TACGAGAAAA
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PLpu348      CGAATTTTTT TTTTAATAAA AAAAAAGTAA AAAAGTTCTT ACCAATCTTT TGTTTGGAAT TTTCTATATA TCTTATCTCA GAAATACGAG AAAAAAAACG
PLth353      CATTAACGAA TTTTTTTTTT AATAAAAAAA AAGTAAAAAA GTTCTTACCA ATCTTTTGTT TGGAATTTTC TATATATCTT ATCTCAGAAA TACGAGAAAA
PLti308      CGAATTTTTT TTTTAAGTAA AAAAGTTCTT ACCAATCTTT TGTTTGGAAT TTTCTATATA TCTTATCTCA GAAATACGAG AAAAAAAAAA AAACGAATGA
PLti181      CGAATTTTTT TTTTAAGTAA AAAAGTTCTT ACCAATCTTT TGTTTGGAAT TTTCTATATA TCTTATCTCA GAAATACGAG AAAAAAAAAA AAACGAATGA
PLti233      CGAATTTTTT TTTTAAGTAA AAAAGTTCTT ACCAATCTTT TGTTTGGAAT TTTCTATATA TCTTATCTCA GAAATACGAG AAAAAAAAAA AAACGAATGA
PLti595      CGAATTTTTT TTTTAAGTAA AAAAGTTCTT ACCAATCTTT TGTTTGGAAT TTTCTATATA TCTTATCTCA GAAATACGAG AAAAAAAAAA AACGAATGAT
PLma329      ATTAACGAAT TTTTTTTTTT TTTTAGTAAA AAAGTTCTTA CCAATCTTTT GTTTGGAATT TTCTATATAT CTTATCTCAG AAATACGAGA AAAAAAAAAA
PLma200      CATTAACGAA TTTTTTTTTT AATAAAAAAA AAGTAAAAAA GTTCTTACCA ATCTTTTGTT TGGAATTTTC TATATATCTT ATCTCAGAAA TACGAGAAAA
PLma404      ATTAACGAAT TTTTTTTTTT TTTTAGAAAA AAAGTTCTTA CCAATCTTTT GTTGGGAATT TTCTATATAT CTTATCTCAG AAATCCGAGA AAAAAAAAAC
PLma405      ATTAACGAAT TTTTTTTTTT TTTTAGAAAA AAAGTTCTTA CCAATCTTTT GTTGGGAATT TTCTATATAT CTTATCTCAA AAATCCGAGA AAAAAAAAAC
PLma598      ATTAACGAAT TTTTTTTTTT TTTTAGTAAA AAAGTTCTTA CCAATCTTTT GTTTGGAATT TTCTATATAT CTTATCTCAG AAATACGAGA AAAAAAAAAA
PLac134      ATAATATAAT ATATTATATA TTAACGAATT TTTTTTTTTT TAAGTAAAAA AGTTCTTACC AATCTTTTGT TTGGAATTTT CTATATATCT TATCTCAGAA
PLas570      AATTTTTTTT ATTAAAAAAA AAAGTAAAAA AGTTCTTACC AATCTTTTGT TTGGAATTTT CTATATATCT TATCTCAGAA ATACGAGAAA AAAAAAAACG
PLab383      TTATATATTA ACTAATTTTT TTTATTAAAA AAAAAAGTAA AAAAGTTCTT ACCAATCTTT TGTTTGGAAT TTTCTATATA TCTTATCTCA GAAATACGAG
PLpe634      CGAATTTTTT TTATTAAAAA AAAAGTAAAA AAGTTCTTAC CAATCTTTTG TTTGGAATTT TCTATATATC TTATCTCAGA AATACGAGAA AAAAAAAAAC
PLmu137      ATTTTTTTTA TTAAAAAAAA AGTAAAAAAG CTCTTACCAA TCTTTTGTTT GGAATTTTCT ATATATCTTA TCTCAGAAAT ACGAGAAAAA AAAAAACGAA
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PLmu318      ATTTTTTTTA TTAAAAAAAA AGTAAAAAAG CTCTTACCAA TCTTTTGTTT GGAATTTTCT ATATATCTTA TCTCAGAAAT ACGAGAAAAA AAAAAACGAA
PLmu630      ATTTTTTTTA TTAAAAAAAA AGTAAAAAAG CTCTTACCAA TCTTTTGTTT GGAATTTTCT ATATATCTTA TCTCAGAAAT ACGAGAAAAA AAAAAACGAA
PLar153      GAATTTTTTT TACTAAAAAA AAAGTAAAAA AGTTCTTACC AATCTTTTGT TTGGAATTTT CTATATATCT TATCTCAGAA ATACGAGAAA AAAAAAAACG
PLar239      GAATTTTTTT TACTAAAAAA AAAGTAAAAA AGTTCTTACC AATCTTTTGT TTGGAATTTT CTATATATCT TATCTCAGAA ATACGAGAAA AAAAAAAACG
PLar252      GAATTTTTTT TACTAAAAAA AAAGTAAAAA AGTTCTTACC AATCTTTTGT TTGGAATTTT CTATATATCT TATCTCAGAA ATACGAGAAA AAAAAAAAAC
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PLcr599      ATTAACGAAT TTTTTTTATT AAAAAAAAAA GTAAAAAAGT TCTTACCAAT CTTTTGTTTG GAATTTTCTA TATATCTTAT CTCAGAAATA CGAAAAAAAA
PMni032      ATAATATAAT ATATTATATA TTAACGAATT TTTTTTTTTT TAAGTAAAAA AGTTCTTACC AATCTTTTGT TTGGAATTTT CTATATATCT TATCTCAGAA
PMni097      AATTTCTTTT ATTAAAAAAA AAGTAAAAAA GTTCTTACCA ATCTTTTGTT TGGAATTTTC TATATATCTT ATCTCAGAAA TACGAGAAAA AAAAAAACGA
PMni105      AATTTCTTTT ATTAAAAAAA AAGTAAAAAA GTTCTTACCA ATCTTTTGTT TGGAATTTTC TATATATCTT ATCTCAGAAA TACGAGAAAA AAAAAAAACG
PMni633      GAATTTCTTT TATTAAAAAA AAAGTAAAAA AGTTCTTACC AATCTTTTGT TTGGAATTTT CTATATATCT TATCTCAGAA ATACGAGAAA AAAAAAAAAC
PMni228      ATTTCTTTTA TTAAAAAAAA AGTAAAAAAG TTCTTACCAA TCTTTTGTTT GGAATTTTCT ATATATCTTA TCTCAGAAAT ACGAGAAAAA AAAAAAAACG
PMne349      CGAATTTTTT TTATTAAAAA AAAAGTAAAA AAGTTCTTAC CAATCTTTTG TTTGGAATTT TCTATATATC TTATCTCAGA AATACGAGAA AAAAAAAAAC
PMne632      AATTTTTTTT ATTAAAAAAA AAGTAAAAAA GTTCTTACCA ATCTTTTGTT TGGAATTTTC TATATATCTT ATCTCAGAAA TACGAGAAAA AAAAAAACGA
PMsy001      GAATTTTTTT TATTAAAAAA AAAGTAAAAA AGTTCTTACC AATCTTTTGT TTGGAATTTT CTATATATCT TATCTCAGAA ATACGAGAAA AAAAAAAAAC
PMsy635      ATTTTTTTTA TTAAAAAAAA AAGTAAAAAA GTTCTTACCA ATCTTTTGTT TGGAATTTTC TATATATCTT ATCTCAGAAA TACGAGAAAA AAAAAAACGA
PMpa059      ATTTTTTTTA TTAAAAAAAA AGTAAAAAAG TTCTTACCAA TCTTTTGTTT GGAATTTTCT ATATATCTTA TCTCAGAAAT ACGAGAAAAA AAAAAACGAA
PMpa296      ATTTTTTTTA TTAAAAAAAA AGTAAAAAAG TTCTTACCAA TCTTTTGTTT GGAATTTTCT ATATATCTTA TCTCAGAAAT ACGAGAAAAA AAAAAACGAA
PMpa249      ATTTTTTTTA TTAAAAAAAA AGTAAAAAAG CTCTTACCAA TCTTTTGTTT GGAATTTTCT ATATATCTTA TCTCAGAAAT ACGAGAAAAA AAAAAACGAA
PMpa005      ATTTTTTTTA TTAAAAAAAA AGTAAAAAAG CTCTTACCAA TCTTTTGTTT GGAATTTTCT ATATATCTTA TCTCAGAAAT ACGAGAAAAA AAAAAACGAA
PMve442      TTTTTTTTAT TAAAAAAAAA GTAAAAAAGT TCTTACCAAT CTTTTGTTTG GAATTTTCTA TATATCTTAT CTCAGAAATA CGAGAAAAAA AAAAACGAAT
PMhi149      TTTTTTTATA AAAAAAAGTA AAAAAGTTCT TACCAATCTT TTGTTTGGAA TTTTCTATAT ATCTTATCTC AGAAATACGA GAAAAAAAAA ACGAATGATG
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PMal338    AATATTAACG AATTTTTTTT TAATATAATA AAAAAAAAAG TAAAAAAGTT CTTACCAATC TTTTGTTTGG AATTTTCTAT ATATCTTATC TCAGAAATAC
PMal440    CATTAACGAA TTTTTTTTTT AATAAAAAAA AAAGTAAAAA AGTTCTTACC AATCTTTTGT TTGGAATTTT CTATATATCT TATCTCAGAA ATACGAGAAA
PMal539    AAATATTAAC GAATTTTTTT TTAATATAAA TAAAAAAAAA AAGTAAAAAA GTTCTTCCCA ATCTTTTGTT TGGAATTTTC TATATATCTT ATCTCAGAAA
PMto189    AATATTAACG AATTTTTTTT TAATATAATA AAAAAAAAAG TAAAAAAGTT CTTACCAATC TTTTGTTTGG AATTTTCTAT ATATCTTATC TCAGAAATAC
PMto489    AATATTAACG AATTTTTTTT TAATATAATA AAAAAAAAAG TAAAAAAGTT CTTACCAATC TTTTGTTTGG AATTTTCTAT ATATCTTATC TCAGAAATAC
PMto479    TATTAACGAA TTTTTTTTTA ATATAATAAA AAAAAAAAGT AAAAAAGTTC TTACCAATCT TTTGTTTGGA ATTTTCTATA TATCTTATCT CAGAAATACG
PMmo496    AAATATTAAC GAATTTTTTT TTAATATAAA TAAAAAAAAA AAGTAAAAAA GTTCTTACCA ATCTTTTGTT TGGAATTTTC TATATATCTT ATCTCAGAAA
PMmo332    AAATATTAAC GAATTTTTTT TTAATATAAA TAAAAAAAAA AAGTAAAAAA GTTCTTACCA ATCTTTTGTT TGGAATTTTC TATATATCTT ATCTCAGAAA
PMmo493    AAATATTAAC GAATTTTTTT TTAATATAAA TAAAAAAAAA AAGTAAAAAA GTTCTTACCA ATCTTTTGTT TGGAATTTTC TATATATCTT ATCTCAGAAA
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PMmo499    AAATATTAAC GAATTTTTTT TTAATATAAA TAAAAAAAAA AAGTAAAAAA GTTCTTCCCA ATCTTTTGTT TGGAATTTTC TATATATCTT ATCTCAGAAA
PAhi270    ATATATTATA TATTAACGAA TTCTTTTAAA ATAAAAAAAA AAATGAATGA TGAATGATAG AAATTGAGAT ATTTGAAATA TTTAAACAAT AAAAAAAAAT
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PAhi455    ATATATTATA TATTAACGAA TTCTTTTAAA ATAAAAAAAA AATGAATGAT GAATGATAGA AATTGAGATA TTTGAAATAT TTAAACAATA AAAAAAAAATA
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PMca389    ATATATTATA TATTAACGAA TTCTTTTAAA ATAAAAAAAA ACGAATGATG AATGATAGAA ATTGAGATAT TTGAAATATT TAAACAATAA AAAAAAATAC
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PMca350    AATATATTAT ATATTAACGA ATTCTTTTAA AATAAAAAAA AAAATGAATG ATGAATGATA GAAATTGAGA TATTTGAAAT ATTTAAACAA TAAAAAAAAA
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PMae351    CGAATTTATT AAAAAGAAAA AAAAAGTAAA AAAGTTCTTA CCAATCTTTT GTTTGGAATT TTCTATATAT CTTATCTCAG AAATACGATA AAAAAAAACG
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PMtr352    CGAATTTATT AAAAAGAAAA AAAAGTAAAA AAGTTCTTAC CAATCTTTTG TTTGGAATTT TCTATATATC TTATCTCAGA AATAACGATA AAAAAAAACG
PMtr393    CGAATTTATT AAAAAGAAAA AAAAGTAAAA AAGTTCTTAC CAATCTTTTG TTTGGAATTT TCTATATATC TTATCTCAGA AATACGATAA AAAAAAACGA
PMtr254    CGAATTTATT AAAAAGAAAA AAAAGTAAAA AAGTTCTTAC CAATCTTTTG TTTGGAATTT TCTATATATC TTATCTCAGA AATACGATAA AAAAAAACGA
PMat628    ATATATTATA TATTAACGAA TTCTTTTAAA ATAAAAAAAA AAATGAATGA TGAATGATAG AAATTGAGAT ATTTGAAATA TTTAAACAAT AAAAAAAAAT
PAlo461    ACTATAGTAT .......... .......... .......... .......... .......... .......... .......... .......... ..........
PAlo462    ACTATAGTAT .......... .......... .......... .......... .......... .......... .......... .......... ..........
PAlo596    ACTATAGTAT .......... .......... .......... .......... .......... .......... .......... .......... ..........
PAlu459    ATTAACTAAT TTTTTAAAAA TAAAAAAAAA ACGAATGATG AATGATAGAA ATTGAGATAT TTGAAATAGT TAAACAATAA AAAAAAATAC TATAGTAT..
PAlu460    ATTAACTAAT TTTTTAAAAA TAAAAAAAAA AACGAATGAT GAATGATAGA AATTGAGATA TTTGAAATAG TTAAACAATA AAAAAAAATA CTATAGTAT.
PAlu616    ATTAACTAAT TTTTTAAAAA TAAAAAAAAA ACGAATGATG AATGATAGAA ATTGAGATAT TTGAAATAGT TAAACAATAA AAAAAAATAC TATAGTAT..
PLph002    TTTTTAAAAT CAAAAAAAAA AGTAAAAAAG TTCTTACCAA TCTTTTGTTT GGAATTTTCT ATATATCTTA TCTCAGAAAT ACGAGAAAAA AAAAACGAAT
PLph628    TTTTTAAAAT CAAAAAAAAA AGTAAAAAAG TTCTTACCAA TCTTTTGTTT GGAATTTTCT ATATATCTTA TCTCAGAAAT ACGAGAAAAA AAAAACGAAT
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PMtf394    AACGAATTTT TTTAAAAGAA AAAAAGTAAA AAAGTTCTTA CCAATCTTTT GTAAAGTTTT TATTTTAGAG TAAAAATAAA GAATTGGAAT TTTCTATATA
PMtf070    AACGAATTTT TTTAAAAGAA AAAAAGTAAA AAAGTTCTTA CCAATCTTTT GTAAAGTTTT TATTTTAGAG TAAAAATAAA GAATTGGAAT TTTCTATATA
PMtf499    AACGAATTTT TTTAAAAGAA AAAAAGTAAA AAAGTTCTTA CCAATCTTTT GTAAAGTTTT TATTTTAGAG TAAAAATAAA GAATTGGAAT TTTCTATATA
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PMma415        AACGAATTTT TTTAAAAGAA AAAAAGTAAA AAAGTTCTTA CCAATCTTTT GTAAAGTTTT TATTTTAGAG TAAAAATAAA GAATTGGAAT TTTCTATATA
PMma279        AACGAATTTT TTTAAAAGAA AAAAAGTAAA AAAGTTCTTA CCAATCTTTT GTAAAGTTTT TATTTTAGAG TAAAAATAAA GAATTGGAAT TTTCTATATA
PAof604        GAATTTTTTT AAAATAGAAA AAAGTAAAAA AGTTCTTACC AATCTTTTGT AAAGTTTTTA TTTTAGAGTA AAAATAAAGA ATTGGAATTT TCTATATATC
PAof511        GAATTTTTTT AAAATAGAAA AAAGTAAAAA AGTTCTTACC AATCTTTTGT AAAGTTTTTA TTTTAGAGTA AAAATAAAGA ATTGGAATTT TCTATATATC
PAof512        GAATTTTTTT AAAATAGAAA AAAGTAAAAA AGTTCTTACC AATCTTTTGT AAAGTTTTTA TTTTAGAGTA AAAATAAAGA ATTGGAATTT TCTATATATC
PAof513        GAATTTTTTT AAAATAGAAA AAAGTAAAAA AGTTCTTACC AATCTTTTGT AAAGTTTTTA TTTTAGAGTA AAAATAAAGA ATTGGAATTT TCTATATATC
PAof330        GAATTTTTTA AAAATAGAAA AAAAGTAAAA AAGTTCTTAC CAATCTTTTG TAAAGTTTTT ATTTTAGAGT AAAAATAAAG AATTGGAATT TTCTATATAT
PAca345        GAATTTTTTT AAAATAGAAA AAAAGTAAAA AAGTTCTTAC CAATCTTTTG TAAAGTTTTT ATTTTAGAGT AAAAATAAAG AATTGGAATT TTCTATATAT
PAca594        GAATTTTTTT AAAATAGAAA AAAAGTAAAA AAGTTCTTAC CAATCTTTTG TAAAGTTTTT ATTTTAGAGT AAAAATAAAG AATTGGAATT TTCTATATAT
PAca471        ATATATTATA TATTAACGAA TTCTTTTAAA ATAAAAAAAA AATGAATGAT GAATGATAGA AATTGAGATA TTTGAAATAT TTAAACAATA AAAAAAAATA
PAar427        GAATTTTTTT AAAATAGAAA AAAAGTAAAA AAGTTCTTAC CAATCTTTTG TAAAGTTTTT ATTTTAGAGT AAAAATAAAG AATTGGAATT TTCTATATAT
PAsp140        ATTAACGAAT TTTTAAAAAA TAGAAAAAAG GTAAAAAAGT TCTTACCAAT CTTTTGTAAA GTTTTTATTT TAGAGTAAAA ATAAAGAATT GGAATTTTCT
Pros422        ATTAACGAAT TTTTAAAAAA TAGAAAAAAG GTAAAAAAGT TCTTACCAAT CTTTTGTAAA GTTTTTATTT TAGAGTAAAA ATAAAGAATT GGAATTTTCT
PMsh0325       ATAATATATT AAATATTAAG TTAACGATTT TTTTAAAATA AAATAAAAGT AAAAAAGTTC TTACCAAATC TTTTGTAAAG TATTTTTTTA GAGTAAAAAT


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                      410        420        430        440        450        460        470        480        490        500
PLpl285        AAAAAAAACG AATGATGAAT GATAGAAATT GAGATATTTG AAATATTTAA ACAATAAAAA AAAATACTAT ACTAT..... .......... ..........
PLbr141        ATACGAGAAA AAAAAAACGA ATGATGAATG ATAGAAATTG AGATATTTGA AATATTTAAA CAATAAAAAA AAATACTATA CTAT...... ..........
PLfl414        AAAAAACGAA TGATGAATGA TAGAAATTGA GATATTTGAA ATATTTAAAC AATAAAAAAA AATACTATAC TAT....... .......... ..........
PLfl000        AAAAAACGAA TGATGAATGA TAGAAATTGA GATATTTGAA ATATTTAAAC AATAAAAAAA AATACTATAC TAT....... .......... ..........
PLag308        AAAAAAAACG AATGATGAAT GATAGAAATT GAGATATTTG AAATATTTAA ACAATAAAAA AAATACTATA CTAT...... .......... ..........
PLtp564        AATGATGAAT GATAGAAATT GAAATATTTG AAATATTTAA ACAATAAAAA AAAATACTAT ACTAT..... .......... .......... ..........
PLtp354        AAAAAACGAA TGATGAATGA TAGAAATTGA GATATTTGAA ATATTTAAAC AATAAAAAAA AATACTATAC TAT....... .......... ..........
PLtr117        AAAAAAAAAA CGAATGATGA ATGATAGAAA TTGAGATATT TGAAATATTT AAACAATAAA AAAAAATACT ATACTAT... .......... ..........
PLtr357        AAAAAAAACG AATGATGAAT GATAGAAATT GAGATATTTG AAATATTTAA ACAATAAAAA AAAATACTAT ACTAT..... .......... ..........
PLtr359        AAAAAAACGA ATGATGAATG ATAGAAATTG AGATATTTGA AATATTTAAA CAATAAAAAA AATACTATAC TAT....... .......... ..........
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PLol451        AAAAAAAACG AATGATGAAT GATAGAAATT GAGATATTTG AAATATTTAA ACAATAAAAA AAAATACTAT ACTAT..... .......... ..........
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PLpu450        AAAAAACGAA TGATGAATGA TAGAAATTGA GATATTTGAA ATATTTAAAC AATAAAAAAA AATACTATAC TAT....... .......... ..........
PLpu348        AATGATGAAT GATAGAAATT GAAATATTTG AAATATTTAA ACAATAAAAA AAAATACTAT ACTAT..... .......... .......... ..........
PLth353        AAAAAACGAA TGATGAATGA TAGAAATTGA GATATTTGAA ATATTTAAAC AATAAAAAAA AATACTATAC TAT....... .......... ..........
PLti308        TGAATGATAG AAATTGAGAT ATTTGAAATA TTTAAACAAT AAAAAAAAAT ACTATAACTA TACTAT.... .......... .......... ..........
PLti181        TGAATGATAG AAATTGAGAT ATTTGAAATA TTTAAACAAT AAAAAAAAAT ACTATACTAT .......... .......... .......... ..........
PLti233        TGAATGATAG AAATTGAGAT ATTTGAAATA TTTAAACAAT AAAAAAAAAT ACTATACTAT .......... .......... .......... ..........
PLti595        GAATGATAGA AATTGAGATA TTTGAAATAT TTAAACAATA AAAAAAAATA CTATACTAT. .......... .......... .......... ..........
PLma329        AACGAATGAT GAATGATAGA AATTGAGATA TTTGAAATAT TTAAACAATA AAAAAAAAAT ACTATAGTAT .......... .......... ..........
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PLma200      AAAAAAACGA ATGATGAATG ATAGAAATTG AGATATTTGA AATATTTAAA CAATAAAAAA AAATACTATA CTAT...... .......... ..........
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PLma405      GAATGATGAA TGATAGAAAT TGAGATATTT GAAATATTTA AACAATAAAA AAAAAATACT ATAGTA.... .......... .......... ..........
PLma598      CGAATGATGA ATGATAGAAA TTGAGATATT TGAAATATTT AAACAATAAA AAAAAAATAC TATAGTAT.. .......... .......... ..........
PLac134      ATACGAGAAA AAAAAAAACG AATGATAGAA ATTGAGATAT TTGAAATATT TAAACAATAA AAAAAAATAC CTATAGTAT. .......... ..........
PLas570      AATGATGAAT GATAGAAATT GAGATATTTG AAATATTTAA ACAATAAAAA AAATACTATA GTAT...... .......... .......... ..........
PLab383      AAAAAAAAAA AAACGAATGA TAGAAATTGA AATATTTGAA ATATTTAAAC AATAAAAAAA ATACTATAGT AT........ .......... ..........
PLpe634      GAATGATGAA TGATAGAAAT TGAGATATTT GAAATATTTA AACAATAAAA AAAATACTAT AGTAT..... .......... .......... ..........
PLmu137      TGATGAATGA TAGAAATTGA GATATTTGAA ATATTTAAAC AATAAAAAAA ATACTATAGT AT........ .......... .......... ..........
PLmu319      TGATGAATGA TAGAAATTGA GATATTTGAA ATATTTAAAC AATAAAAAAA ATACTATAGT AT........ .......... .......... ..........
PLmu318      TGATGAATGA TAGAAATTGA GATATTTGAA ATATTTAAAC AATAAAAAAA ATACTATAGT AT........ .......... .......... ..........
PLmu630      TGATGAATGA TAGAAATTGA GATATTTGAA ATATTTAAAC AATAAAAAAA ATACTATAGT AT........ .......... .......... ..........
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PLar239      AATGATAGAA ATTGAGATAT TTGAAATATT TAAACAATAA AAAAAATACT ATAGTAT... .......... .......... .......... ..........
PLar252      GAATGATAGA AATTGAGATA TTTGAAATAT TTAAACAATA AAAAAAATAC TATAGTAT.. .......... .......... .......... ..........
PLcr076      AAAACGAATG ATGAATGATA GAAATTGAGA TATTTGAAAT ATTTAAACAA TAAAAAAAAT ACTATAGTAT .......... .......... ..........
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PLcr235      AAACGAATGA TGAATGATAG AAATTGAGAT ATTTGAAATA TTTAAACAAT AAAAAAAAAT CTATAGTAT. .......... .......... ..........
PLcr599      AAACGAATGA TGAATGATAG AAATTGAGAT ATTTGAAATA TTTAAACAAT AAAAAAAAAT CTATAGTAT. .......... .......... ..........
PMni032      ATACGAGAAA AAAAAAAACG AATGATAGAA ATTGAGATAT TTGAAATATT TAAACAATAA AAAAAAATAC TATAGTAT.. .......... ..........
PMni097      ATGATGAATG ATAGAAATTG AGATATTTGA AATATTTAAA CAATAAAAAA AATACTATTA CTATAGTAT. .......... .......... ..........
PMni105      AATGATGAAT GATAGAAATT GAGATATTTG AAATATTTAA ACAATAAAAA AAATACTATT ACTATAGTAT .......... .......... ..........
PMni633      GAATGATGAA TGATAGAAAT TGAGATATTT GAAATATTTA AACAATAAAA AAAATACTAT TACTATAGTA T......... .......... ..........
PMni228      AATGATGAAT GATAGAAATT GAGATATTTG AAATATTTAA ACAATAAAAA AAATACTATT ACTATAGTAT .......... .......... ..........
PMne349      GAATGATGAA TGATAGAAAT TGAGATATTT GAAATATTTA AACAATAAAA AAAATACTAT AGTAT..... .......... .......... ..........
PMne632      ATGATGAATG ATAGAAATTG AGATATTTGA AATATTTAAA CAAAAAAAAA AATACTATAG TAT....... .......... .......... ..........
PMsy001      GAATGATGAA TGATAGAAAT TGAGATATTT GAAATATTTA AACAATAAAA AAAATACTAT AGTAT..... .......... .......... ..........
PMsy635      ATGATGAATG ATAGAAATTG AGATATTTGA AATATTTAAA CAATAAAAAA AATACTATAG TAT....... .......... .......... ..........
PMpa059      TGATGAATGA TAGAAATTGA GATATTTGAA ATATTTAAAC AATAAAAAAA ATACTATAGT AT........ .......... .......... ..........
PMpa296      TGATGAATGA TAGAAATTGA GATATTTGAA ATATTTAAAC AATAAAAAAA ATACTATAGT AT........ .......... .......... ..........
PMpa249      TGATGAATGA TAGAAATTGA GATATTTGAA ATATTTAAAC AATAAAAAAA ATACTATAGT AT........ .......... .......... ..........
PMpa005      TGATGAATGA TAGAAATTGA GATATTTGAA ATATTTAAAC AATAAAAAAA ATACTATAGT AT........ .......... .......... ..........
PMve442      GATGAATGAT AGAAATTGAG ATATTTGAAA TATTTAAACA ATAAAAAAAA TACTATAGTA T......... .......... .......... ..........
PMhi149      AATGATAGAA ATTGAGATAT TTGAAATATT TAAACAATAA AAAAAAATAC TATACTAT.. .......... .......... .......... ..........
PMhi602      AATGATAGAA ATTGAGATAT TTGAAATATT TAAACAATAA AAAAAAATAC TATACTAT.. .......... .......... .......... ..........
PMhi631      ATGAATGATA GAAATTGGGA TATTTGAAAT ATTTAAACAA TAAAAAAAAT ACTATACTAT .......... .......... .......... ..........
PMal338      GAGAAAAAAA AAAAAACGAA TGATGAATGA TAGAAATTGA GATATTTGAA ATATTTAAAC AATAAAAAAA AAATACTATA CTAT...... ..........
PMal440      AAAAAACGAA TGATGAATGA TAGAAATTGA GATATTTGAA ATATTTAAAC AATAAAAAAA AATACTATAC TAT....... .......... ..........
PMal539      TACGAGAAAA AAAAAACGAA TGATGAATGA TAGAAATTGA GATATTTGAA ATATTTAAAC AATAAAAAAA AATACTATAC TAT....... ..........
PMto189      GAGAAAAAAA AAAAAACGAA TGATGAATGA TAGAAATTGA GATATTTGAA ATATTTAAAC AATAAAAAAA AAATACTATA CTAT...... ..........
PMto489      GAGAAAAAAA AAAAAACGAA TGATGAATGA TAGAAATTGA GATATTTGAA ATATTTAAAC AATAAAAAAA AATACTATAC TAT....... ..........
PMto479      AGAAAAAAAA AAAAACGAAT GATGAATGAT AGAAATTGAG ATATTTGAAA TATTTAAACA ATAAAAAAAA AATACTATAC TAT....... ..........
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PMmo496      TACGAGAAAA AAAAAAACGA ATGATGAATG ATAGAAATTG AGATATTTGA AATATTTAAA CAATAAAAAA AAATACTATA CTAT...... ..........
PMmo332      TACGAGAAAA AAAAAACGAA TGATGAATGA TAGAAATTGA GATATTTGAA ATATTTAAAC AATAAAAAAA AATACTATAC TAT....... ..........
PMmo493      TACGAGAAAA AAAAAACGAA TGATGAATGA TAGAAATTGA GATATTTGAA ATATTTAAAC AATAAAAAAA AATACTATAC TAT....... ..........
PMmo494      TACGAGAAAA AAAAAACGAA TGATGAATGA TAGAAATTGA GATATTTGAA ATATTTAAAC AATAAAAAAA AATACTATAC TAT....... ..........
PMmo499      TACGAGAAAA AAAAAACGAA TGATGAATGA TAGAAATTGA GATATTTGAA ATATTTAAAC AATAAAAAAA AATACTATAC TAT....... ..........
PAhi270      ACTATAGTAT .......... .......... .......... .......... .......... .......... .......... .......... ..........
PAhi454      ACTATAGTAT .......... .......... .......... .......... .......... .......... .......... .......... ..........
PAhi455      CTATAGTAT. .......... .......... .......... .......... .......... .......... .......... .......... ..........
PAhi456      CTATAGTAT. .......... .......... .......... .......... .......... .......... .......... .......... ..........
PAhi458      ACTATAGTAT .......... .......... .......... .......... .......... .......... .......... .......... ..........
PAhi356      AAAAAAAAAA CGAATGATGA ATGATAGAAA TTGAGATATT TGAAATATTT AAACAATAAA AAAAAATACT ATACTAT... .......... ..........
PMca389      TATAGTAT.. .......... .......... .......... .......... .......... .......... .......... .......... ..........
PMca391      CTATAGTAT. .......... .......... .......... .......... .......... .......... .......... .......... ..........
PMca463      ACTATAGTAT .......... .......... .......... .......... .......... .......... .......... .......... ..........
PMca350      TACTATAGTA T......... .......... .......... .......... .......... .......... .......... .......... ..........
PMae465      ATGATGAATG ATAGAAATTG AGATATTTGA AATATTTAAA CAATAAAAAA AAATACTATA GTAT...... .......... .......... ..........
PMae468      ATGATGAATG ATAGAAATTG AGATATTTGA AATATTTAAA CAATAAAAAA AAATACTATA GTAT...... .......... .......... ..........
PMae351      AATGATGAAT GATAGAAATT GAGATATTTG AAATATTTAA ACAATAAAAA AAAATACTAT AGTAT..... .......... .......... ..........
PMtr392      ATGATGAATG ATAGAAATTG AGATATTTGA AATATTTAAA CAATAAAAAA AAATACTATA GTAT...... .......... .......... ..........
PMtr352      AATGATGAAT GATAGAAATT GAGATATTTG AAATATTTAA ACAATAAAAA AAAATACTAT AGTAT..... .......... .......... ..........
PMtr393      ATGATGAATG ATAGAAATTG AGATATTTGA AATATTTAAA CAATAAAAAA AAATACTATA GTAT...... .......... .......... ..........
PMtr254      ATGATGAATG ATAGAAATTG AGATATTTGA AATATTTAAA CAATAAAAAA AAATACTATA GTAT...... .......... .......... ..........
PMat628      ACTATAGTAT .......... .......... .......... .......... .......... .......... .......... .......... ..........
PAlo461      .......... .......... .......... .......... .......... .......... .......... .......... .......... ..........
PAlo462      .......... .......... .......... .......... .......... .......... .......... .......... .......... ..........
PAlo596      .......... .......... .......... .......... .......... .......... .......... .......... .......... ..........
PAlu459      .......... .......... .......... .......... .......... .......... .......... .......... .......... ..........
PAlu460      .......... .......... .......... .......... .......... .......... .......... .......... .......... ..........
PAlu616      .......... .......... .......... .......... .......... .......... .......... .......... .......... ..........
PLph002      GATGAATGAT AGAAATTGAG ATATTTGAAA TATTTAAAAA ATAAAAAAAA AAAATACTAT ACTCT..... .......... .......... ..........
PLph628      GATGAATGAT AGAAATTGAG ATATTTGAAA TATTTAAAAA ATAAAAAAAA AAAATACTAT ACTCT..... .......... .......... ..........
PLph629      GATGAATGAT AGAAATTGAG ATATTTGAAA TATTTAAAAA ATAAAAAAAA AAAATACTAT ACTCT..... .......... .......... ..........
PMtf394      TTTTATATCA GAAATACGAG AAAAAACGAA TGATGAATGA TAGAAATTGA GATATTTGAA ATATTTAAAC AATAAAAAAA AATACTATAG TATTATAGTA
PMtf070      TTTTATATCA GAAATACGAG AAAAAACGAA TGATGAATGA TAGAAATTGA GATATTTGAA ATATTTAAAC AATAAAAAAA AATACTATAG TAT.......
PMtf499      TTTTATATCA GAAATACGAG AAAAAACGAA TGATGAATGA TAGAAATTGA GATATTTGAA ATATTTAAAC AATAAAAAAA AATACTATAG TAT.......
PMma415      TTTTATCTCA GAAATACGAG AAAAAACGAA TGATGAATGA TAGAAATTGA GATATTTGAA ATATTTAAAC AATAAAAAAA AATACTATAG TAT.......
PMma279      TTTTATCTCA GAAATACGAG AAAAAACGAA TGATGAATGA TAGAAATTGA GATATTTGAA ATATTTAAAC AATAAAAAAA AATACTATAG TAT.......
PAof604      TTATCTCAGA AATACGAGAA AAAACGAATG ATGAATGATA GAAATTGAGA TATTTGAAAT ATTTAAACAA TAAAAAAAAA TACTATAGTA T.........
PAof511      TTATCTCAGA AATACGAGAA AAAACGAATG ATGAATGATA GAAATTGAGA TATTTGAAAT ATTTAAACAA TAAAAAAAAA TACTATAGTA T.........
PAof512      TTATCTCAGA AATACGAGAA AAAACGAATG ATGAATGATA GAAATTGAGA TATTTGAAAT ATTTAAACAA TAAAAAAAAA TACTATAGTA T.........
PAof513      TTATCTCAGA AATACGAGAA AAAACGAATG ATGAATGATA GAAATTGAGA TATTTGAAAT ATTTAAACAA TAAAAAAAAA TCCTATAGTA T.........
PAof330      CTTATCTCAG AAATACGAGA AAAAACGAAT GATGAATGAT AGAAATTGAG ATATTTGAAA TATTTAAACA ATAAAAAAAA AATACTATAG TAT.......
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PAca345      CTTATCTCAG AAATACGAGA AAAAACGAAT GATGAATGAT AGAAATTGAG ATATTTGAAA TATTTAAACA ATAAAAAAAA ATACTATAGT AT........
PAca594      CTTATCTCAG AAATACGAGA AAAAACGAAT GATGAATGAT AGAAATTGAG ATATTTGAAA TATTTAAACA ATAAAAAAAA ATACTATAGT AT........
PAca471      CTATAGTAT. .......... .......... .......... .......... .......... .......... .......... .......... ..........
PAar427      CTTATCTCAG AAATACGAGA AAAAACGAAT GATGAATGAT AGAAATTGAG ATATTTGAAA TATTTAAACA ATAAAAAAAA ATACTATAGT AT........
PAsp140      ATATATCTTA TCTCAGAAAT ACGAGAAAAA ACGAATGATG AATGATAGAA ATTGAGATAT TTGAAATATT TAAACAATAA AAAAAATACT ATACTAT...
Pros422      ATATATCTTA TCTCAGAAAT ACGAGAAAAA ACGAATGATG AATGATAGAA ATTGAGATAT TTGAAATATT TAAACAATAA AAAAAAGACT ATACTAT...
PMsh325      AAATAAAAGA TAGAGATTGG AATTTTCTAT ATATCTTATT CTTATCTCAG AAATAAGATA AAAAAAGAAT GATGAATGAT AGAGATTGAA ATCTTTGAAA
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                        10         20         30         40         50         60         70         80         90        100
TLpl285         AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTT---AT TGGTTCAAAG TTCCTTATGT TTCTCACTCA TCCTATTCTT TTTT------
TLob144         AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTT---AT TGGTTCAAAG TTCCTTATGT TTCTCACTCA TCCTATTCTT TTTT------
TLbr141         AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTT---AT TGGTTCAAAG TTCCTTATGT TTCTCACTCA TCCTATTCTT TTTT------
TLol451         AaAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTT---AT TGGTTCAAAG TTCCTTATGT TTCTCACTCA TCCTATTCTT TTTT------
TLol004         AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTT---AT TGGTTCAAAG TTCCTTATGT TTCTCACTCA TCCTATTCTT TTTT------
TLfl414         AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTT---AT TGGTTCAAAG TTCCTTATGT TTCTCACTCA TCCTATTCTT TTTT------
TLfl000         AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTT---AT TGGTTCAAAG TTCCTTATGT TTCTCACTCA TCCTATTCTT TTTT------
TLag308         AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTT---AT TGGTTCAAAG TTCCTTATGT TTCTCACTCA TCCTATTCTT TTTT------
TLtp564         AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTT---AT TGGTTCAAAG TTCCTTATGT TTCTCACTCA TCCTATTCTT TTTT------
TLtp354         AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTT---AT TGGTTCAAAG TTCCTTATGT TTCTCACTCA TCCTATTCTT TTTT------
TLtr117         AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTT---AT TGGTTCAAAG TTCCTTATGT TTCTCACTCA TCCTATTCTT TTTT------
TLtr357         AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTT---AT TGGTTCAAAG TTCCTTATGT TTCTCACTCA TCCTATTCTT TTTT------
TLtr359         AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTT---AT TGGTTCAAAG TTCCTTATGT TTCTCACTCA TCCTATTCTT TTTT------
TLtr169         AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTT---AT TGGTTCAAAG TTCCTTATGT TTCTCACTCA TCCTATTCTT TTTT------
TLpu348         AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTT---AT TGGTTCAAAG TTCCTTATGT TTCTCACTCA TCCTATTCTT TTTT------
TLpu450         AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTT---AT TGGTTCAAAG TTCCTTATGT TTCTCACTCA TCCTATTCTT TTTT------
TLpu555         AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTT---AT TGGTTCAAAG TTCCTTATGT TTCTCACTCA TCCTATTCTT TTTT------
TLth353         AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTT---AT TGGTTCAAAG TTCCTTATGT TTCTCACTCA TCCTATTCTT TTTT------
TLmo346         AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTT--AT TGGTTCAAAG TTCCTTATGT TTCTCACTCA TCCTATTCTT TTTT------
TLmo515         AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTT--AT TGGTTCAAAG TTCCTTATGT TTCTCACTCA TCCTATTCTT TTTT------
TLti595         AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTT--AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TLti181         AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTT--AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TLti233         AaAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTT--AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TLti308         AAAag-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTT--AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TLac134         AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTT--AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TLcr031         AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTTT-AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TLcr599         AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTTT-AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TLcr235         AAAaG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTTT-AT TGGTTCAAAG TTcCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TLmu137         AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTTT-AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TLmu319         AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTTT-AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TLmu630         AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTTT-AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TMpa005         AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTTT-AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TMpa249         AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTTT-AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TMpa059         AaAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTTT-AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TMpa296         AaAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTTT-AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TMsy001         AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTTT-AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TMsy635         --AAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTTT-AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TMni032         AAAag-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTTT-AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
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TMni097      AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTTT-AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TMni633      AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTTT-AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TMni228      AaAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTTT-AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TMne349      AaAAg-CCCG TTTGCTAtCT ATTTATTTTa TcctACCCTT Ttttttt-AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TMne632      AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCTTT TTTTTTT-AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TMve442      AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTTT-AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TLar153      AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTTT-AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TLar378      AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTTT-AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TLar239      AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTTT-AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TLar252      AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTTT-AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TLas570      AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTTT-AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TLab383      AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTTT-AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TLpe634      AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTTT-AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TLma598      AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTT--AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TLma329      AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTT--AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TLma200      AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTT--AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TLma404      AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTT--AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TMhi602      AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTT--AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TMhi149      AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTT--AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TMhi631      AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTT--AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TAhi356      AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTT---AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT CTTTTTT---
TAhi270      AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTT---AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TAhi454      AAaAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTT---AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TAhi455      AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTT---AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TAhi456      AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTT---AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TAhi458      AAaAG-CCCG tTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTT---AT TGGTTCAAAG TTCCTTATGT TtcTCATTCA TCCTATTcTT TTTT------
TAlu460      AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTTT-AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TAlu616      AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTTT-AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TMat628      AAAAGG-CCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTT---AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TAlo596      AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTT---AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTGTT TTTT------
TAlo461      AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTT---AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTGTT TTTT------
TAlo462      AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTT---AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTGTT TTTT------
TAof330      AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTGTT--AG TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTTACATTT
TAof604      AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTGTT--AG TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTTACATTT
TAof511      AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTGTT--AG TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTTACATTT
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TAof513      AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTGTT--AG TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTTACATTT
TAca345      AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTGTT--AG TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTTACATTT
TAca594      AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTGTT--AG TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTTACATTT
TAca471      AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTGTT--AG TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTTACATTT
TAar427      AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTGTT--AG TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTTACATTT
TMtr452      AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTT--AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
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TMtr453         AaAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTT--AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TMtr352         AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTT--AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TMtr254         AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTT--AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TMae351         AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTT--AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TMae465         AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTT--AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TMae468         AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTT--AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TMcc361         AAAAGGCC-G TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTT---AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TMca463         AAAAGGCC-G TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTT---AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TMal440         AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTT---AT TGGTTCAAAG TTCCTTATGT TTCTCACTCA TCCTATTCTT TTTT------
TMal539         AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTTT-AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TMal338         AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTT--AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TMmo493         AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTTT-AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TMmo494         AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTTT-AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TMmo332         AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTTT-AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TMmo496         AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTTT-AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TMmo499         AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTTT-AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TMmo593         AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTTT-AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TMto479         AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTT--AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TMto189         AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTT--AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TMto489         AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTT--AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TMtf601         AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTTT-AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TMtf070         AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTTT-AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TMtf499         AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTTT-AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TMma415         AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTTT-AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TMma600         AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTTT-AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TMma600         AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTTT-AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TLph002         AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTT--AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TLph628         AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTT--AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TLph629         AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTT--AT TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
Tros422         AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTGTT--AG TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TAsp140         AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTGTT--AG TGGTTCAAAG TTCCTTATGT TTCTCATTCA TCCTATTCTT TTTT------
TMsh325         AAAAG-CCCG TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTGTT--AG TGGTTCAAAA TTCCTTATGT TTCTTATTCA TCCTATTCTT TTTT------


                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                       110        120        130        140        150        160        170        180        190        200
TLpl285         ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATAT--- -ATATATAT- -----CATAT ACGTACAAAT CTCTTGAGCA
TLob144         ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATAT--- -ATATATAT- -----CATAT ACGTACAAAT CTCTTGAGCA
TLbr141         ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATAT--- -ATATATAT- -----CATAT ACGTACAAAT CTCTTGAGCA
TLol451         ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATAT--- -ATATATAT- -----CATAT ACGTACAAAT CTCTTGAGCA
TLol004         ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATAT--- -ATATATAT- -----CATAT ACGTACAAAT CTCTTGAGCA
TLfl414         ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATAT--- -ATATATAT- -----CATAT ACGTACAAAT CTCTTGAGCA
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TLfl000       ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATAT--- -ATATATAT- -----CATAT ACGTACAAAT CTCTTGAGCA
TLag308       ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATAT--- -ATATATAT- -----CATAT ACGTACAAAT CTCTTGAGCA
TLtp564       ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATAT--- -ATATATAT- -----CATAT ACGTACAAAT CTCTTGAGCA
TLtp354       ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATAT--- -ATATATAT- -----CATAT ACGTACAAAT CTCTTGAGCA
TLtr117       ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATAT--- -ATATATAT- -----CATAT ACGTACAAAT CTCTTGAGCA
TLtr357       ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATAT--- -ATATATAT- -----CATAT ACGTACAAAT CTCTTGAGCA
TLtr359       ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATAT--- -ATATATAT- -----CATAT ACGTACAAAT CTCTTGAGCA
TLtr169       ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATAT--- -ATATATAT- -----CATAT ACGTACAAAT CTCTTGAGCA
TLpu348       ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATAT--- -ATATATAT- -----CATAT ACGTACAAAT CTCTTGAGCA
TLpu450       ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATAT--- -ATATATAT- -----CATAT ACGTACAAAT CTCTTGAGCA
TLpu555       ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATAT--- -ATATATAT- -----CATAT ACGTACAAAT CTCTTGAGCA
TLth353       ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATAT--- -ATATATAT- -----CATAT ACGTACAAAT CTCTTGAGCA
TLmo346       ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATAT--- -ATATATAT- -----CATAT ACGTACAAAT CTCTTGAGCA
TLmo515       ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATAT--- -ATATATAT- -----CATAT ACGTACAAAT CTCTTGAGCA
TLti595       ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATATTGT GATATATATA TATATCATAT ACGCACAAAT CTCTTGAGAA
TLti181       ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATATTGT GATATATATA TATATCATAT ACGCACAAAT CTCTTGAGAA
TLti233       ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATATTGT GATATATATA TATATCATAT ACGCACAAAT CTCTTGAGAA
TLti308       ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATATTGT GATATATATA TATATCATAT ACGCACAAAT CTCTTGAGAA
TLac134       ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATATTGT GATATATATA TAT--CATAT ACGTACAAAT CTCTTGAGCA
TLcr031       ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATATTGT GATATATATA TAT--TATAT ACGTACAAAT CTCTTGAGCA
TLcr599       ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATATTGT GATATATATA TAT--TATAT ACGTACAAAT CTCTTGAGCA
TLcr235       ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATATTGT GATATATATA TAT--TATAT ACGTACAAAT CTCTTGAGCA
TLmu137       ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATATTGT AATATATATA TAT--TATAT ACGTACAAAT CTCTTGAGCA
TLmu319       ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATATTGT AATATATATA TAT--TATAT ACGTACAAAT CTCTTGAGCA
TLmu630       ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATATTGT AATATATATA TAT--TATAT ACGTACAAAT CTCTTGAGCA
TMpa005       ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATATTGT AATATATATA TAT--TATAT ACGTACAAAT CTCTTGAGCA
TMpa249       ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATATTGT AATATATATA TAT--TATAT ACGTACAAAT CTCTTGAGCA
TMpa059       ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATATTGT AATATATATA TAT--TATAT ACGTACAAAT CTCTTGAGCA
TMpa296       ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATATTGT GATATATATA TAT--CATAT ACGTACAAAT CTCTTGAGCA
TMsy001       ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATATTGT GATATATATA TAT--TATAT ACGTACAAAT CTCTTGAGCA
TMsy635       ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATATTGT GATATATATA TAT--TATAT ACGTACAAAT CTCTTGAGCA
TMni032       ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATATTGT GATATATATA TAT--TATAT ACGTACAAAT CTCTTGAGCA
TMni097       ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATATTGT GATATATATA TAT--TATAT ACGTACAAAT CTCTTGAGCA
TMni633       ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATATTGT GATATATATA TAT--TATAT ACGTACAAAT CTCTTGAGCA
TMni228       ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATATTGT GATATATATA TAT--TATAT ACGTACAAAT CTCTTGAGCA
TMne349       ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATATTGT GATATATATA TAT--TATAT ACGTACAAAT CTCTTGAGCA
TMne632       ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATATTGT GATATATATA TAT--TATAT ACGTACAAAT CTCTTGAGCA
TMve442       ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATATTGT AATATATATA TAT--TATAT ACGTACAAAT CTCTTGAGCA
TLar153       ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATATTGT GATATATATA TAT--CATAT ACGTACAAAT CTCTTGAGCA
TLar378       ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATATTGT GATATATATA TAT--CATAT ACGTACAAAT CTCTTGAGCA
TLar239       ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATATTGT GATATATATA TAT--CATAT ACGTACAAAT CTCTTGAGCA
TLar252       ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATATTGT GATATATATA TAT--CATAT ACGTACAAAT CTCTTGAGCA
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TLas570      ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATATTGT GATATATATA TAT--CATAT ACGTACAAAT CTCTTGAGCA
TLab383      ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATATTGT GATATATATA TAT--CATAT ACGTACAAAT CTCTTGAGCA
TLpe634      ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATATTGT GATATATATA TAT--CATAT ACGTACAAAT CTCTTGAGCA
TLma598      ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATATTGT GATATATATA TAT--CATAT ACGTACAAAT CTCGTGAGCA
TLma329      ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATATTGT GATATATATA TAT--CATAT ACGTACAAAT CTCGTGAGCA
TLma200      ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATATTGT GATATATATA TAT--CATAT ACGTACAAAT CTCGTGAGCA
TLma404      ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATATTGT GATATATATA TAT--CATAT ACGTACAAAT CTCGTGAGCA
TMhi602      ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATAT--- -ATATAT--- -----CATAT ACGTACAAAT CTCTTGACCA
TMhi149      ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATAT--- -ATATAT--- -----CATAT ACGTACAAAT CTCTTGACCA
TMhi631      ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATAT--- -ATATAT--- -----CATAT ACGTACAAAT CTCTTGACCA
TAhi356      ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATATTGT GATATATAT- -----CATAT ACGTACAAAT CTCTTGAGCA
TAhi270      ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATATTGT GATATATAT- -----CATAT ACGTACAAAT CTCTTGAGCA
TAhi454      ---ACAAACG TATCCTAGCA GAATTTTGTT CTCTatATCA CAAGTCTTGT GATATATTGT GATATATAT- -----CATAT ACGTACAAAT CTCTTGAGCA
TAhi455      ---ACAAACG TATCCTAGCA GAATTTTGTT CTCTatATCA CAAGTCTTGT GATATATTGT GATATATAT- -----CATAT ACGTACAAAT CTCTTGAGCA
TAhi456      ---ACAAACG TATCCTAGCA GAATTTTGTT CTCTatATCA CAAGTCTTGT GATATATTGT GATATATAT- -----CATAT ACGTACAAAT CTCTTGAGCA
TAhi458      ---ACAAACG TATCCTAGCa GAATTTTGTT CTCTAtATCA CAAGTCTTGT GATATATTGT GATATATAT- -----CATAT ACGTACAAAT CTCTTGAGCA
TAlu460      ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATATTGT GATATATAT- -----CATAT ACGTACAAAT CTCTTGAGCA
TAlu616      ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATATTGT GATATATAT- -----CATAT ACGTACAAAT CTCTTGAGCA
TMat628      ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATATTGT GATATATAT- -----CATAT ACGTACAAAT CTCTTGAGCA
TAlo596      ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATATTGT GATATATAT- -----CATAT ACGTACAAAT CTCTTGAGCA
TAlo461      ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATATTGT GATATATAT- -----CATAT ACGTACAAAT CTCTTGAGCA
TAlo462      ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATATTGT GATATATAT- -----CATAT ACGTACAAAT CTCTTGAGCA
TAof330      TTTACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATATTGT GATATATATA TAT--GATAT ACGTACAAAT CTCTTGAGCA
TAof604      TTTACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATATTGT GATATATATA TAT--GATAT ACGTACAAAT CTCTTGAGCA
TAof511      TTTACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATATTGT GATATATATA TAT--GATAT ACGTACAAAT CTCTTGAGCA
TAof512      TTTACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATATTGT GATATATATA TAT--GATAT ACGTACAAAT CTCTTGAGCA
TAof513      TTTACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATATTGT GATATATATA TAT--GATAT ACGTACAAAT CTCTTGAGCA
TAca345      TTTACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATATTGT GATATATATA TAT--GATAT ACGTACAAAT CTCTTGAGCA
TAca594      TTTACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATATTGT GATATATATA TAT--GATAT ACGTACAAAT CTCTTGAGCA
TAca471      TTTACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATATTGT GATATATATA TAT--GATAT ACGTACAAAT CTCTTGAGCA
TAar427      TTTACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATATTGT GATATATATA TAT--GATAT ACGTACAAAT CTCTTGAGCA
TMtr452      ---ACAAACG TATCCTAGCA GAATTTCGTT CTCT-TATCA CAAGTCTTGT GATATATTGT GATATATAT- -----CATAT ACGTACAAAT CTCTTGAGCA
TMtr453      ---ACAAACG TATCCTAGCA GAATTTCGTT CTCT-TATCA CAAGTCTTGT GATATATTGT GATATATAT- -----CATAT ACGTACAAAT CTCTTGAGCA
TMtr352      ---ACAAACG TATCCTAGCA GAATTTCGTT CTCT-TATCA CAAGTCTTGT GATATATTGT GATATATAT- -----CATAT ACGTACAAAT CTCTTGAGCA
TMtr254      ---ACAAACG TATCCTAGCA GAATTTCGTT CTCT-TATCA CAAGTCTTGT GATATATTGT GATATATAT- -----CATAT ACGTACAAAT CTCTTGAGCA
TMae351      ---ACAAACG TATCCTAGCA GAATTTCGTT CTCT-TATCA CAAGTCTTGT GATATATTGT GATATATAT- -----CATAT ACGTACAAAT CTCTTGAGCA
TMae465      ---ACAAACG TATCCTAGCA GAATTTCGTT CTCT-TATCA CAAGTCTTGT GATATATTGT GATATATAT- -----CATAT ACGTACAAAT CTCTTGAGCA
TMae468      ---ACAAACG TATCCTAGCA GAATTTCGTT CTCT-TATCA CAAGTCTTGT GATATATTGT GATATATAT- -----CATAT ACGTACAAAT CTCTTGAGCA
TMcc361      ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATATTGT GATATATAT- -----CATAT ACGTACAAAT CTCTTGAGCA
TMca463      ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATATTGT GATATATAT- -----CATAT ACGTACAAAT CTCTTGAGCA
TMal440      ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATAT--- -ATATAT--- -----CATAT ACGTACAAAT CTCTTGAGCA
TMal539      ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATAT--- -ATATAT--- -----CATAT ACGTACAAAT CTCTTGAGCA
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TMal338       ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATAT--- -ATAT----- -----CATAT ACGTACAAAT CTCTTGAGCA
TMmo493       ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATAT--- -ATATAT--- -----CATAT ACGTACAAAT CTCTTGAGCA
TMmo494       ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATAT--- -ATATAT--- -----CATAT ACGTACAAAT CTCTTGAGCA
TMmo332       ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATAT--- -ATATAT--- -----CATAT ACGTACAAAT CTCTTGAGCA
TMmo496       ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATAT--- -ATATAT--- -----CATAT ACGTACAAAT CTCTTGAGCA
TMmo499       ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATAT--- -ATATAT--- -----CATAT ACGTACAAAT CTCTTGAGCA
TMmo593       ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATAT--- -ATATAT--- -----CATAT ACGTACAAAT CTCTTGAGCA
TMto479       ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATAT--- -ATATAT--- -----CATAT ACGTACAAAT CTCTTGAGCA
TMto189       ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATAT--- -ATATAT--- -----CATAT ACGTACAAAT CTCTTGAGCA
TMto489       ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATAT--- -ATATAT--- -----CATAT ACGTACAAAT CTCTTGAGCA
TMtf601       ---ACAAACG TATGCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATATTGT GATATATATA T----GATAT ACGTACAAAT CTCTTGAGCA
TMtf070       ---ACAAACG TATGCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATATTGT GATATATATA T----GATAT ACGTACAAAT CTCTTGAGCA
TMtf499       ---ACAAACG TATGCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATATTGT GATATATATA T----GATAT ACGTACAAAT CTCTTGAGCA
TMma415       ---ACAAACG TATGCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATATTGT GATATATATA T----GATAT ACGTACAAAT CTCTTGAGCA
TMma600       ---ACAAACG TATGCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATATTGT GATATATATA T----GATAT ACGTACAAAT CTCTTGAGCA
TMma600       ---ACAAACG TATGCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATATTGT GATATATATA T----GATAT ACGTACAAAT CTCTTGAGCA
TLph002       ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATATTGT GATATATATA TAT--CATAT ACGTACAAAT CTCTTGAGCA
TLph628       ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATATTGT GATATATATA TAT--CATAT ACGTACAAAT CTCTTGAGCA
TLph629       ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATATTGT GATATATATA TAT--CATAT ACGTACAAAT CTCTTGAGCA
Tros422       ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATATTGT GATATATATA TAT--GATAT ACGTACAAAT CTCTTGAGCA
TAsp140       ---ACAAACG TATCCTAGCA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATATTGT GATATATATA TAT--GATAT ACGTACAAAT CTCTTGAGCA
TMsh325       ---ACAAGCG TATCCTAGTA GAATTTTGTT CTCT-TATCA CAAGTCTTGT GATATATTGT GATATATATA T----GATAT ACGTACAAAT CTCTTGAGCA


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                     210        220        230        240        250        260        270        280        290        300
TLpl285       AGGAATACCT ATTT------ -GAATGATTC ATAATCCATA TGATTACTCA TATGGAAATT TACAAAGTCT TCCTTTTGAA GATCAAAGAA ATTCCTGTTC
TLob144       AGGAATACCT ATTT------ -GAATGATTC ATAATCCATA TGATTACTCA TATGGAAATT TACAAAGTCT TCCTTTTGAA GATCAAAGAA ATTCCTGTTC
TLbr141       AGGAATACCT ATTT------ -GAATGATTC ATAATCCATA TGATTACTCA TATGGAAATT TACAAAGTCT TCCTTTTGAA GATCAAAGAA ATTCCTGTTC
TLol451       AGGAATACCT ATTT------ -GAATGATTC ATAATCCATA TGATTACTCA TATGGAAATT TACAAAGTCT TCCTTTTGAA GATCAAAGAA ATTCCTGTTC
TLol004       AGGAATACCT ATTT------ -GAATGATTC ATAATCCATA TGATTACTCA TATGGAAATT TACAAAGTCT TCCTTTTGAA GATCAAAGAA ATTCCTGTTC
TLfl414       AGGAATACCT ATTT------ -GAATGATTC ATAATCCATA TGATTACTCA TATGGAAATT TACAAAGTCT TCCTTTTGAA GATCAAAGAA ATTCCTGTTC
TLfl000       AGGAATACCT ATTT------ -GAATGATTC ATAATCCATA TGATTACTCA TATGGAAATT TACAAAGTCT TCCTTTTGAA GATCAAAGAA ATTCCTGTTC
TLag308       AGGAATACCT ATTT------ -GAATGATTC ATAATCCATA TGATTACTCA TATGGAAATT TACAAAGTCT TCCTTTTGAA GATCAAAGAA ATTCCTGTTC
TLtp564       AGGAATACCT ATTT------ -GAATGATTC ATAATCCATA TGATTACTCA TATGCAAATT TACAAAGTCT TCCTTTTGAA GATCAAAGAA ATTCCTGTTC
TLtp354       AGGAATGCCT ATTT------ -GAATGATTC ATAATCCATA TGATTACTCA TATGGAAATT TACAAAGTCT TCCTTTTGAA GATCAAAGAA ATTCCTGTTC
TLtr117       AGGAATACCT ATTT------ -GAATGATTC ATAATCCATA TGATTACTCA TATGGAAATT TACAAAGTCT TCCTTTTGAA GATCAAAGAA ATTCCTGTTC
TLtr357       AGGAATACCT ATTT------ -GAATGATTC ATAATCCATA TGATTACTCA TATGGAAATT TACAAAGTCT TCCTTTTGAA GATCAAAGAA ATTCCTGTTC
TLtr359       AGGAATACCT ATTT------ -GAATGATTC ATAATCCATA TGATTACTCA TATGGAAATT TACAAAGTCT TCCTTTTGAA GATCAAAGAA ATTCCTGTTC
TLtr169       AGGAATACCT ATTT------ -GAATGATTC ATAATCCATA TGATTACTCA TATGGAAATT TACAAAGTCT TCCTTTTGAA GATCAAAGAA ATTCCTGTTC
TLpu348       AGGAATACCT ATTT------ -GAATGATTC ATAATCCATA TGATTACTCA TATGCAAATT TACAAAGTCT TCCTTTTGAA GATCAAAGAA ATTCCTGTTC
TLpu450       AGGAATGCCT ATTT------ -GAATGATTC ATAATCCATA TGATTACTCA TATGGAAATT TACAAAGTCT TCCTTTTGAA GATCAAAGAA ATTCCTGTTC
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TLpu555     AGGAATACCT ATTT------ -GAATGATTC ATAATCCATA TGATTACTCA TATGCAAATT TACAAAGTCT TCCTTTTGAA GATCAAAGAA ATTCCTGTTC
TLth353     AGGAATACCT ATTT------ -GAATGATTC ATAATCCATA TGATTACTCA TATGGAAATT TACAAAGTCT TCCTTTTGAA GATCAAAGAA ATTCCTGTTC
TLmo346     AGGAATACCT ATTT------ -GAATGATTC ATAATCCATA TGATTACTCA TATGGAAATT TACAAAGTCT TCCTTTTGAA GATCAAAGAA ATTCCTGTTC
TLmo515     AGGAATACCT ATTT------ -GAATGATTC ATAATCCATA TGATTACTCA TATGGAAATT TACAAAGTCT TCCTTTTGAA GATCAAAGAA ATTCCTGTTC
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TAhi456      GAGACTTTAA A-------TT TAATA----- CGTTTTCGTT TTTTTTT--- -GTTTTCATT TTGAATTGAC ATAGACCCAA GTCGTCTAGT ATTATGATGA
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TAlu460      GAGACTTTAA A-------TT TAATA----- CGTTTTCGTT TTTTTTT--- -GTTTTCATT TTGAATTGAC ATAGACCCAA GTCGTCTAGT ATTATGATGA
TAlu616      GAGACTTTAA A-------TT TAATA----- CGTTTTCGTT TTTTTTT--- -GTTTTCATT TTGAATTGAC ATAGACCCAA GTCGTCTAGT ATTATGATGA
TMat628      GAGACTTTAA A-------TT TAATA----- CGTTTTCGTT TTTTTTT--- -GTTTTCATT TTGAATTGAC ATAGACCCAA GTCGTCTAGT ATTATGATGA
TAlo596      GAGACTTTAA A-------TT TAATACAATA CGTTTTCGTT TTTTTTT--- -GTTTTCATT TTGAATTGAC ATAGACCCAA GTCGTCTAGT ATTATGATGA
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TAlo461      GAGACTTTAA A-------TT TAATACAATA CGTTTTCGTT TTTTTTT--- -GTTTTCATT TTGAATTGAC ATAGACCCAA GTCGTCTAGT ATTATGATGA
TAlo462      GAGACTTTAA A-------TT TAATACAATA CGTTTTCGTT TTTTTTT--- -GTTTTCATT TTGAATTGAC ATAGACCCAA GTCGTCTAGT ATTATGATGA
TAof330      GAGACTTTAA A-------TT TAATA----- CTTTTTCATT TTTTTTTTT- -GTTTTCATT TTTAATTGAC ATAGACCCAA GTCGTCTAGT ATTATGATGA
TAof604      GAGACTTTAA A-------TT TAATA----- CTTTTTCATT TTTTTTTT-- -GTTTTCATT TTTAATTGAC ATAGACCCAA GTCGTCTAGT ATTATGATGA
TAof511      GAGACTTTAA A-------TT TAATA----- CTTTTTCATT TTTTTTTT-- -GTTTTCATT TTTAATTGAC ATAGACCCAA GTCGTCTAGT ATTATGATGA
TAof512      GAGACTTTAA A-------TT TAATA----- CTTTTTCATT TTTTTTTT-- -GTTTTCATT TTTAATTGAC ATAGACCCAA GTCGTCTAGT ATTATGATGA
TAof513      GAGACTTTAA A-------TT TAATA----- CTTTTTCATT TTTTTTTT-- -GTTTTCATT TTTAATTGAC ATAGACCCAA GTCGTCTAGT ATTATGATGA
TAca345      GAGACTTTAA A-------TT TAATA----- CTTTTTCATT TTTTTTTT-- -GTTTTCATT TTTAATTGAC ATAGACCCAA GTCGTCTAGT ATTATGATGA
TAca594      GAGACTTTAA A-------TT TAATA----- CTTTTTCATT TTTTTTTT-- -GTTTTCATT TTTAATTGAC ATAGACCCAA GTCGTCTAGT ATTATGATGA
TAca471      GAGACTTTAA A-------TT TAATA----- CTTTTTCATT TTTTTTTT-- -GTTTTCATT TTTAATTGAC ATAGACCCAA GTCGTCTAGT ATTATGATGA
TAar427      GAGACTTTAA A-------TT TAATA----- CTTTTTCATT TTTTTTTT-- -GTTTTCATT TTTAATTGAC ATAGACCCAA GTCGTCTAGT ATTATGATGA
TMtr452      GAGACTTTAA A-------TT TAATA----- CGTTTTCGTT TTTTTGTT-- -GTTTTCATT TTGAATTGAC ATAGACCCAA GTCGTCTAGT ATTATGATGA
TMtr453      GAGACTTTAA A-------TT TAATA----- CGTTTTCGTT TTTTTGTT-- -GTTTTCATT TTGAATTGAC ATAGACCCAA GTCGTCTAGT ATTATGATGA
TMtr352      GAGACTTTAA A-------TT TAATA----- CGTTTTCGTT TTTTTGTT-- -GTTTTCATT TTGAATTGAC ATAGACCCAA GTCGTCTAGT ATTATGATGA
TMtr254      GAGACTTTAA A-------TT TAATA----- CGTTTTCGTT TTTTTGTT-- -GTTTTCATT TTGAATTGAC ATAGACCCAA GTCGTCTAGT ATTATGATGA
TMae351      GAGACTTTAA A-------TT TAATA----- CGTTTTCGTT TTTTTGTT-- -GTTTTCATT TTGAATTGAC ATAGACCCAA GTCGTCTAGT ATTATGATGA
TMae465      GAGACTTTAA A-------TT TAATA----- CGTTTTCGTT TTTTTGTT-- -GTTTTCATT TTGAATTGAC ATAGACCCAA GTCGTCTAGT ATTATGATGA
TMae468      GAGACTTTAA A-------TT TAATA----- CGTTTTCGTT TTTTTGTT-- -GTTTTCATT TTGAATTGAC ATAGACCCAA GTCGTCTAGT ATTATGATGA
TMcc361      GAGACTTTAA A-------TT TAATA----- CGTTTTCGTT TTTTTTT--- -GTTTTCATT TTGAATTGAC ATAGACCCAA GTCGTCTAGT ATTATGATGA
TMca463      GAGACTTTAA A-------TT TAATA----- CGTTTTCGTT TTTTTTTT-- -GTTTTCATT TTGAATTGAC ATAGACCCAA GTCGTCTAGT ATTATGATGA
TMal440      GAGACTTTAA A-------TT TAATA----- CGTTTTCGTT TTTTTTT--- -GTTTTCATT TTGAATTGAC ATAGACCCAA GTCGTCTAGT ATTATGATGA
TMal539      GAGACTTGAA A-------TT TAATA----- CGTTTTCGTT TTTTTTT--- -GTTTTCATT TTGAATTGAC ATAGACCCAA GTCGTCTAGT ATTATGATGA
TMal338      GAGACTTGAA A-------TT TAATA----- CGTTTTCGTT TTTTTTTT-- -GTTTTCATT TTGAATTGAC ATAGACCCAA GTCGTCTAGT ATTATGATGA
TMmo493      GAGACTTGAA A-------TT TAATA----- CGTTTTCGTT TTTTTTT--- -GTTTTCATT TTGAATTGAC ATAGACCCAA GTCGTCTAGT ATTATGATGA
TMmo494      GAGACTTGAA A-------TT TAATA----- CGTTTTCGTT TTTTTTT--- -GTTTTCATT TTGAATTGAC ATAGACCCAA GTCGTCTAGT ATTATGATGA
TMmo332      GAGACTTGAA A-------TT TAATA----- CGTTTTCGTT TTTTTTT--- -GTTTTCATT TTGAATTGAC ATAGACCCAA GTCGTCTAGT ATTATGATGA
TMmo496      GAGACTTGAA A-------TT TAATA----- CGTTTTCGTT TTTTTTT--- -GTTTTCATT TTGAATTGAC ATAGACCCAA GTCGTCTAGT ATTATGATGA
TMmo499      GAGACTTGAA A-------TT TAATA----- CGTTTTCGTT TTTTTTT--- -GTTTTCATT TTGAATTGAC ATAGACCCAA GTCGTCTAGT ATTATGATGA
TMmo593      GAGACTTGAA A-------TT TAATA----- CGTTTTCGTT TTTTTTT--- -GTTTTCATT TTGAATTGAC ATAGACCCAA GTCGTCTAGT ATTATGATGA
TMto479      GAGACTTGAA A-------TT TAATA----- CGTTTTCGTT TTTTTTTT-- -GTTTTCATT TTGAATTGAC ATAGACCCAA GTCGTCTAGT ATTATGATGA
TMto189      GAGACTTGAA A-------TT TAATA----- CGTTTTCGTT TTTTTTTT-- -GTTTTCATT TTGAATTGAC ATAGACCCAA GTCGTCTAGT ATTATGATGA
TMto489      GAGACTTGAA A-------TT TAATA----- CGTTTTCGTT TTTTTTTT-- -GTTTTCATT TTGAATTGAC ATAGACCCAA GTCGTCTAGT ATTATGATGA
TMtf601      GAGACTTTAA ACTTTAAATT TAATA----- CTTTTTCGTT TTTTTTTTT- -GTTTTCATT TTGAATTGAC ATAGACCCAA GTCGTCTAGT ATTATGATGA
TMtf070      GAGACTTTAA ACTTTAAATT TAATA----- CTTTTTCGTT TTTTTTT--- -GTTTTCATT TTGAATTGAC ATAGACCCAA GTCGTCTAGT ATTATGATGA
TMtf499      GAGACTTTAA ACTTTAAATT TAATA----- CTTTTTCGTT TTTTTTT--- -GTTTTCATT TTGAATTGAC ATAGACCCAA GTCGTCTAGT ATTATGATGA
TMma415      GAGACTTTAA A-------TT TAATA----- CTTTTTCGTT TTTTTTTT-- -GTTTTCATT TTGAATTGAC ATAGACCCAA GTCGTCTAGT ATTATGATGA
TMma600      GAGACTTTAA A-------TT TAATA----- CTTTTTCGTT TTTTTTTTTT -GTTTTCATT TTGAATTGAC ATAGACCCAA GTCGTCTAGT ATTATGATGA
TMma600      GAGACTTTAA A-------TT TAATA----- CTTTTTCGTT TTTTTTTTTT -GTTTTCATT TTGAATTGAC ATAGACCCAA GTCGTCTAGT ATTATGATGA
TLph002      GAGACTTTAA A-------TT TAATA----- CGTTTTCGTT TTTTTTTT-- -GTTTTCATT TTGAATTGAC ATAGACCCAA GTCGTCTAGT ATTATGATGA
TLph628      GAGACTTTAA A-------TT TAATA----- CGTTTTCGTT TTTTTTTT-- -GTTTTCATT TTGAATTGAC ATAGACCCAA GTCGTCTAGT ATTATGATGA
TLph629      GAGACTTTAA A-------TT TAATA----- CGTTTTCGTT TTTTTTTT-- -GTTTTCATT TTGAATTGAC ATAGACCCAA GTCGTCTAGT ATTATGATGA
Tros422      GAGACTTTAA A-------TT TAATA----- CTTTTTCATT TTTTTTTTTT TGTTTTCATT TTTAATTGAC ATAGACCCAA GTCGTCTAGT ATTATGATGA
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TAsp140         GAGACTTTAA A-------TT TAATA----- CTTTTTCATT TTTTTTTTTT TGTTTTCATT TTTAATTGAC ATAGACCCAA GTCGTCTAGT ATTATGATGA
TMsh325         GAGACTTTTA A-------TT TAATA----- CTTTTTCGTT TTTTTTTT-- -GTTTTCATT TTTAATTGAC ATAGACCCAA GTCATCTAGT ATTATGATGA


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                       410        420        430        440        450        460        470        480        490        500
TLpl285         TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCAC---- ---------- ---------- ----------
TLob144         TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCAC---- ---------- ---------- ----------
TLbr141         TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCAC---- ---------- ---------- ----------
TLol451         TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCAC---- ---------- ---------- ----------
TLol004         TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCAC---- ---------- ---------- ----------
TLfl414         TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCAC---- ---------- ---------- ----------
TLfl000         TAATGCGCTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCACCAGG TTCAAATA-- ---------- ----------
TLag308         TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCAC---- ---------- ---------- ----------
TLtp564         TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCAC---- ---------- ---------- ----------
TLtp354         TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCAC---- ---------- ---------- ----------
TLtr117         TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCAC---- ---------- ---------- ----------
TLtr357         TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCAC---- ---------- ---------- ----------
TLtr359         TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCAC---- ---------- ---------- ----------
TLtr169         TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCAC---- ---------- ---------- ----------
TLpu348         TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCAC---- ---------- ---------- ----------
TLpu450         TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCAC---- ---------- ---------- ----------
TLpu555         TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCAC---- ---------- ---------- ----------
TLth353         TAATGCGTTG GTAATGGGCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCAC---- ---------- ---------- ----------
TLmo346         TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCACccAG TTCAAATATG GTTCCTGGC- ----------
TLmo515         TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCAC---- ---------- ---------- ----------
TLti595         TATCCCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCAC---- ---------- ---------- ----------
TLti181         TATCCCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCaC---- ---------- ---------- ----------
TLti233         TATCCCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGtCaC---- ---------- ---------- ----------
TLti308         TATCCCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCaC---- ---------- ---------- ----------
TLac134         TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCAC---- ---------- ---------- ----------
TLcr031         TAATGCGTTG GTAGTGGTCG GGATAGTTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCT TGTCACC-AG TTCAAARATG ---------A TAATGCGTTG
TLcr599         TAATGCGTTG GTAGTGGTCG GGATAGTTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCT TGTCACC-AG TTCAAAGATG ---------A TAATGCGTTG
TLcr235         TAATGCGTTG GTAGTGGTCG GGATAGTTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCT TGTCACC-AG TTCAAAKATG ---------A TAATGCGTTG
TLmu137         TAATGCGTTG GTAGTGGTCG GGATAGTTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCT TGTCACC-AG TTCAAARATG ---------A TAATGCGTTG
TLmu319         TAATGCGTTG GTAGTGGTCG GGATAGTTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCT TGTCACC-AG TTCAAAGATG ---------A TAATGCGTTG
TLmu630         TAATGCGTTG GTAGTGGTCG GGATAGTTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCACCAGG TTCAAATATG ---------A TAATGCGTTG
TMpa005         TAATGCGTTG GTAGTGGTCG GGATAGTTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCACC-AG TTCAAAKATG ---------A TAATGCGTTG
TMpa249         TAATGCGTTG GTAGTGGTCG GGATAGTTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCT TGTCACC-AG TTCAAAKATG ---------A TAATGCGTTG
TMpa059         TAATGCGTTG GTAGTGGTCG GGATAGTTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCT TGTCACC-AG TTCAAAKATG ---------A TAATGCGTTG
TMpa296         TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCaC---- ---------- ---------- ----------
TMsy001         -AATGCGTTG GTAGTGGTCG GGATAGTTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCACC-AG TTCAAARATG ---------A TAATGCGTTG
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TMsy635      -AATGCGTTG GTAGTGGTCG GGATAGTTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCT TGTCACC-AG TTCAAAKATG ---------A TAATGCGTTG
TMni032      -AATGCGTTG GTAGTGGTCG GGATAGTTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCACC-AG TTCAAAKATG ---------A TAATGCGTTG
TMni097      -AATGCGTTG GTAGTGGTCG GGATAGTTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCT TGTCACC-AG TTCAAAKATG ---------A TAATGCGTTG
TMni633      -AATGCGTTG GTAGTGGTCG GGATAGTTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCT TGTCACC-AG TTCAAATATG ---------A TAATGCGTTG
TMni228      -AATGCGTTG GTAGTGGTCG GGATAGTTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCT TGTCACC-AG TTCAAAKATG ---------A TAATGCGTTG
TMne349      TAATGCGTTG GTAGtGGTCG GGATAGTTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCACC-AG TTCAAATATG ---------A TAATGCGTTG
TMne632      TAATGCGTTG GTAGTGGTCG GGATAGTTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCt TGTCACC-AG TTCAAATATG ---------A TAATGCGTTG
TMve442      TAATGCGTTG GTAGTGGTCG GGATAGTTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCT TGTCACC-AG TTCAAAGATG ---------A TAATGCGTTG
TLar153      TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCAC---- ---------- ---------- ----------
TLar378      TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG tGTCaC---- ---------- ---------- ----------
TLar239      TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAgAGGACTG AAAATCCTCG TGTCaC---- ---------- ---------- ----------
TLar252      TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCAC---- ---------- ---------- ----------
TLas570      TAATGCGTTG GTAGTGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCAC---- ---------- ---------- ----------
TLab383      TAATGCGTTG GTAGTGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCaC---- ---------- ---------- ----------
TLpe634      TAATGCGTTG GTAGTGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCACCA-- ---------- ---------- ----------
TLma598      TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCAC---- ---------- ---------- ----------
TLma329      TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCAC---- ---------- ---------- ----------
TLma200      TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCAC---- ---------- ---------- ----------
TLma404      TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCAC---- ---------- ---------- ----------
TMhi602      TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCAC---- ---------- ---------- ----------
TMhi149      TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCAC---- ---------- ---------- ----------
TMhi631      TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCACCAGG TTCAAATAAA ---------- ----------
TAhi356      TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCAC---- ---------- ---------- ----------
TAhi270      TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCAC---- ---------- ---------- ----------
TAhi454      TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCaC---- ---------- ---------- ----------
TAhi455      TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGtCaC---- ---------- ---------- ----------
TAhi456      TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCAC---- ---------- ---------- ----------
TAhi458      TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGtCaC---- ---------- ---------- ----------
TAlu460      TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCAC---- ---------- ---------- ----------
TAlu616      TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCAC---- ---------- ---------- ----------
TMat628      TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCACCAGG TTCAAATA-- ---------- ----------
TAlo596      TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCAC---- ---------- ---------- ----------
TAlo461      TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCACC-AG TTCAAATATG GtTCCTGGC- ----------
TAlo462      TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCACC-AG TTCAAATATG GTTCCTGGC- ----------
TAof330      TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCAC---- ---------- ---------- ----------
TAof604      TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCAC---- ---------- ---------- ----------
TAof511      TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCAC---- ---------- ---------- ----------
TAof512      TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCAC---- ---------- ---------- ----------
TAof513      TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCAC---- ---------- ---------- ----------
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TAca594      TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCAC---- ---------- ---------- ----------
TAca471      TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCAC---- ---------- ---------- ----------
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TAar427     TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCAC---- ---------- ---------- ----------
TMtr452     TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCaC---- ---------- ---------- ----------
TMtr453     TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCaC---- ---------- ---------- ----------
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TMae468     TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCAC---- ---------- ---------- ----------
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TMal440     TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCAC---- ---------- ---------- ----------
TMal539     TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCAC---- ---------- ---------- ----------
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TMmo493     TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCAC---- ---------- ---------- ----------
TMmo494     TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCAC---- ---------- ---------- ----------
TMmo332     TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCAC---- ---------- ---------- ----------
TMmo496     TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCAC---- ---------- ---------- ----------
TMmo499     TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCAC---- ---------- ---------- ----------
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TMto479     TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCAC---- ---------- ---------- ----------
TMto189     TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCAC---- ---------- ---------- ----------
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TMtf601     TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCAC---- ---------- ---------- ----------
TMtf070     TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCAC---- ---------- ---------- ----------
TMtf499     TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCAC---- ---------- ---------- ----------
TMma415     TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCAC---- ---------- ---------- ----------
TMma600     TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCAC---- ---------- ---------- ----------
TMma600     TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCAC---- ---------- ---------- ----------
TLph002     TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCAC---- ---------- ---------- ----------
TLph628     TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCAC---- ---------- ---------- ----------
TLph629     TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCAC---- ---------- ---------- ----------
Tros422     TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCAC---- ---------- ---------- ----------
TAsp140     TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCAC---- ---------- ---------- ----------
TMsh325     TAATGCGTTG GTAATGGTCG GGATAGCTCA GTTGGTAGAG CAGAGGACTG AAAATCCTCG TGTCAC---- ---------- ---------- ----------
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ITS *Alcea*

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           10         20         30         40         50         60         70         80         90        100
Iros422      gtCGTAACAA GGTTTCCGTA GGTGAaCCTG CGGAAGGATC ATTGTCGAAA CCTGCCTAGC AGAATGACCC GTGAATGTGA TATCAAACAA TCGAATGAGG
Ipal140      GTCGTAACAA GGTTTCCGTA GGTGAaCCTG CGGAAGGATC ATTGTCGAAA CCTGCCTAGC AGAATGACCC GTGAATGTGA TATCAAACAA TTGAATGAGG
Iarb624      GTCGTAACAA GGTTTCCGTA GGTGAACCTG CGGAAGGATC ATTGTCGAAA CCTGCCTAGC AGAATGACCC GTGAATGTGA TATCAAACAA TTGAATGAGG
Iauc617      GTCGTAACAA GGTTTCCGTA GGTGAACCTG CGGAAGGATC ATTGTCGAAA CCTGCCTAGC AGAATGACCC GTGAATGTGA TATCAAACAA TT--ATGAGG
Iexc417      GTCGTAACAA GGTTTCCGTA GATGAACCTG CgGAAGGATC ATTGTCGAAA CCTGCCTAGC AGAATGACCC GTGAATGTGA TATCAAACAA TCGAATGAGG
Ifla625      GTCGTAACAA GGTTTCCGTA GGTGAACCTG CGGAAGGATC ATTGTCGAAA CCTGCCTAGC AGAATGACCC GTGAATGTGA TATCAAACAA TCGAATGAGG
Igar611      GTCGTAACAA GGTTTCCGTA GGTGAACCTG CGGAAGGATC ATTGTCGAAA CCTGCCTAGC AGAATGACCC GTGAATGTGA TATCAAACAA TCGAATGAGG
Igla607      GTCGTAACAA GATTTCCGTA GGTGAACCTG CGGAAGGATC ATTGTCGAAA CCTGCCTAGC AGAATGACCC GTGAATGTGA TATCAAACAA TCGAATGAGG
Ikoe609      GTCGTAACAA GGTTTCCGTA GGTGAACCTG CgGAAGGATC ATTGTCGAAA CCTGCCTAGC AGAATGACCC GTGAATGTGA TATCAAACAA TTGAATGAGG
Ikur619      GTCGTAACAA GGTTTCCGTA GGTGAACCTG CGGAAGGATC ATTGTCGAAA CCTGCCTAGC AGAATGACCC GTGAATGTGA TATCAAACAA TTGAATGAGG
Ilon612      GTCGTAACAA GGTTTCCGTA GGTGAACCTG CGGAAGGATC ATTGTCGAAA CCTGCCTAGC AGAATGACCC GTGAATGTGA TATCAAACAA TCGAATGAGG
Irec621      GTCGTAACAA GGTTTCCGTA GGTGAACCTG CGGAAGGATC ATTGTCGAAA CCTGCCTAGC AGAATGACCC GTGAATGTGA TATCAAACAA TTGAATGAGG
Isac620      GTCGTAACAA GGTTTCCGTA GGTGAACCTG CGGAAGGATC ATTGTCGAAA CCTGCCTAGC AGAATGACCC GTGAATGTGA TATCAAACAA TCGAATGAGG
Iset424      GTCGTAACAA GGTTTCCGTA GGTGAACCTG CGGAAGGATC ATTGTCGAAA CCTGCCTAGC AGAATGACCC GTGAATGTGA TATCAAACAA TCGAATGAGG
Ishi618      GTAGTAACAA GGTTTCCGTA GGTGAACCTG CGGAAGGATC ATTGTCGAAA CCTGCCTAGC AGAATGACCC GTGAATGTGA TATCAAACAA TTGAATGAGG
Isul610      GTCGTAACAA GGTTTCCGTA GGTGAACCTG CGGAAGGATC ATTGTCGAAA CCTGCCTAGC AGAATGACCC GTGAATGTGA TATCAAACAA TTGAATGAGG
Itab613      GTCGTAACAA GGTTTCCGTA GGTGAACCTG CGGAAGGATC ATTGTCGAAA CCTGCCTAGC AGAATGACCC GTGAATGTGA TATCAAACAA TTGAATGAGG
Iwil627      GTCGTAACAA GATTTCCGTA GGTGAACCTG CGGAAGGATC ATTGTCGAAA CCTGCCTAGC AGAATGACCC GTGAATGTGA TATCAAACAA TCGAATGAGG
IMtf601      GTCGTAACAA GGTTTCCGTA GGTGA-CCTG CGGAAGGATC ATTGTCGAAA CCTGCCTAGC AGAATGACCC GTGAACGTGA TATCAAA--- CTAAACGAGG
IAof512      GTCGTAACAA GGTTTCCGTA GGTGA-CCTG CGGAAGGATC ATTGTCGAAA CCTGCCTAGC AGAATGACCT GTGAACGTGA TATCAAACAA TTGAACGAGG
IAar427      GTCGTAACAA GGTTTCCGTA GGTGA-CCTG CGGAAGGATC ATTGTCGAA- CCTGCCTAGC AGAATGACCT GTGAACGTGA TATCAAACAA TTGAACGAGG


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                    110        120        130        140        150        160        170        180        190        200
Iros422      GGGTGAGGAT GCATCTTTGC CCCAAACCCC CTCGTTGCCT AGGTGTGCTT GGCCTTTCCC CATTCGTTCT TGGGCGGGTG AGATTACAGG TCTTGTTGCA
Ipal140      GGGTGAGGAT GCATCTTTGC CCCAAACCCC CTCGTTGCCT AGGTGTGCTT GGCCTTTCCT CATTCGTTCT TGGGCGGGTG AGATTATAGG TCTTGTTGCA
Iarb624      GGGTGAGGAT GCATCTTTGC CCCAAACCCC CTCGTTGCCT AGGTGTGCTT GGCCTTTCCC CATTCGTTCT TGGGCGGGTG AGATTACAGG TCTTGTTGCA
Iauc617      GGGTGAGGAT GCATCTTTGC CCCAAACCCC CTCGTTGCCT AGGTGTGCTT GGCCTTTCCC CATTCGTTCT TGGGCGGGTG AGATTACAGG TCTTGTTGCA
Iexc417      GGGTGAGGAT GCATCTTTGC CCCAAACCCC CTCGTTGCCT AGGTGTGCTT GGCCTTTCCC CATTCGTTCT TGGGCGGGTG AGATTACAGG TCTTGTTGCA
Ifla625      GGGTGAGGAT GCATCTTTGC CCCAAACCCC CTCGTTGCCT AGGTGTGCTT GGCCTTTCCC CATTCGTTCT TGGGCGGGTG AGATTACAGG TCTTGTTGCA
Igar611      GGGTGAGGAT GCATCTTTGC CCCAAACCCC CTCGTTGCCT AGGTGTGCTT GGCCTTTCCC CATTCGTTCT TGGGCGGGTG AGATTACAGA TCTTGTTGCA
Igla607      GGGTGAGGAT GCATCTTTGC CCCAAACCCC CTCGTTGCCT AGGTGTGCTT GGCCTTTACC CATTCGTTCT TGGGCGGGTG AGATTACAGG TCTTGTTGCA
Ikoe609      GGGTGAGGAT GCATCTTTGC CCCAAACCCC CTCGTTGCCT AGGTGTGCTT GGCCTTTCCC CATTCGTTCT TGGGCGGGTG AGATTACAGG TCTTGTTGCA
Ikur619      GGGTGAGGAT GCATCTTTGC CCCAAACCCC CTCGTTGCCT AGGTGTGCTT GGCCTTTCCC CATTCGTTCT TGGGCGGGTG AGATTACAGG TCTTGTTGCA
Ilon612      GGGTGAGGAT GCATCTTTGC CCCAAACCCC CTCGTTGCCT AGGTGTGCTT GGCCTTTCCC CATTCGTTCT TGGGCGGGTG AGATTACAGG TCTTGTTGCA
Irec621      GGGTGAGGAT GCATCTTTGC CCCAAACCCC CTCGTTGCCT AGGTGTGCTT GGCCTTTCCC CATTCGTTCT TGGGCGGGTG AGATTACAGG TCTTGTTGCA
Isac620      GGGTGAGGAT GCATCTTTGC CCCAAACCCC CTCGTTGCCT AGGTGTGCTT GGCCTTTCCC CATTCGTTCT TGGGCGGGTG AGATTACAGG TCTTGTTGCA
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Iset424         GGGTGAGGAT GCATCTTTGC CCCAAACCCC CTCGTTGCCT AGGTGTGCTT GGCCTTTCCC CATTCGTTCT TGGGCGGGTG AGATTACAGG TCTTGTTGCA
Ishi618         GGGTGAGGAT GCATCTTTGC CCCAAACCCC CTCGTTGCCT AGGTGTGCTT GGCCTTTCCC CATTCGTTCT TGGGCGGGTG AGATTACAGG TCTTGTTGCA
Isul610         GGGTGAGGAT GCATCTTTGC CCCAAACCCC CTCGTTGCCT AGGTGTGCTT GGCCTTTCCC CATTCGTTCT TGGGCGGGTG AGATTACAGG TCTTGT-GCA
Itab613         GGGTGAGGAT GCATCTTTGC CCCAAACCCC CTCGTTGCCT AGGTGTGCTT GGCCTTTCCC CATTCGTTCT TGGGCGGGTG AGATTACAGG TCTTGTTGCA
Iwil627         GGGTGAGGAT GCATCTTTGC CCCAAACCCC CTCGTTGCCT AGGTGTGCTT GGCCTTTACC CATTCGTTCT TGGGCGGGTG AGATTACAGG TCTTGTTGCA
IMtf601         GGGCGCGGAT GCATCCATGC CCCAAACTCC CTCGATGCCT TGGTGCGCAG AGCCCGGCCG CATCCGCCCT CGGGCGGGTG AG-TT--GGG TTTTGTCACA
IAof512         GGGTGAGGAT GCATCCTTGC CCCAAACCCC CTCGCTGCCT TGGTGTGATT GGATTCTCCC CACTCGCTCT TGGGCGGGTG AGATGTCAGG TCTTGTCGCA
IAar427         GGGTGAGGAT GCATCCTTGC CCCAAACCCC CTCGCTGCCT TGGTGTGATT GGATTCTCCC CACTCGCTCT TGGGCGGGTG AGATGTCAGG TCTTGTCGCA


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                       210        220        230        240        250        260        270        280        290        300
Iros422         CTCA-GGTAA AA-TGAACAA CCCCCGGCGC GAATTGCGTC AAGGAATTAA AAATGAAAAG AGTGCACGTC TACTGTCATC GTCCCGTATG CGGTGTTTGT
Ipal140         CTCA-GGTAA AA-TGAACAA CCCCCGGCGC GAATTGCGTC AAGGAATTAA AAATGAAAAG AGTGCACG-C TACTGTCATC GTCCCGTATG CGGTGTTTGT
Iarb624         CTCA-GGTAA AA-TGAACAA CCCCCGGCGC GAATTGCGTC AAGGAATTAA AAATGAAAAG AGTGCACGTC TACTGTCATC GTCCCGTATG CGGTGTTTGT
Iauc617         CTCA-GGTAA AA-TGAACAA CCCCCGGCGC GAATTGCGTC AAGGAATTAA AAATGAAAAG AGTTCACGTC TACTGTCATC GTCCCGTATG CGGTGTTTGT
Iexc417         CTCA-GGTAA AA-TGAACAA CCCCCGGCGC GAATTGCGTC AAGGAATTAA AAATGAAAAG AGTGCACGTC TACTGTCATC GTCCCGTATG CGGTGTTTGT
Ifla625         CTCA-GGTAA AA-TGAACAA CCCCCGGCGC GAATTGCGTC AAGGAATTAA AAATGAAAAG AGTGCACGTC TACTGTCATC GTCCCGTATG CGGTGTTTGT
Igar611         CTCA-GGTAA AA-TGAACAA CCCCCGGCGC GAATTGCGTC AAGGAATTAA AAATGAAAAG AGTGCACGTC TACTGTCATC GTCCCGTATG CGGTGTTTGT
Igla607         CTCA-GGTAA AA-TGAACAA CCCCCGGCGC GAATTGCGTC AAGGAATTAA AAATGAAAAG AGTGCACGTC TACTGTCATC GTCCCGTATG CGGTGTTTGT
Ikoe609         CTCA-GGTAA AA-TTAACAA CCCCCGGCGC GAATTGCGTC AAGGAATTAA AAATGAAAAG AGTGCACGTC TACTGTCATC GTCCCGTATG CGGTGTTTGT
Ikur619         CTCA-GGTAA AA-TGAACAA CCCCCGGCGC GAATTGCGTC AAGGAATTAA AAATGAAAAG AGTGCACGTC TACTGTCATC GTCCCGTATG CGGTGTTTGT
Ilon612         CTCA-GGTAA AA-TGAACAA CCCCCGGCGC GAATTGCGTC AAGGAATTAA AAATGAAAAG AGTGCACGTC TACTGTCATC GTCCCGTATG CGGTGTTTGT
Irec621         CTCA-GGTAA AA-TKAACAA CCCCCGGCGC GAATTGCGTC AAGGAATTAA AAATGAAAAG AGTGCACGTC TACTGTCATC GTCCCGTATG CGGTGTTTGT
Isac620         CTCA-GGTAA AA-TGAACAA CCCCCGGCGC GAATTGCGTC AAGGAATTAA AAATGAAAAG AGTGCACGTC TACTGTCATC GTCCCGTATG CGGTGTTTGT
Iset424         CTCA-GGTAA AA-TGAACAA CCCCCGGCGC GAATTGCGTC AAGGAATTAA AAATGAAAAG AGTGCACGTC TACTGTCATC GTCCCGTATG CGGTGTTTGT
Ishi618         CTCA-GGTAA AA-TKAACAA CCCCCGGCGC GAATTGCGTC AAGGAATTAA AAATGAAAAG AGTGCACGTC TACTGTCATC GTCCCGTATG CGGTGTTTGT
Isul610         CTCA-GATAA AA-TGAACAA CCCCCGGCGC GAATTGCGTC AAGGAATTAA AAATGAAAAG AGTGCACGTC TACTGTCATC GTCCCGTATG CGGTGTTTGT
Itab613         CTCA-GGTAA AA-TGAACAA CCCCCGGCGC GAATTGCGTC AAGGAATTAA AAATGAAAAG AGTGCACGTC TACTGTCATC GTCCCGTATG CGGTGTTTGT
Iwil627         CTCA-GGTAA AA-TGAACAA CCCCCGGCGC GAATTGCGTC AAGGAATTAA AAATGAAAAG AGTGCACGTC TACTGTCATC GTCCCGTATG CGGTGTTTGT
IMtf601         CTAAAGGTCA AAACGAACAA CCCCCGGCGC GAATTGCGTC AAGGAAT-AA AAATGAAA-G AGTGCACGTT TGCTGTCCAC GTCCCGTGCG CGGTGTCTGT
IAof512         CTCG-GGCAA AA-TGAACAA CCCCCGGCGC GAATCGCGTC AAGGAATTAA AAATGAAAAG GGTGCGCGTC TACTGTCGTC GTCCCGTACG CGGTGTTTGT
IAar427         CTCG-GGCAA AA-TGAACAA CCCCCGGCGC GAATTGCGTC AAGGAATTAA AAATGAAAAG GGTGCACGTC TACTGTCGTC GTCCCGTACG CGGTGTTTGT


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                       310        320        330        340        350        360        370        380        390        400
Iros422         GTGGCAGTGA CGCTGTTACT TTTGTCGTGA AA--TACAAA A-CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA GCGAAATGCG
Ipal140         GTGGCAGTGA CGCTGTTACT TTTGTCGTGA AA--TACAAA A-CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA GCGAAATGCG
Iarb624         GTGGCAGTGA CGCTGTTACT TTTGTCGTGA AA--TACAAA A-CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA GCGAAATGCG
Iauc617         GTGGCAGTGA CGCTGTTACT TTTGTCGTGA AA--TACAAA A-CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA GCGAAATGCG
Iexc417         GTGGCAGTGA CGCTGTTACT TTTGTCGTGA AA--TACAAA A-CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA GCGAAATGCG
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Ifla625        GTGGCAGTGA CGCTGTTACT TTTGTCGTGA AA--TACAAA A-CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA GCGAAATGCG
Igar611        GTGGCAGTGA CGCTGTTACT TTTGTCGTGA AA--TACAAA A-CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA GCGAAATGCG
Igla607        GTGGCAGTGA CGCTGTTACT TTTGTCGTGA AA--TACAAA A-CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA GCGAAATGCG
Ikoe609        GTGGCAGTGA CGCTGTTACT TTTGTCGTGA AA--TACAAA A-CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA GCGAAATGCG
Ikur619        GTGGCAGTGA CGCTGTTACT TTTGTCGTGA AA--TACAAA A-CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA GCGAAATGCG
Ilon612        GTGGCAGTGA CGCTGTTACT TTTGTCGTGA AA--TACAAA A-CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA GCGAAATGCG
Irec621        GTGGCAGTGA CGCTGTTACT TTTGTCGTGA AA--TACAAA A-CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA GCGAAATGCG
Isac620        GTGGCAGTGA CGCTGTTACT TTTGTCGTGA AA--TACAAA A-CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA GCGAAATGCG
Iset424        GTGGCAGTGA CGCTGTTACT TTTGTCGTGA AA--TACAAA A-CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA GCGAAATGCG
Ishi618        GTGGCAGTGA CGCTGTTACT TTTGTCGTGA AA--TACAAA A-CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA GCGAAATGCG
Isul610        GTGGCAGTGA CGCTGTTACT TTTGTCGTGA AA--TACAAA A-CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA GCGAAATGCG
Itab613        GTGGCAGTGA CGCTGTTACT TTTGTCGTGA AA--TACAAA A-CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA GCGAAATGCG
Iwil627        GTGGCAGTGA CGCTGTTACT TTTGTCGTGA AA--TACAAA A-CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA GCGAAATGCG
IMtf601        GTGGCGGCGA CGGTGTTACT TCTGTCGTGA AAAATAAAAA AACGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA GCGAAATGCG
IAof512        GCGGCAGTGA CGCTGTTACT CTAGTCGTGA AAA-TACAAA A-CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA GCGAAATGCG
IAar427        GCGGCAGTGA CGCTGTTACT CTAGTCGTGA AAA-TACAAA A-CGACTCTC GGCAACGGAT ATCTCGGCTC TCGCATCGAT GAAGAACGTA GCGAAATGCG


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                      410        420        430        440        450        460        470        480        490        500
Iros422        ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCATT AGGCCGAGGG CACGTCTGCC TGGGTGTCAC
Ipal140        ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCATT AGGCCGAGGG CACGTCTGCC TGGGTGTCAC
Iarb624        ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCATT AGGCCGAGGG CACGTCTGCC TGGGTGTCAC
Iauc617        ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCATT AGGCCGAGGG CACGTCTGCC TGGGTGTCAC
Iexc417        ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCATT AGGCCGAGGG CACGTCTGCC TGGGTGTCAC
Ifla625        ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCATT AGGCCGAGGG CACGTCTGCC TGGGTGTCAC
Igar611        ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCATT AGGCCGAGGG CACGTCTGCC TGGGTGTCAC
Igla607        ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCATT AGGCCGAGGG CACGTCTGCC TGGGTGTCAC
Ikoe609        ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCATT AGGCCGAGGG CACGTCTGCC TGGGTGTCAC
Ikur619        ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCATT AGGCCGAGGG CACGTCTGCC TGGGTGTCAC
Ilon612        ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCATT AGGCCGAGGG CACGTCTGCC TGGGTGTCAC
Irec621        ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCATT AGGCCGAGGG CACGTCTGCC TGGGTGTCAC
Isac620        ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCATT AGGCCGAGGG CACGTCTGCC TGGGTGTCAC
Iset424        ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCATT AGGCCGAGGG CACGTCTGCC TGGGTGTCAC
Ishi618        ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCATT AGGCCGAGGG CACGTCTGCC TGGGTGTCAC
Isul610        ATACTTGGTG TGAATTGCAg AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCATT AGGCCGAGGG CACGTCTGCC TGGGTGTCAC
Itab613        ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCATT AGGCCGAGGG CACGTCTGCC TGGGTGTCAC
Iwil627        ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCATT AGGCCGAGGG CACGTCTGCC TGGGTGTCAC
IMtf601        ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CCAAGCCATT AGGCCGAGGG CACGTCTGCC TGGGTGTCAC
IAof512        ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CGAAGCCATT AGGCCGAGGG CACGTCTGCC TGGGTGTCAC
IAar427        ATACTTGGTG TGAATTGCAG AATCCCGTGA ACCATCGAGT CTTTGAACGC AAGTTGCGCC CGAAGCCATT AGGCCGAGGG CACGTCTGCC TGGGTGTCAC
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                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                       510        520        530        540        550        560        570        580        590        600
Iros422         GCATCGTCGC CCCAATCAAA CCCTAAGCCA TCGCGCTACG GTTGCATTGT GGGCGGAAAT TGGCCTCCCG TGTGCTCACC GCTCATGGTT GGCCTAAAAT
Ipal140         GCATCGTCGC CCCAATCAAA CCCTAAGCCA TCGCGCTACG GTTGGAATGT GGGCGGAAAT TGGCCTCCCG TGTGCTCACC GCTCATGGTT GGCCTAAAAT
Iarb624         GCATCGTCGC CCCAATCAAA CCCTAAGCCA TCGCGCTACG GTTGCATTGT GGGCGGAAAT TGGCCTCCCG TGTGCTCACC GCTCATGGTT GGCCTAAAAT
Iauc617         GCATCGTCGC CCCAATCAAA CCCTAAGCCA TCGCGCTACG GTTGCAATGT GGGCGGAAAT TGGCCTCCCG TGTGCTCACC GCTCATGGTT GGCCTAAAAT
Iexc417         GCATCGTCGC CCCAATCAAA CCCTAAGCCA TCGCGCTACG GTTGCATTGT GGGCGGAAAT TGGCCTCCCG TGTGCTCACC GCTCATGGTT GGCCTAAAAT
Ifla625         GCATCGTCGC CCCAATCAAA CCCTAAGCCA TCGCGCTACG GTTGCATTGT GGGCGGAAAT TGGCCTCCCG TGTGCTCACC GCTCATGGTT GGCCTAAAAT
Igar611         GCATCGTCGC CCCAATCAAA CCCTAAGCCA TCGCGCTACG GTTGTATTGT GGGCGGAAAT TGGCCTCCCG TGTGCTCACC GCTCATGGTT GGCCTAAAAT
Igla607         GCATCGTCGC CCCAATCAAA CCCTAAGCCA TCGCGCTACG GTTGCATTGT GGGCGGAAAT TGGCCTCCCG TGTGCTCACC GCTCATGGTT GGCCTAAAAT
Ikoe609         GCATCGTCGC CCCAATCAAA CCCTAAGCCA TCGCGCTACG GTTGCATTGT GGGCGGAAAT TGGCCTCCCG TGTGCTCACC GCTCATGGTT GGCCTAAAAT
Ikur619         GCATCGTCGC CCCAATCAAA CCCTAAGCCA TCGCGCTACG GTTGCATTGT GGGCGGAAAT TGGCCTCCCG TGTGCTCACC GCTCATGGTT GGCCTAAAAT
Ilon612         GCATCGTCGC CCCAATCAAA CCCTAAGCCA TCGCGCTACG GTTGCATTGT GGGCGGAAAT TGGCCTCCCG TGTGCTCACC GCTCATGGTT GGCCTAAAAT
Irec621         GCATCGTCGC CCCAATCAAA CCCTAAGCCA TCGCGCTACG GTTGCATTGT GGGCGGAAAT TGGCCTCCCG TGTGCTCACC GCTCATGGTT GGCCTAAAAT
Isac620         GCATCGTCGC CCCAATCAAA CCCTAAGCCA TCGCGCTACG GTTGCATTGT GGGCGGAAAT TGGCCTCCCG TGTGCTCACC GCTCATGGTT GGCCTAAAAT
Iset424         GCATCGTCGC CCCAATCAAA CCSTAAGCCA TCGCGCTACG GTTGCATTGT GGGCGGAAAT TGGCCTCCCG TGTGCTCACC GCTCATGGTT GGCCTAAAAT
Ishi618         GCATCGTCGC CCCAATCAAA CCCTAAGCCA TCGCGCTACG GTTGCATTGT GGGCGGAAAT TGGCCTCTCG TGTGCTCACC GCTCATGGTT GGCCTAAAAT
Isul610         GCATCGTCGC CCCAATCAAA CCCTAAGCCA TCGAGCTACG GTTGCAtTGT GGGCGGAAAT TGGCCTCCCG TGTGCTCACC GCTCATGGTT GGCCTAAAAT
Itab613         GCATCGTCGC CCCAATCAAA CCCTAAGCCA TCGCGCTACG GTTGCATTGT GGGCGGAAAT TGGCCTCCCG TGTGCTCACC GCTCATGGTT GGCCTAAAAT
Iwil627         GCATCGTCGC CCCAATCAAA CCCTAAGCCA TCGCGCTACG GTTGCATTGT GGGCGGAAAT TGGCCTCCCG TGTGCTCACC GCTCATGGTT GGCCTAAAAT
IMtf601         GCATCGTTGC CCCCACCAAA CCATAACCCA TCGGGCCTTG GTTGAAGTGT GGGCGGAAAT TGGCCTCCCG TGCGCTCACC GCTCGCGGTT GGCCTAAATC
IAof512         GCATCGTCGC CCCCATCAAA CCCTAAGCCG TCGGGCTGCG GTTGCAATGT GGGCGGAAAT TGGCCTCCCG TGTGCTCACC GCTCGTGGTT GGCCTAAAAT
IAar427         GCATCGTCGC CCCCATCAAA CCCTAAGCCG TCGGGCTGCG GTTGCAATGT GGGCGGAAAT TGGCCTCCCG TGTGCTCACC GCTCGTGGTT GGCCTAAAAT


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                       610        620        630        640        650        660        670        680        690        700
Iros422         TTGGTCCTCG GCGATGAATT GCCGC-GACA ATCGGTGGGA ATGCTTAATA AGCTGCCTCG TTAGTTATCG TGTGTGCTCG TTGATTTGGA CCCTTTTGAC
Ipal140         TTGGTCCTCG GCGATGAATT GCCGC-GACA ATCGGTGGGA ATGCTTAATA AGCTGCCTCG TTAGTTATCG TGTGTGCTCG TTGATTAGGA CCCTTTTGAC
Iarb624         TTGGTCCTCG GCGATGAATT GCCGC-GACA ATCGGTGGGA ATGCTTAATA AGCTGCCTCG TTAGTTATCG TGTGTGCTCG TTGATTTGGA CCCTTTTGAC
Iauc617         TTGGTCCTCG GCGATGAATT GCCGC-GACA ATCGGTGGGA ATGCTTAATA AGCTGCCTCG TTAGTTATCG TGTGTGCTCG TTGATTTGGA CCCTTTTGAC
Iexc417         TTGGTCCTCG GCGATGAATT GCCGC-GACA ATCGGTGGGA ATGCTTAATA AGCTGCCTCG TTAGTTATCG TGTGTGCTCG TTGATTTGGA CCCTTTTGAC
Ifla625         TTGGTCCTCG GCGATGAATT GCCGC-GACA ATCGGTGGGA ATGCTTAATA AGCTGCCTCG TTAGTTATCG TGTGTGCTCG TTGATTTGGA CCCTTTTGAC
Igar611         TTGGTCCTCG GCGATGAATT GCCGC-GACA ATCGGTGGGA ATGCTTAATA AGCTGCCTCG TTAGTTATCG TGTGTGCTCG TTGATTTGGA CCCTTTTGAC
Igla607         TTGGTCCTCG GCGATGAATT GCCGC-GACA ATCGGTGGGA ATGCTTAATA AGCTGCCTCG TTAGTTATCG TGTGTGCTCG TTGATTTGGA CCCTTTTGAC
Ikoe609         TTGGTCCTCG GCGATGAATT GCCGC-GACA ATCGGTGGGA ATGCTTAATA AGCTGCCTCG TTAGTTATCG TGTGTgCTCG TTGATTTGgA CCCTTTTGAC
Ikur619         TTGGTCCTCG GCGATGAATT GCCGC-GACA ATCGGTGGGA ATGCTTAATA AGCTGCCTCG TTAGTTATCG TGTGTGCTCG TTGATTTGGA CCCTTTTGAC
Ilon612         TTGGTCCTCG GCGATGAATT GCCGC-GACA ATCGGTGGGA ATGCTTAATA AGCTGCCTCG TTAGTTATCG TGTGTGCTCG TTGATTTGGA CCCTTTTGAC
Irec621         TTGGTCCTCG GCGATGAATT GCCGC-GACA ATCGGTGGGA ATGCTTAATA AGCTGCCTCG TTAGTTATCG TGTGTGCTCG TTGATTTGGA CCCTTTTGAC
Isac620         TTGGTCCTCG GCGATGAATT GCCGC-GACA ATCGGTGGGA ATGCTTAATA AGCTGCCTCG TTAGTTATCG TGTGTGCTCG TTGATTTGGA CCCTTTTGAC
Iset424         TTGGTCCTCG GCGATGAATT GCCGC-GACA ATCGGTGGGA ATGCTTAATA AGCTGCCTCG TTAGTTATCG TGTGTGCTCG TTGATTTGGA CCCTTTTGAC
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Ishi618     TTGGTCCTCG GCGATGAATT GCCGC-GACA ATCGGTGGGA ATGCTTAATA AGCTGCCTCG TTAGTTATCG TGTGTGCTCG TTGATTTGGA CCCTTTTGAC
Isul610     TTGGTCCTCG GCGATGAATT GCCGC-GACA ATCGGTGGGA ATGCTTAATA AGCTGCCTCG TTAGTTATCG TGTGTGCTCG TTGATTTGGA CCCTTTTGAC
Itab613     TTGGTCCTCG GCGATGAATT GCCGC-GACA ATCGGTGGGA ATGCTTAATA AGCTGCCTCG TTAGTTATCG TGTGTGCTCG TTGATTTGGA CCCTTTTGAC
Iwil627     TTGGTCCTCG GCGATGAATT GCCGC-GACA ATCGGTGGGA ATGCTTAATA AGCTGCCTCG TTAGTTATCG TGTGTGCTCG TTGATTTGGA CCCTTTTGAC
IMtf601     TGAGTCCTCG GCGATGAAGC GCCGC-GACA ATCGGTGGGA ATGCTCTT-- AGCTGCCTCG TTCGGAGTCG CGTGTGCTCG TTGATTGGGA CCCTTCTGAC
IAof512     TCAGTCCTCG GCGATGAATT GCCTGCGACA ATCGGTGGGA ATGCTTT--G AGCTGCCTCG TTAGTTGTCG TGTGTGCTCG TTGATTAGGA CCCTTTTGAC
IAar427     TCAGTCCTCG GCGATGAATT GCCGC-GACA ATCGGTGGGA ATGCTTT--G AGCTGCCTCG TTAGTTGTCG TGTGTGCTCG TTGATTAGGA CCCTTTTGAC
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            ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   710        720        730        740        750        760
Iros422     CCTTTT-GGC ATCACTATGT CGATGCTCGC ATCGGGACCC CAGGTCAGGC GGGATTACCC
Ipal140     CCTTTT-GGC ATCACTATGT CGATGCTCGC ATCGGGACCC CAGGTCAGGC GGGATTACCC
Iarb624     CCTTTT-GGC ATCACTATGT CGATGCTCGC ATCGGGACCC CAGGTCAGGC GGGATTACCC
Iauc617     CCTTTT-GGC ATCACTATGT CGATGCTCGC ATCGGGACCC CAGGTCAGGC GGGATTACCC
Iexc417     CCTTTT-GGC ATCACTATGT CGATGCTCGC ATCGGGACCC CAGGTCAGGC GGGATTACCC
Ifla625     CCTTTT-GGC ATCACTATGT CGATGCTCGC ATCGGGACCC CAGGTCAGGC GGGATTACCC
Igar611     CCTTTT-GGC ATCACTATGT CGATGCTCGC ATCGGGACCC CAGGTCAGGC GGGATTACCC
Igla607     CCTTTT-GGC ATCACTATGT CGATGCTCGC ATCGGGACCC CAGGTCAGGC GGGATTACCC
Ikoe609     CCTTTT-GGC ATCACTATGT CGATGCTCGC ATCGGGACCC CAGGTCAGGC GGGATTACCC
Ikur619     CCTTTT-GGC ATCACTATGT CGATGCTCGC ATCGGGACCC CAGGTCAGGC GGGATTACCC
Ilon612     CCTTTT-GGC ATCACTATGT CGATGCTCGC ATCGGGACCC CAGGTCAGGC GGGATTACCC
Irec621     CCTTTT-GGC ATCACTATGT CGATGCTCGC ATCGGGACCC CAGGTCAGGC GGGATTACCC
Isac620     CCTTTT-GGC ATCACTATGT CGATGCTCGC ATCGGGACCC CAGGTCAGGC AGGATTACCC
Iset424     CCTTTT-GGC ATCACTATGT CGATGCTCGC ATCGGGACCC CAGGTCAGGC GGGATTACCC
Ishi618     CCTTTT-GGC ATCACTATGT CGATGCTCGC ATCGGGACCC CAGGTCAGGC GGGATTACCC
Isul610     CCTTTT-GGC ATCACTATGT CGATGCTCGC ATCGGGACCC CAGGTCAGGC GGGATTACCC
Itab613     CCTTTT-GGC ATCACTATGT CGATGCTCGC ATCGGGACCC CAGGTCAGGC GGGATTACCC
Iwil627     CCTTTT-GGC ATCACTATGT CGATGCTCGC ATCGGGACCC CAGGTCAGGC GGGATTACCC
IMtf601     CCTTTTTGGC ATTGCAACGT CGATGCTCGC ATCGCGACCC CAGGTCAGGC GGGATTACCC
IAof512     CCTTCT-GGC ATCGCAATGC CGGTGCTCGC ATCGGGACCC CAGGTCAGGC GGGATTACCC
IAar427     CCTTCT-GGC ATCGCAATGC CGGTGCTCGC ATCGGGACCC CAGGTCAGGC GGGATTaccc
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*psb*A-*trn*H *Alcea*

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                   ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                           10         20         30         40         50         60         70         80         90        100
Ppal140            TCGAAGCTCC AtCTACAAAT GGATAAGACT TTGGTTTTAG TGTATACGAG TTTTTGAAAA TAAAGGAGCA ATACCAACAC TCTTGATAGA ACAAGAAATT
Pros422            TCGAAGCTCC AtCTACAAAT GGATAAGACT TTGGTTTTAG TGTATACGAG TTTTTGAAAA TAAAGGAGCA ATACCAACAC TCTTGATAGA ACAAGAAATT
Pauc617            TCGAAGCTCC ATCTACAAAT GGATAAGACT TTGGTTTTAG TGTATACGAG TTTTTGAAAA TAAAGGAGCA ATAACCAATT TCTTGTTCTA TCAAGAGTGT
Pexc417            TCGAAGCTCC ATCTACAAAT GGATAAGACT TTGGTTTTAG TGTATACGAG TTTTTGAAAA TAAAGGAGCA ATACCAACAC TCTTGATAGA ACAAGAAATT
Pkoe609            TCGAAGCTCC ATCTACAAAT GGATAAGACT TTGGTTTTAG TGTATACGAG TTTTTGAAAA TAAAGGAGCA ATACCAACAC TCTTGATAGA ACAAGAAATT
Pkur619            TCGAAGCTCC ATCTACAAAT GGATAAGACT TTGGTTTTAG TGTATACGAG TTTTTGAAAA TAAAGGAGCA ATACCAACAC TCTTGATAGA ACAAGAAATT
Plon612            TCGAAGCTCC ATCTACAAAT GGATAAGACT TTGGTTTTAG TGTATACGAG TTTTTGAAAA TAAAGGAGCA ATACCAACAC TCTTGATAGA ACAAGAAATT
Ppal140            TCGAAGCTCC ATCTACAAAT GGATAAGACT TTGGTTTTAG TGTATACGAG TTTTTGAAAA TAAAGGAGCA ATACCAACAC TCTTGATAGA ACAAGAAATT
Prec621            TCGAAGCTCC ATCTACAAAT GGATAAGACT TTGGTTTTAG TGTATACGAG TTTTTGAAAA TAAAGGAGCA ATACCAACAC TCTTGATAGA ACAAGAAATT
Prhy618            TCGAAGCTCC ATCTACAAAT GGATAAGACT TTGGTTTTAG TGTATACGAG TTTTTGAAAA TAAAGGAGCA ATACCAACAC TCTTGATAGA ACAAGAAATT
Prug420            TCGAAGCTCC ATCTACAAAT GGATAAGACT TTGGTTTTAG TGTATACGAG TTTTTGAAAA TAAAGGAGCA ATACCAACAC TCTTGATAGA ACAAGAAATT
Psac620            TCGAAGCTCC ATCTACAAAT GGATAAGACT TTGGTTTTAG TGTATACGAG TTTTTGAAAA TAAAGGAGCA ATACCAACAC TCTTGATAGA ACAAGAAATT
Pset424            TCGAAGCTCC AtCTACAAAT GGATAAGACT TTGGTTTTAG TGTATACGAG TTTTTGAAAA TAAAGGAGCA ATACCAACAC TCTTGATAGA ACAAGAAATT
Pshi618            TCGAAGCTCC ATCTACAAAT GGATAAGACT TTGGTTTTAG TGTATACGAG TTTTTGAAAA TAAAGGAGCA ATACCAACAC TCTTGATAGA ACAAGAAATT
Psul610            TCGAAGCTCC ATCTACAAAT GGATAAGACT TTGGTTTTAG TGTATACGAG TTTTTGAAAA TAAAGGAGCA ATACCAACAC TCTTGATAGA ACAAGAAATT
Ptab613            TCGAAGCTCC ATCTACAAAT GGATAAGACT TTGGTTTTAG TGTATACGAG TTTTTGAAAA TAAAGGAGCA ATACCAACAC TCTTGATAGA ACAAGAAATT
Pwil627            TCGAAGCTCC ATCTACAAAT GGATAAGACT TTGGTTTTAG TGTATACGAG TTTTTGAAAA TAAAGGAGCA ATACCAACAC TCTTGATAGA ACAAGAAATT
PMtf394            TCGAAGCTCC ATCTACAAAT GGATAAGACT TTGGTTTTAG TGTATACGAG TTTTTGAAAA TAAAGGAGCA ATACCAACAT TCTTGATAAA ACAAGAAATT
PAof512            TCGAAGCTCC ATCTACAAAT GGATAAGACT TTGGTTTTAG TGTATACGAG TTTTTGAAAA TAAAGGAGCG ATACCAACAC TCTTGATAGA ACAAGAAATT
PAar427            TCGAAGCTCC ATCTACAAAT GGATAAGACT TTGGTTTTAG TGTATACGAG TTTTTGAAAA TAAAGGAGCG ATACCAACAC TCTTGATAGA ACAAGAAATT


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                          110        120        130        140        150        160        170        180        190        200
Ppal140            GGTTATTGCT CCTTTATTTA GATTTAGTAG TCTTTTTTTC GTTACACTTT TTTTTCTTTA CATTTACATA AGTTTGTTTT TTCTTTACTT TAACTTTTTT
Pros422            GGTTATTGCT CCTTTATTTA GATTTAGTAG TCTTTTTTTC GTTACACTTT TTTTTCTTTA CATTTACATA AGTTTGTTTT TTCTTTACTT TAACTTTTTT
Pauc617            TGGTATTGCT CCTTTATTTA GATTTAGTAG TCTTTTTTTC GTTACACTTT TTTTTCTTTA CATTTACATA AGTTTGTTTT TTCTTTACTT TAACTTTTTT
Pexc417            GGTTATTGCT CCTTTATTTA GATTTAGTAG TCTTTTTTTC GTTACACTTT TTTTTCTTTA CATTTACATA AGTTTGTTTT TTCTTTACTT TAACTTTTTT
Pkoe609            GGTTATTGCT CCTTTATTTA GATTTAGTAG TCTTTTTTTC GTTACACTTT TTTTTCTTTA CATTTACATA AGTTTGTTTT TTCTTTACTT TAACTTTTTT
Pkur619            GGTTATTGCT CCTTTATTTA GATTTAGTAG TCTTTTTTTC GTTACACTTT TTTTTCTTTA CATTTACATA AGTTTGTTTT TTCTTTACTT TAACTTTTTT
Plon612            GGTTATTGCT CCTTTATTTA GATTTAGTAG TCTTTTTTTC GTTACACTTT TTTTTCTTTA CATTTACATA AGTTTGTTTT TTCTTTACTT TAACTTTTTT
Ppal140            GGTTATTGCT CCTTTATTTA GATTTAGTAG TCTTTTTTTC GTTACACTTT TTTTTCTTTA CATTTACATA AGTTTGTTTT TTCTTTACTT TAACTTTTTT
Prec621            GGTTATTGCT CCTTTATTTA GATTTAGTAG TCTTTTTTTC GTTACACTTT TTTTTCTTTA CATTTACATA AGTTTGTTTT TTCTTTACTT TAACTTTTTT
Prhy618            GGTTATTGCT CCTTTATTTA GATTTAGTAG TCTTTTTTTC GTTACACTTT TTTTTCTTTA CATTTACATA AGTTTGTTTT TTCTTTACTT TAACTTTTTT
Prug420            GGTTATTGCT CCTTTATTTA GATTTAGTAG TCTTTTTTTC GTTACACTTT TTTTTCTTTA CATTTACATA AGTTTGTTTT TTCTTTACTT TAACTTTTTT
Psac620            GGTTATTGCT CCTTTATTTA GATTTAGTAG TCTTTTTTTC GTTACACTTT TTTTTCTTTA CATTTACATA AGTTTGTTTT TTCTTTACTT TAACTTTTTT
Pset424            GGTTATTGCT CCTTTATTTA GATTTAGTAG TCTTTTTTTC GTTACACTTT TTTTTCTTTA CATTTACATA AGTTTGTTTT TTCTTTACTT TAACTTTTTT
Pshi618            GGTTATTGCT CCTTTATTTA GATTTAGTAG TCTTTTTTTC GTTACACTTT TTTTTCTTTA CATTTACATA AGTTTGTTTT TTCTTTACTT TAACTTTTTT
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Psul610     GGTTATTGCT CCTTTATTTA GATTTAGTAG TCTTTTTTTC GTTACACTTT TTTTTCTTTA CATTTACATA AGTTTGTTTT TTCTTTACTT TAACTTTTTT
Ptab613     GGTTATTGCT CCTTTATTTA GATTTAGTAG TCTTTTTTTC GTTACACTTT TTTTTCTTTA CATTTACATA AGTTTGTTTT TTCTTTACTT TAACTTTTTT
Pwil627     GGTTATTGCT CCTTTATTTA GATTTAGTAG TCTTTTTTTC GTTACACTTT TTTTTCTTTA CATTTACATA AGTTTGTTTT TTCTTTACTT TAACTTTTTT
PMtf394     GTTTATTGCT CCTTTATTTA TATTTAGTAG TCTTTTTTTC GTTACACTTT TTTTTCTTTA CATTTACATA AGTTTGTTTT TTCTTTACTT TAACTTTTTT
PAof512     GGTTATTGCT CCTTTATTTA GATTTAGTAG TCTTTTTTTC GTTACACTTT TTTTTCTTTA CATTTACATA AGTTTGTTTT TTCTTTACTT TAACTTTTTT
PAar427     GGTTATTGCT CCTTTATTTA GATTTAGTAG TCTTTTTTTC GTTACACTTT TTTTTCTTTA CATTTACATA AGTTTGTTTT TTCTTTACTT TAACTTTTTT


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                   210        220        230        240        250        260        270        280        290        300
Ppal140     ATTTTACCTT ATTTATTTCT GATTATCATA AGAAATAAAA AAAAA--GGA TTTTTTAATG AGTTTGATTT CATTTTATTG GATTTGACTT AGTATTATAC
Pros422     ATTTTACCTT ATTTATTTCT GATTATCATA AGAAATAAAA AAAAA--GGA TTTTTTAATG AGTTTGATTT CATTTTATTG GATTTGACTT AGTATTATAC
Pauc617     ATTTTACCTT ATTTATTTCT GATTATCATA AGAAATAAAA AAAAA--GGA TTTTTTAATG AGTTTGATTT CATTTTATTG GATTTGACTT AGTATTATAC
Pexc417     ATTTTACCTT ATTTATTTCT GATTATCATA AGAAATAAAA AAAAA--GGA TTTTTTAATG AGTTTGATTT CATTTTATTG GATTTGACTT AGTATTATAC
Pkoe609     ATTTTACCTT ATTTATTTCT GATTATCATA AGAAATAAAA AAAAA--GGA TTTTTTAATG AGTTTGATTT CATTTTATTG GATTTGACTT AGTATTATAC
Pkur619     ATTTTACCTT ATTTATTTCT GATTATCATA AGAAATAAAA AAAAA--GGA TTTTTTAATG AGTTTGATTT CATTTTATTG GATTTGACTT AGTATTATAC
Plon612     ATTTTACCTT ATTTATTTCT GATTATCATA AGAAATAAAA AAAAA--GGA TTTTTTAATG AGTTTGATTT CATTTTATTG GATTTGACTT AGTATTATAC
Ppal140     ATTTTACCTT ATTTATTTCT GATTATCATA AGAAATAAAA AAAAA--GGA TTTTTTAATG AGTTTGATTT CATTTTATTG GATTTGACTT AGTATTATAC
Prec621     ATTTTACCTT ATTTATTTCT GATTATCATA AGAAATAAAA AAAAA--GGA TTTTTTAATG AGTTTGATTT CATTTTATTG GATTTGACTT AGTATTATAC
Prhy618     ATTTTACCTT ATTTATTTCT GATTATCATA AGAAATAAAA AAAAA--GGA TTTTTTAATG AGTTTGATTT CATTTTATTG GATTTGACTT AGTATTATAC
Prug420     ATTTTACCTT ATTTATTTCT GATTATCATA AGAAATAAAA AAAAA--GGA TTTTTTAATG AGTTTGATTT CATTTTATTG GATTTGACTT AGTATTATAC
Psac620     ATTTTACCTT ATTTATTTCT GATTATCATA AGAAATAAAA AAAAA--GGA TTTTTTAATG AGTTTGATTT CATTTTATTG GATTTGACTT AGTATTATAC
Pset424     ATTTTACCTT ATTTATTTCT GATTATCATA AGAAATAAAA AAAAA--GGA TTTTTTAATG AGTTTGATTT CATTTTATTG GATTTGACTT AGTATTATAC
Pshi618     ATTTTACCTT ATTTATTTCT GATTATCATA AGAAATAAAA AAAAA--GGA TTTTTTAATG AGTTTGATTT CATTTTATTG GATTTGACTT AGTATTATAC
Psul610     ATTTTACCTT ATTTATTTCT GATTATCATA AGAAATAAAA AAAAA--GGA TTTTTTAATG AGTTTGATTT CATTTTATTG GATTTGACTT AGTATTATAC
Ptab613     ATTTTACCTT ATTTATTTCT GATTATCATA AGAAATAAAA AAAAA--GGA TTTTTTAATG AGTTTGATTT CATTTTATTG GATTTGACTT AGTATTATAC
Pwil627     ATTTTACCTT ATTTATTTCT GATTATCATA AGAAATAAAA AAAAA--GGA TTTTTTAATG AGTTTGATTT CATTTTATTG GATTTGACTT AGTATTATAC
PMtf394     ATTTTACCTT ATTTATTTCT GATTATCATA AGAAATCAAA TAAAAAAGGA TTTTTTAATG AGTTTGATTT CATTTTATTG GATTTGACTT AGTATTATAC
PAof512     ATTTTACCTT ATTTATTTCT GATTATCATA AGAAATAAAA AAAA---GGA TTTTTTAATG AGTTTGATTT CGTTTTATTG GATTTGACTT AGTATTATAC
PAar427     ATTTTACCTT ATTTATTTCT GATTATCATA AGAAATAAAA AAAA---GGA TTTTTTAATG AGTTTGATTT CGTTTTATTG GATTTGACTT AGTATTATAC


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                   310        320        330        340        350        360        370        380        390        400
Ppal140     GTTCGTTATG TAATAATATA TTATATATTA AATTAACGAA TTTTTAAAAA ATAGAAAAAA GGTAAAAAAG TTCTTACCAA TCTTTTGTAA AGTTTTTATT
Pros422     GTTCGTTATG TAATAATATA TTATATATTA AATTAACGAA TTTTTAAAAA ATAGAAAAAA GGTAAAAAAG TTCTTACCAA TCTTTTGTAA AGTTTTTATT
Pauc617     GTTCGTTATG TAATAATATA TTATATATTA AATTAACGAA TTTTTAAAAA ATAGAAAAAA GGTAAAAAAG TTCTTACCAA TCTTTTGTAA AGTTTTTATT
Pexc417     GTTCGTTATG TAATAATATA TTATATATTA AATTAACGAA TTTTTAAAAA ATAGAAAAAA GGTAAAAAAG TTCTTACCAA TCTTTTGTAA AGTTTTTATT
Pkoe609     GTTCGTTATG TAATAATATA TTATATATTA AATTAACGAA TTTTTAAAAA ATAGAAAAAA GGTAAAAAAG TTCTTACCAA TCTTTTGTAA AGTTTTTATT
Pkur619     GTTCGTTATG TAATAATATA TTATATATTA AATTAACGAA TTTTTAAAAA ATAGAAAAAA GGTAAAAAAG TTCTTACCAA TCTTTTGTAA AGTTTTTATT
Plon612     GTTCGTTATG TAATAATATA TTATATATTA AATTAACGAA TTTTTAAAAA ATAGAAAAAA GGTAAAAAAG TTCTTACCAA TCTTTTGTAA AGTTTTTATT
Ppal140     GTTCGTTATG TAATAATATA TTATATATTA AATTAACGAA TTTTTAAAAA ATAGAAAAAA GGTAAAAAAG TTCTTACCAA TCTTTTGTAA AGTTTTTATT
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Prec621      GTTCGTTATG TAATAATATA TTATATATTA AATTAACGAA TTTTTAAAAA ATAGAAAAAA GGTAAAAAAG TTCTTACCAA TCTTTTGTAA AGTTTTTATT
Prhy618      GTTCGTTATG TAATAATATA TTATATATTA AATTAACGAA TTTTTAAAAA ATAGAAAAAA GGTAAAAAAG TTCTTACCAA TCTTTTGTAA AGTTTTTATT
Prug420      GTTCGTTATG TAATAATATA TTATATATTA AATTAACGAA TTTTTAAAAA ATAGAAAAAA GGTAAAAAAG TTCTTACCAA TCTTTTGTAA AGTTTTTATT
Psac620      GTTCGTTATG TAATAATATA TTATATATTA AATTAACGAA TTTTTAAAAA ATAGAAAAAA GGTAAAAAAG TTCTTACCAA TCTTTTGTAA AGTTTTTATT
Pset424      GTTCGTTATG TAATAATATA TTATATATTA AATTAACGAA TTTTTAAAAA ATAGAAAAAA GGTAAAAAAG TTCTTACCAA TCTTTTGTAA AGTTTTTATT
Pshi618      GTTCGTTATG TAATAATATA TTATATATTA AATTAACGAA TTTTTAAAAA ATAGAAAAAA GGTAAAAAAG TTCTTACCAA TCTTTTGTAA AGTTTTTATT
Psul610      GTTCGTTATG TAATAATATA TTATATATTA AATTAACGAA TTTTTAAAAA ATAGAAAAAA GGTAAAAAAG TTCTTACCAA TCTTTTGTAA AGTTTTTATT
Ptab613      GTTCGTTATG TAATAATATA TTATATATTA AATTAACGAA TTTTTAAAAA ATAGAAAAAA GGTAAAAAAG TTCTTACCAA TCTTTTGTAA AGTTTTTATT
Pwil627      GTTCGTTATG TAATAATATA TTATATATTA AATTAACGAA TTTTTAAAAA ATAGAAAAAA GGTAAAAAAG TTCTTACCAA TCTTTTGTAA AGTTTTTATT
PMtf394      GTTCGTTATG TAATAATATA TTATATATTA A-----CGAA TTTTTTT--A AAAGAAAAAA AGTAAAAAAG TTCTTACCAA TCTTTTGTAA AGTTTTTATT
PAof512      GTTCGTTATG TAATAATATA TTATATATTA A-----CGAA TTTTTTTAAA ATAGAAAAAA -GTAAAAAAG TTCTTACCAA TCTTTTGTAA AGTTTTTATT
PAar427      GTTCGTTATG TAATAATATA TTATATATTA A-----CGAA TTTTTTTAAA ATAGAAAAAA AGTAAAAAAG TTCTTACCAA TCTTTTGTAA AGTTTTTATT


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                    410        420        430        440        450        460        470        480        490        500
Ppal140      TTAGAGTAAA AATAAAGAAT TGGAATTTTC TATATATCTT ATCTCAGAAA TACGAGAAAA AACGAATGAT GAATGATAGA AATTGAGATA TTTGAAATAT
Pros422      TTAGAGTAAA AATAAAGAAT TGGAATTTTC TATATATCTT ATCTCAGAAA TACGAGAAAA AACGAATGAT GAATGATAGA AATTGAGATA TTTGAAATAT
Pauc617      TTAGAGTAAA AATAAAGAAT TGGAATTTTC TATATATCTT ATCTCAGAAA TACGAGAAAA AACGAATGAT GAATGATAGA AATTGAGATA TTTGAAATAT
Pexc417      TTAGAGTAAA AATAAAGAAT TGGAATTTTC TATATATCTT ATCTCAGAAA TACGAGAAAA AACGAATGAT GAATGATAGA AATTGAGATA TTTGAAATAT
Pkoe609      TTAGAGTAAA AATAAAGAAT TGGAATTTTC TATATATCTT ATCTCAGAAA TACGAGAAAA AACGAATGAT GAATGATAGA AATTGAGATA TTTGAAATAT
Pkur619      TTAGAGTAAA AATAAAGAAT TGGAATTTTC TATATATCTT ATCTCAGAAA TACGAGAAAA AACGAATGAT GAATGATAGA AATTGAGATA TTTGAAATAT
Plon612      TTAGAGTAAA AATAAAGAAT TGGAATTTTC TATATATCTT ATCTCAGAAA TACGAGAAAA AACGAATGAT GAATGATAGA AATTGAGATA TTTGAAATAT
Ppal140      TTAGAGTAAA AATAAAgAAT TGGAATTTTc TATATATCTT ATcTCAGAAA TACGAGAAAA AACGAATGAT GAATGATAGA AATTGAGATA TTTGAAATAT
Prec621      TTAGAGTAAA AATAAAGAAT TGGAATTTTC TATATATCTT ATCTCAGAAA TACGAGAAAA AACGAATGAT GAATGATAGA AATTGAGATA TTTGAAATAT
Prhy618      TTAGAGTAAA AATAAAGAAT TGGAATTTTC TATATATCTT ATCTCAGAAA TACGAGAAAA AACGAATGAT GAATGATAGA AATTGAGATA TTTGAAATAT
Prug420      TTAGAGTAAA AATAAAGAAT TGGAATTTTC TATATATCTT ATCTCAGAAA TACGAGAAAA AACGAATGAT GAATGATAGA AATTGAGATA TTTGAAATAT
Psac620      TTAGAGTAAA AATAAAGAAT TGGAATTTTC TATATATCTT ATCTCAGAAA TACGAGAAAA AACGAATGAT GAATGATAGA AATTGAGATA TTTGAAATAT
Pset424      TTAGAGTAAA AATAAAGAAT TGGAATTTTC TATATATCTT ATCTCAGAAA TACGAGAAAA AACGAATGAT GAATGATAGA AATTGAGATA TTTGAAATAT
Pshi618      TTAGAGTAAA AATAAAGAAT TGGAATTTTC TATATATCTT ATCTCAGAAA TACGAGAAAA AACGAATGAT GAATGATAGA AATTGAGATA TTTGAAATAT
Psul610      TTAGAGTAAA AATAAAGAAT TGGAATTTTC TATATATCTT ATCTCAGAAA TACGAGAAAA AACGAATGAT GAATGATAGA AATTGAGATA TTTGAAATAT
Ptab613      TTAGAGTAAA AATAAAGAAT TGGAATTTTC TATATATCTT ATCTCAGAAA TACGAGAAAA AACGAATGAT GAATGATAGA AATTGAGATA TTTGAAATAT
Pwil627      TTAGAGTAAA AATAAAGAAT TGGAATTTTC TATATATCTT ATCTCAGAAA TACGAGAAAA AACGAATGAT GAATGATAGA AATTGAGATA TTTGAAATAT
PMtf394      TTAGAGTAAA AATAAAGAAT TGGAATTTTC TATATATTTT ATATCAGAAA TACGAGAAAA AACGAATGAT GAATGATAGA AATTGAGATA TTTGAAATAT
PAof512      TTAGAGTAAA AATAAAGAAT TGGAATTTTC TATATATCTT ATCTCAGAAA TACGAGAAAA AACGAATGAT GAATGATAGA AATTGAGATA TTTGAAATAT
PAar427      TTAGAGTAAA AATAAAGAAT TGGAATTTTC TATATATCTT ATCTCAGAAA TACGAGAAAA AACGAATGAT GAATGATAGA AATTGAGATA TTTGAAATAT


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                                     510        520        530        540        550        560
                 Ppal140      TTAAACAATA AAAAAAA-TA CTATACTATT ATAGTAGAGG GGCGGATGTA GCCAAGTGGa TCAAGGCAG
                 Pros422      TTAAACAATA AAAAAAA-GA CTATACTATT ATAGTAGAGG GGCGGATGTA GCCAAGTGGa TCAAGGCAG
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Pauc617      TTAAACAATA AAAAAAA-TA CTATACTATT ATAGTAGAGG GGCGGATGTA GCCAAGTGGA TCAAGGCAG
Pexc417      TTAAACAATA AAAAAAA-TA CTATACTATT ATAGTAGAGG GGCGGATGTA GCCAAGTGGA TCAAGGCAG
Pkoe609      TTAAACAATA AAAAAAA-TA CTATACTATT ATAGTAGAGG GGCGGATGTA GCCAAGTGGA TCAAGGCAG
Pkur619      TTAAACAATA AAAAAAA-TA CTATACTATT ATAGTAGAGG GGCGGATGTA GCCAAGTGGA TCAAGGCAG
Plon612      TTAAACAATA AAAAAAA-TA CTATACTATT ATAGTAGAGG GGCGGATGTA GCCAAGTGGA TCAAGGCAG
Ppal140      TTAAACAATA AAAAAAA-TA CTATACTATT ATAGTAGAGG GGCGGATGTA GCCAAGTGGA TCAAGGCAG
Prec621      TTAAACAATA AAAAAAA-TA CTATACTATT ATAGTAGAGG GGCGGATGTA GCCAAGTGGA TCAAGGCAG
Prhy618      TTAAACAATA AAAAAAA-TA CTATACTATT ATAGTAGAGG GGCGGATGTA GCCAAGTGGA TCAAGGCAG
Prug420      TTAAACAATA AAAAAAA-TA CTATACTATT ATAGTAGAGG GGCGGATGTA GCCAAGTGGA TCAAGGCAG
Psac620      TTAAACAATA AAAAAAA-TA CTATACTATT ATAGTAGAGG GGCGGATGTA GCCAAGTGGA TCAAGGCAG
Pset424      TTAAACAATA AAAAAAA-TA CTATACTATT ATAGTAGAGG GGCGGATGTA GCCAAGTGGA TCAAGGCAG
Pshi618      TTAAACAATA AAAAAAA-TA CTATACTATT ATAGTAGAGG GGCGGATGTA GCCAAGTGGA TCAAGGCAG
Psul610      TTAAACAATA AAAAAAA-TA CTATACTATT ATAGTAGAGG GGCGGATGTA GCCAAGTGGA TCAAGGCAG
Ptab613      TTAAACAATA AAAAAAA-TA CTATACTATT ATAGTAGAGG GGCGGATGTA GCCAAGTGGA TCAAGGCAG
Pwil627      TTAAACAATA AAAAAAA-TA CTATACTATT ATAGTAGAGG GGCGGATGTA GCCAAGTGGA TCAAGGCAG
PMtf394      TTAAACAATA AAAAAAAATA CTATAGTATT ATAGTAGAGG GGCGGATGTA GCCAAGTGGA TCAAGGCAG
PAof512      TTAAACAATA AAAAAAAATA CTATAGTATT ATAGTAGAGG GGCGGATGTA GCCAAGTGGA TCAAGGCAG
PAar427      TTAAACAATA AAAAAAAATA CTATAGTATT ATAGTAGAGG GGCGGATGTA GCCAAGTGGA TCAAGGCAG
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*trn*L-*trn*F *Alcea*

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                        10         20         30         40         50         60         70         80         90        100
Tros422        TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTGTTAGTG G-TTCAAAGT TCCTTATGTT TCTCATTCAT CCTATTCTTT TTTACA---- -----AACGT
Tpal140        TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTGTTAGTG G-TTCAAAGT TCCTTATGTT TCTCATTCAT CCTATTCTTT TTTACA---- -----AACGT
Tauc617        TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTGTTAGTG G-TTCAAAGT TCCTTATGTT TCTCATTCAT CCTATTCTTT TTTACA---- -----AACGT
Texc417        TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTGTTAGTG G-TTCAAAGT TCCTTATGTT TCTCATTCAT CCTATTCTTT TTTACA---- -----AACGT
Tkoe609        TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTGTTAGTG G-TTCAAAGT TCCTTATGTT TCTCATTCAT CCTATTCTTT TTTACA---- -----AACGT
Tkur619        TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTGTTAGTG G-TTCAAAGT TCCTTATGTT TCTCATTCAT CCTATTCTTT TTTACA---- -----AACGT
Tlon612        TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTGTTAGTG G-TTCAAAGT TCCTTATGTT TCTCATTCAT CCTATTCTTT TTTACA---- -----AACGT
Trec621        TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTGTTAGTG G-TTCAAAGT TCCTTATGTT TCTCATTCAT CCTATTCTTT TTTACA---- -----AACGT
Trhy618        TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTGTTAGTG G-TTCAAAGT TCCTTATGTT TCTCATTCAT CCTATTCTTT TTTACA---- -----AACGT
Trug420        TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTGTTAGTG G-TTCAAAGT TCCTTATGTT TCTCATTCAT CCTATTCTTT TTTACA---- -----AACGT
Tsac620        TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTGTTAGTG G-TTCAAAGT TCCTTATGTT TCTCATTCAT CCTATTCTTT TTTACA---- -----AACGT
Tset424        TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTGTTAGTG G-TTCAAAGT TCCTTATGTT TCTCATTCAT CCTATTCTTT TTTACA---- -----AACGT
Tshy618        TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTGTTAGTG G-TTCAAAGT TCCTTATGTT TCTCATTCAT CCTATTCTTT TTTACA---- -----AACGT
Tsul610        TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTGTTAGTG G-TTCAAAGT TCCTTATGTT TCTCATTCAT CCTATTCTTT TTTACA---- -----AACGT
Ttab613        TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTGTTAGTG G-TTCAAAGT TCCTTATGTT TCTCATTCAT CCTATTCTTT TTTACA---- -----AACGT
Twil627        TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTGTTAGTG G-TTCAAAGT TCCTTATGTT TCTCATTCAT CCTATTCTTT TTTACA---- -----AACGT
TAof512        TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTGTTAGTG G-TTCAAAGT TCCTTATGTT TCTCATTCAT CCTATTCTTT TTTACATTTT TTACAAACGT
TAar427        TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTGTTAGTG G-TTCAAAGT TCCTTATGTT TCTCATTCAT CCTATTCTTT TTTACATTTT TTACAAACGT
TMtf601        TTTGCTATCT ATTTATTTTA TCCTACCCTT TTTTTTTATT GGTTCAAAGT TCCTTATGTT TCTCATTCAT CCTATTCTTT TTTACA---- -----AACGT


               ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                       110        120        130        140        150        160        170        180        190        200
Tros422        ATCCTAGCAG AATTTTGTTC TCTTATCACA AGTCTTGTGA TATATTGTGA TATATATATA TGATATACGT ACAAATCTCT TGAGCAAGGA ATACCTATTT
Tpal140        ATCCTAGCAG AATTTTGTTC TCTTATCACA AGTCTTGTGA TATATTGTGA TATATATATA TGATATACGT ACAAATCTCT TGAGCAAGGA ATACCTATTT
Tauc617        ATCCTAGCAG AATTTTGTTC TCTTATCACA AGTCTTGTGA TATATTGTGA TATATATATA TGATATACGT ACAAATCTCT TGAGCAAGGA ATACCTATTT
Texc417        ATCCTAGCAG AATTTTGTTC TCTTATCACA AGTCTTGTGA TATATTGTGA TATATATATA TGATATACGT ACAAATCTCT TGAGCAAGGA ATACCTATTT
Tkoe609        ATCCTAGCAG AATTTTGTTC TCTTATCACA AGTCTTGTGA TATATTGTGA TATATATATA TGATATACGT ACAAATCTCT TGAGCAAGGA ATACCTATTT
Tkur619        ATCCTAGCAG AATTTTGTTC TCTTATCACA AGTCTTGTGA TATATTGTGA TATATATATA TGATATACGT ACAAATCTCT TGAGCAAGGA ATACCTATTT
Tlon612        ATCCTAGCAG AATTTTGTTC TCTTATCACA AGTCTTGTGA TATATTGTGA TATATATATA TGATATACGT ACAAATCTCT TGAGCAAGGA ATACCTATTT
Trec621        ATCCTAGCAG AATTTTGTTC TCTTATCACA AGTCTTGTGA TATATTGTGA TATATATATA TGATATACGT ACAAATCTCT TGAGCAAGGA ATACCTATTT
Trhy618        ATCCTAGCAG AATTTTGTTC TCTTATCACA AGTCTTGTGA TATATTGTGA TATATATATA TGATATACGT ACAAATCTCT TGAGCAAGGA ATACCTATTT
Trug420        ATCCTAGCAG AATTTTGTTC TCTTATCACA AGTCTTGTGA TATATTGTGA TATATATATA TGATATACGT ACAAATCTCT TGAGCAAGGA ATACCTATTT
Tsac620        ATCCTAGCAG AATTTTGTTC TCTTATCACA AGTCTTGTGA TATATTGTGA TATATATATA TGATATACGT ACAAATCTCT TGAGCAAGGA ATACCTATTT
Tset424        ATCCTAGCAG AATTTTGTTC TCTTATCACA AGTCTTGTGA TATATTGTGA TATATATATA TGATATACGT ACAAATCTCT TGAGCAAGGA ATACCTATTT
Tshy618        ATCCTAGCAG AATTTTGTTC TCTTATCACA AGTCTTGTGA TATATTGTGA TATATATATA TGATATACGT ACAAATCTCT TGAGCAAGGA ATACCTATTT
Tsul610        ATCCTAGCAG AATTTTGTTC TCTTATCACA AGTCTTGTGA TATATTGTGA TATATATATA TGATATACGT ACAAATCTCT TGAGCAAGGA ATACCTATTT
Ttab613        ATCCTAGCAG AATTTTGTTC TCTTATCACA AGTCTTGTGA TATATTGTGA TATATATATA TGATATACGT ACAAATCTCT TGAGCAAGGA ATACCTATTT
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Twil627         ATCCTAGCAG AATTTTGTTC TCTTATCACA AGTCTTGTGA TATATTGTGA TATATATATA TGATATACGT ACAAATCTCT TGAGCAAGGA ATACCTATTT
TAof512         ATCCTAGCAG AATTTTGTTC TCTTATCACA AGTCTTGTGA TATATTGTGA TATATATATA TGATATACGT ACAAATCTCT TGAGCAAGGA ATACCTATTT
TAar427         ATCCTAGCAG AATTTTGTTC TCTTATCACA AGTCTTGTGA TATATTGTGA TATATATATA TGATATACGT ACAAATCTCT TGAGCAAGGA ATACCTATTT
TMtf601         ATGCTAGCAG AATTTTGTTC TCTTATCACA AGTCTTGTGA TATATTGTGA TATATATAT- -GATATACGT ACAAATCTCT TGAGCAAGGA ATACCTATTT


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                       210        220        230        240        250        260        270        280        290        300
Tros422         GAATTTTGAA TGATTCATAA TCCATATGAT TACTCATATG GAAATTTACA AAGTCTTCCT TTTGAAGATC CAAGAAATTC CTGTTCGAGA CTTTAAA---
Tpal140         GAATTTTGAA TGATTCATAA TCCATATGAT TACTCATATG GAAATTTACA AAGTCTTCCT TTTGAAGATC CAAGAAATTC CTGTTCGAGA CTTTAAA---
Tauc617         GAATTTTGAA TGATTCATAA TCCATATGAT TACTCATATG GAAATTTACA AAGTCTTCCT TTTGAAGATC CAAGAAATTC CTGTTCGAGA CTTTAAA---
Texc417         GAATTTTGAA TGATTCATAA TCCATATGAT TACTCATATG GAAATTTACA AAGTCTTCCT TTTGAAGATC CAAGAAATTC CTGTTCGAGA CTTTAAA---
Tkoe609         GAATTTTGAA TGATTCATAA TCCATATGAT TACTCATATG GAAATTTACA AAGTCTTCCT TTTGAAGATC CAAGAAATTC CTGTTCGAGA CTTTAAA---
Tkur619         GAATTTTGAA TGATTCATAA TCCATATGAT TACTCATATG GAAATTTACA AAGTCTTCCT TTTGAAGATC CAAGAAATTC CTGTTCGAGA CTTTAAA---
Tlon612         GAATTTTGAA TGATTCATAA TCCATATGAT TACTCATATG GAAATTTACA AAGTCTTCCT TTTGAAGATC CAAGAAATTC CTGTTCGAGA CTTTAAA---
Trec621         GAATTTTGAA TGATTCATAA TCCATATGAT TACTCATATG GAAATTTACA AAGTCTTCCT TTTGAAGATC CAAGAAATTC CTGTTCGAGA CTTTAAA---
Trhy618         GAATTTTGAA TGATTCATAA TCCATATGAT TACTCATATG GAAATTTACA AAGTCTTCCT TTTGAAGATC CAAGAAATTC CTGTTCGAGA CTTTAAA---
Trug420         GAATTTTGAA TGATTCATAA TCCATATGAT TACTCATATG GAAATTTACA AAGTCTTCCT TTTGAAGATC CAAGAAATTC CTGTTCGAGA CTTTAAA---
Tsac620         GAATTTTGAA TGATTCATAA TCCATATGAT TACTCATATG GAAATTTACA AAGTCTTCCT TTTGAAGATC CAAGAAATTC CTGTTCGAGA CTTTAAA---
Tset424         GAATTTTGAA TGATTCATAA TCCATATGAT TACTCATATG GAAATTTACA AAGTCTTCCT TTTGAAGATC CAAGAAATTC CTGTTCGAGA CTTTAAA---
Tshy618         GAATTTTGAA TGATTCATAA TCCATATGAT TACTCATATG GAAATTTACA AAGTCTTCCT TTTGAAGATC CAAGAAATTC CTGTTCGAGA CTTTAAA---
Tsul610         GAATTTTGAA TGATTCATAA TCCATATGAT TACTCATATG GAAATTTACA AAGTCTTCCT TTTGAAGATC CAAGAAATTC CTGTTCGAGA CTTTAAA---
Ttab613         GAATTTTGAA TGATTCATAA TCCATATGAT TACTCATATG GAAATTTACA AAGTCTTCCT TTTGAAGATC CAAGAAATTC CTGTTCGAGA CTTTAAA---
Twil627         GAATTTTGAA TGATTCATAA TCCATATGAT TACTCATATG GAAATTTACA AAGTCTTCCT TTTGAAGATC CAAGAAATTC CTGTTCGAGA CTTTAAA---
TAof512         GAA------- TGATTCATAA TCCATATGAT TACTCATATG GAAATTTACA AAGTCTTCCT TTTGAAGATC CAAGAAATTC CTGTTCGAGA CTTTAAA---
TAar427         GAA------- TGATTCATAA TCCATATGAT TACTCATATG GAAATTTACA AAGTCTTCCT TTTGAAGATC CAAGAAATTC CTGTTCGAGA CTTTAAA---
TMtf601         GAA------- TGATTCATAA TCCATACGAT TACTCATATG GAAATTTACA AAGTCTTCCT TTTGAAGATC CAAGAAATTC CTGTTCGAGA CTTTAAACTT


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                       310        320        330        340        350        360        370        380        390        400
Tros422         ----TTTAAT ACTTTTTCAT TTTTTTTTTT TTGTTTTCAT TTTTAATTGA CATAGACCCA AGTCGTCTAG TATTATGATG ATAATGCGTT GGTAATGGTC
Tpal140         ----TTTAAT ACTTTTTCAT TTTTTTTTTT TTGTTTTCAT TTTTAATTGA CATAGACCCA AGTCGTCTAG TATTATGATG ATAATGCGTT GGTAATGGTC
Tauc617         ----TTTAAT ACTTTTTCAT TTTTTTTTTT TTGTTTTCAT TTTTAATTGA CATAAACCCA AGTCGTCTAG TATTATGATG ATAATGCGTT GGTAATGGTC
Texc417         ----TTTAAT ACTTTTTCAT TTTTTTTTTT TTGTTTTCAT TTTTAATTGA CATAAACCCA AGTCGTCTAG TATTATGATG ATAATGCGTT GGTAATGGTC
Tkoe609         ----TTTAAT ACTTTTTCAT TTTTTTTTTT TTGTTTTCTT TTTTAATTGA CATAAACCCA AGTCGTCTAG TATTATGATG ATAATGCGTT GGTAAGGGTC
Tkur619         ----TTTAAT ACTTTTTCAT TTTTTTTTTT TTGTTTTCAT TTTTAATTGA CATAAACCCA AGTCGTCTAG TATTATGATG ATAATGCGTT GGTAATGGTC
Tlon612         ----TTTAAT ACTTTTTCAT TTTTTTTTTT TTGTTTTCAT TTTTAATTGA CATAAACCCA AGTCGTCTAG TATTATGATG ATAATGCGTT GGTAATGGTC
Trec621         ----TTTAAT ACTTTTTCAT TTTTTTTTTT TTGTTTTCAT TTTTAATTGA CATAAACCCA AGTCGTCTAG TATTATGATG ATAATGCGTT GGTAATGGTC
Trhy618         ----TTTAAT ACTTTTTCAT TTTTTTTTTT TTGTTTTCAT TTTTAATTGA CATAAACCCA AGTCGTCTAG TATTATGATG ATAATGCGTT GGTAATGGTC
Trug420         ----TTTAAT ACTTTTTCAT TTTTTTTTTT TTGTTTTCAT TTTTAATTGA CATAAACCCA AGTCGTCTAG TATTATGATG ATAATGCGTT GGTAATGGTC
Tsac620         ----TTTAAT ACTTTTTCAT TTTTTTTTTT TTGTTTTCAT TTTTAATTGA CATAAACCCA AGTCGTCTAG TATTATGATG ATAATGCGTT GGTAATGGTC
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Tset424      ----TTTAAT ACTTTTTCAT TTTTTTTTTT TTGTTTTCAT TTTTAATTGA CATAAACCCA AGTCGTCTAG TATTATGATG ATAATGCGTT GGTAATGGTC
Tshy618      ----TTTAAT ACTTTTTCAT TTTTTTTTTT TTGTTTTCAT TTTTAATTGA CATAAACCCA AGTCGTCTAG TATTATGATG ATAATGCGTT GGTAAGGGTC
Tsul610      ----TTTAAT ACTTTTTCAT TTTTTTTTTT TTGTTTTCAT TTTTAATTGA CATAAACCCA AGTCGTCTAG TATTATGATG ATAATGCGTT GGTAATGGTC
Ttab613      ----TTTAAT ACTTTTTCAT TTTTTTTTTT TTGTTTTCAT TTTTAATTGA CATAAACCCA AGTCGTCTAG TATTATGATG ATAATGCGTT GGTAATGGTC
Twil627      ----TTTAAT ACTTTTTCAT TTTTTTTTTT TTGTTTTCAT TTTTAATTGA CATAAACCCA AGTCGTCTAG TATTATGATG ATAATGCGTT GGTAATGGTC
TAof512      ----TTTAAT ACTTTTTCAT TTTTTTTTT- --GTTTTCAT TTTTAATTGA CATAGACCCA AGTCGTCTAG TATTATGATG ATAATGCGTT GGTAATGGTC
TAar427      ----TTTAAT ACTTTTTCAT TTTTTTTTT- --GTTTTCAT TTTTAATTGA CATAGACCCA AGTCGTCTAG TATTATGATG ATAATGCGTT GGTAATGGTC
TMtf601      TAAATTTAAT ACTTTTTCGT TTTTTTTTTT --GTTTTCAT TTTGAATTGA CATAGACCCA AGTCGTCTAG TATTATGATG ATAATGCGTT GGTAATGGTC


                                    ....|....| ....|....| ....|....| ....|....| ....|..
                                           410        420        430        440
                             Tros422      GGGATAGCTC AGTTGGTAGA GCAGAGGACT GAAAATCCTC GTGTCAC
                             Tpal140      GGGATAGCTC AGTTGGTAGA GCAGAGGACT GAAAATCCTC GTGTCAC
                             Tauc617      GGGATAGCTC ATTTGGTAAA GCAAAGGACT GAAAATCCTC GTGTCCC
                             Texc417      GGGATAGCTC ATTTGGTAAA GCAAAGGACT GAAAATCCTC GTGTCCC
                             Tkoe609      GGGATAGCTC ATTTGGTAAA GCAAAGGACT GAAAATCCTC GTGTCCC
                             Tkur619      GGGATAGCTC ATTTGGTAAA GCAAAGGACT GAAAATCCTC GTGTCAC
                             Tlon612      GGGATAGCTC ATTTGGTAAA GCAAAGGACT GAAAATCCTC GGGTCCC
                             Trec621      GGGATAGCTC ATTTGGTAAA GCAAAGGACT GAAAATCCTC GTGTCAC
                             Trhy618      GGGATAGCTC ATTTGGTAAA GCAAAGGACT GAAAATCCTC GTGTCCC
                             Trug420      GGGATAGCTC ATTTGGTAAA GCAAAGGACT GAAAATCCTC GTGTCAC
                             Tsac620      GGGATAGCTC ATTTGGTAAA GCAAAGGACT GAAAATCCTC GTGTCCC
                             Tset424      GGGATAGCTC ATTTGGTAAA GCAAAGGACT GAAAATCCTC GTGTCAC
                             Tshy618      GGGATAGCTC ATTTGGTAAA GCAAAGGACT GAAAATTCTC GTGTCCC
                             Tsul610      GGGATAGCTC ATTTGGTAAA GCAAAGGACT GAAAATCCTC GTGTCCC
                             Ttab613      GGGATAGCTC ATTTGGTAAA GCAAAGGACT GAAAATCCTC GTGTCAC
                             Twil627      GGGATAGCTC ATTTGGTAAA GCAAAGGACT GAAAATCCTC GTGTCAC
                             TAof512      GGGATAGCTC AGTTGGTAGA GCAGAGGACT GAAAATCCTC GTGTCAC
                             TAar427      GGGATAGCTC AGTTGGTAGA GCAGAGGACT GAAAATCCTC GTGTCAC
                             TMtf601      GGGATAGCTC AGTTGGTAGA GCAGAGGACT GAAAATCCTC GTGTCAC
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                        10         20         30         40         50         60         70         80         90        100
MAar11          TCT-AACCGT CTTCTTAT-- ---CCTATAA CGAACATAAA TCAATTAGAT GGCAAAAGAT AGGATA--GA GAATCCGTTG ATGAATCTAC CTGTATCCGA
Aca594          TCT-AACCGT CTTCTTAT-- ---CCTATAA CGAACATAAA TCAATTAGAT GGCAAAAGAT AGGATA--GA GAATCCGTTG ATGAATCTAC CTGTATCCGA
MAof11          TCT-AACCGT CTTCTTAT-- ---CCTATAA CGAACATAAA TCAATTAGAT GGCAAAAGAT AGGATA--GA GAATCCGTTG ATGAATCTAC CTGTATCCGA
Lol451          TCTGAACCGT CTTCTTAT-- ---CCTATAA CGAACATAAA TCAATTAGAT GGCAAAAGAT AGGATA--GA GAATCCGTTG ATGAATCTAC CTGTCTCCGA
Lob144          TCT-AACCGT CTTCTTAT-- ---CCTATAA CGAACATAAA TCAATTAGAT GGCAAAAGAT AGGATA--GA GAATCCGTTG ATGAATCTAC CTGTCTCCGA
Lbr141          TCTGAACCGT CTTCTTAT-- ---CCTATAA CGAACATAAA TCAATTAGAT GGCAAAAGAT AGGATA--GA GAATCCGTTG ATGAATCTAC CTGTCTCCGA
Lag308          TCT-AACCGT CTTCTTAT-- ---CCTATAA CGAACATAAA TCAATTAGAT GGCAAAAGAT AGGATA--GA GAATCCGTTG ATGAATCTAC CTGTCTCCGA
MLtp11          TCT-AACCGC CTTCTTAT-- ---CCTATAA CGAACATAAA TCAATTAGAT GGTAAAAGAT AGGATA--GA GAATCCGTTG ATGAATCTAC CTGTCTCCGA
Ltr680          TCT-AACCGT CTTCTTAT-- ---CCTATAA CGAACATAAA TCAATTAGAT GGCAAAAGAT AGGATA--GA GAATCCGTTG ATGAATCTAC CTGTCTCCGA
MLfl11          TCT-AACCGT CTTCTTAT-- ---CCTATAA CGAACATAAA TCAATTAGAT GGCAAAAGAT AGGATA--GA GAATCCGTTG ATGAATCTAC CTGTCTCCGA
LplM57          TCT-AACCGT CTTCTTAT-- ---CCTATAA CGAACATAAA TCAATTAGAT GGCAAAAGAT AGGATA--GA GAATCCGTTG ATGAATCTAC CTGTCTCCGA
Lti472          TCT-AACCGT CTTCTTAT-- ---CCTATAA CGAACATAAA TCAATTAGAT GGCAAAAGAT AGGATA--GA GAATCCGTTG ATGAATCTAC CTGTCTCCGA
LthVie          TCT-AACCGT CTTCTTAT-- ---CCTATAA CGAACATAAA TCAATTAGAT GGCAAAAGAT AGGACA--GG -AA-CCGTTG ATGAATCTAC CTGTCTCCGA
MLpu11          TCT-AACCGT CTTCTTAT-- ---CCTATAA CGAACATAAA TCAATTAGAT GGCAAAAGAT AGGATA--GA GAATCCGTTG ATGAATCTAC CTGTCTCCGA
Lmo316          TCT-AACCGT CTTCTTAT-- ---CCTATAA CGAACATAAA TCAATTAGAT GG-AAAAGAT AGGA---CGA GAATCCGTTG ATGAATCTAC CTGTCTCCGA
LacB11          TCT-AACCGT CTTCTTAT-- ---CCTATAA CGAA-ATAAA TCAATTAGAT GG-AAAAGAT AGGATA-GCA GAATCCGTTG ATGAATCTAC CTGTCTCCGA
Lar253          TCT-AACCGT CTTCTTAT-- ---CCTATAA CGAACATAAA TCAATTAGAT GGCAAAAGAT AGGTATAGCA GAATCCGTTG ATGAATCTAC CTGTCTCCGA
MLas11          TCT-AACCGT CTTCTTAT-- ---CCTATAA CGAACATAAA TCAATTAGAT GGCAAAAGAT AGGATA--GA GAATCCGTTG ATGAATCTAC CTGTCTCCGA
MLma11          TCT-AACCGT CTTCTTAT-- ---CCTATAA CGAACATAAA TCAATTAGAT GGCAAAAGAT AGGATA--GA GAATCCGTTG ATGAATCTAC CTGTCTCCGA
Lmu283          TCT-AACCGT CTTCTTAT-- ---CCTATAA CGAACATAAA TCAATTAGAT GG-AAAAGAT AGGATA-CGA GAATCCGTTG ATGAATCTAC CTGTCTCCGA
MLcr11          TCT-AACCGT CTTCTTAT-- ---CCTATAA CGAACATAAA TCAATTAGAT GGCAAAAGAT AGGATA--GA GAATCCGTTG ATGAATCTAC CTGTCTCCGA
LpebM2          TCT-AACCGT CTTCTTAT-- ---CCTATAA CGAACATAAA TCAATTAGAT GGCAAAAGAT AGGATA--GA GAATCCGTTG ATGAATCTAC CTGTCTCCGA
Mni674          TCT-AACCGT CTTCTTAT-- ---CCTATAA CGAACATAAA TCAATTAGAT GGCAAAAGAT AGGATA--GA GAATCCGTTG ATGAATCTAC CTGTCTCCGA
Mpa603          TCT-AACCGT CTTCTTAT-- ---CCTATAA CGAACATAAA TCAATTAGAT GGCAAAAGAT AGGATA--GA GAATCCGTTG ATGAATCTAC CTGTCTCCGA
Msy597          TCT-AACCGT CTTCTTAT-- ---CCTATAA CGAACATAAA TCAATTAGAT GGCAAAAGAT AGGATA--GA GAATCCGTTG ATGAATCTAC CTGTCTCCGA
Mne795          TCT-AACCGT CTTCTTAT-- ---CCTATAA CGAACATAAA TCAATTAGAT GGCAAAAGAT AGGATA--GA GAATCCGTTG ATGAATCTAC CTGTCTCCGA
Mve442          TCT-AACCGT CTTCTTAT-- ---CCTATAA CGAACATAAA TCAATTAGAT GGCAAAAGAT AGGATA--GA GAATCCGTTG ATGAATCTAC CTGTCTCCGA
Mal338          TCT-AACCGT CTTCTTAT-- ---CCTATAA CGAACATAAA TCAATTAGAT GGCAAAAGAT AGGATA--GA GAATCCGTTG ATGAATCTAC CTGTCTCCGA
Mto185          TCT-AACCGT CTTCTTAT-- ---CCTATAA CGAACATAAA TCAATTAGAT GGCAAAAGAT AGGATA--GA GAATCCGTTG ATGAATCTAC CTGTCTCCGA
Mmo593          TCT-AACCGT CTTCTTAT-- ---CCTATAA CGAACATAAA TCAATTAGAT GGCAAAAGAT AGGATA--GA GAATCCGTTG ATGAATCTAC CTGTCTCCGA
Mhi672          TCT-AATCGT CTTCTTAT-- ---CCTATAA CGAACATAAA TCAATTAGAT GGCAAAAGAT AGGATA--GA GAATCCGTTG ATGAATCTAC CTGTCTCCGA
Ahi270          TCT-AACCGT CTTCTTATCT TATCCTATAA CGAACATAAA TCAATTAGAT GGCAAAAGAT AGGATA--GA GAATCCGTTG ATGAATCTAC TTGTCTCCGA
Alo596          TCT-AACCGT CTTCTTATCT TATCCTATAA CGAACATAAA TCAATTAGAT GGCAAAAGAT AGGATA--GA GAATCCGTTG ATGAATCTAC CTGTCTCCGA
AluM53          TCT-AACCGT CTTCTTAT-- ---CCTATAA CGAACATAAA TCAATTAGAT GGCAAAAGAT AGGATA--GA GAATCCGTTG ATGAATCTAC CTGTCTCCGA
Mca572          TCT-AACCGT CTTCTTATCT TATCCTATAA CGAACATAAA TCAATTAGAT GGCAAAAGAT AGGATA--GA GAATCCGTTG ATGAATCTAC TTGTCTCCGA
MMae11          ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Mtr683          ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Mma671          TCT-AACCGT CTTCTTAT-- ---CCTATAA CGAACATAAA TCAATTAGAT GGCAAAAGAT AGGATA--GA GAATCCGTTG ATGAATCTAC CTGTCTCCGA
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Mtf502          TCT-AACCGT CTTCTTAT-- ---CCTATAA CGAACATAAA TCAATTCGAT GGCAAAAGAT AGGATA--GA GAATCCGTTG ATGAATCTAC CTGTCTCCGA
LphM81          TCT-AACCGT CTTCTTAT-- ---CCTATAA CGAACATAAA TCAATTAGAT GGCAAAAGAT AGGATA--GA GAATCCGTTG ATGAATCTAC CTGTCTCCGA
AniM31          ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
MKvi11          TCT-AACCGT CTTCTTAT-- ---CCTATAA CGAACATAAA TCAATTAGAT GGCAAAAGAT AGGATA--GA GAATCCGTTG ATGAATCTAC CTGTCTCCGA
MAros1          TCT-AACCGT CTTCTTAT-- ---CCTATAA CGAACATAAA TCAATTAGAT GGCAAAAGAT AGGATA--GA GAATCCGTTG ATGAATCTAC CTGTCTCCGA
MshM21          TCT-AACCGT CTTCTTAT-- ---CCTATAA CGAACATAAA TCAATTAGAT GGCAAAAGAT AGGATA--GA GAATCCGTTG ATGAATCTAC -----TCCGA


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                       110        120        130        140        150        160        170        180        190        200
MAar11          GGTATCTATT CTTTTTTTAC TAAAATACCT TGTTTTGACT GTATCGCACT ATGTATCATT TAATAACCGA ATAGATCCCC TATCTTTGGT TCAAATCGAA
Aca594          GGTATCTATT CTTTTTTTAC TAAAATACCT TGTTTTGACT GTATCGCACT ATGTATCATT TAATAACCGA ATAGATCCCC TATCTTTGGT TCAAATCGAA
MAof11          GGTATCTATT CTTTTTTTAC TAAAATACCT TGTTTTGACT GTATCGCACT ATGTATCATT TAATAACCGA ATAGATCCCC TATCTTTGGT TCAAATCGAA
Lol451          GGTATCTGTT CTTTTCTTAC TAAAATACCT TGTTTTGACT GTATCGCACT ATGTATCATT TAATAACCGA ATAGATCCCC TATCTTTGGT TCAAATCGAA
Lob144          GGTATCTGTT CTTTTCTTAC TAAAATACCT TGTTTTGACT GTATCGCACT ATGTATCATT TAATAACCGA ATAGATCCCC TATCTTTGGT TCAAATCGAA
Lbr141          GGTATCTGTT CTTTTCTTAC TAAAATACCT TGTTTTGACT GTATCGCACT ATGTATCATT TAATAACCGA ATAGATCCCC TATCTTTGGT TCAAATCGAA
Lag308          GGTATCTGTT CTTTTCTTAC TAAAATACCT TGTTTTGACT GTATCGCACT ATGTATCATT TAATAACCGA ATAGATCCCC TATCTTTGGT TCAAATCGAA
MLtp11          GGTATCTATT CTTTTCTTAC TATAATACCT TGTTTTGACT GTATCGCACT ATGTATCATT TAATAACCGA ATAGGTCCCC TATCTTTGGT TCAAATCGAA
Ltr680          GGTATCTGTT CTTTTCTTAC TAAAATACCT TGTTTTGACT GTATCGCACT ATGTATCATT TAATAACCGA ATAGATCCCC TATCTTTGGT TCAAATCGAA
MLfl11          GGTATCTGTT CTTTTCTTAC TAAAATACCT TGTTTTGACT GTATCGCACT ATGTATCATT TAATAACCGA ATAGATCCCC TATCTTTGGT TCAAATCGAA
LplM57          GGTATCTGTT CTTTTCTTAC TAAAATACCT TGTTTTGACT GTATCGCACT ATGTATCATT TAATAACCGA ATAGATCCCC TATCTTTGGT TCAAATCGAA
Lti472          GGTATCTGTT CTTTTCTTAC TAAAATACCT TGTTTTGACT GTATCGCACT ATGTATCATT TAATAACCAA ATAGATCCCC TATCTTTGGT TCAAATCGAA
LthVie          GGTATCTGTT CTTTTCTTAC TAAAATACCT TGTTTTGACT GTATCGCACT ATGTATCATT TAATAACCGA ATAGATCCCC TATCTTTGGT TCAAATCGAA
MLpu11          GGTATCTGTT CTTTTCTTAC TAAAATACCT TGTTTTGACT GTATCGCACT ATGTATCATT TAATAACCGA ATAGATCCCC TATCTTTGGT TCAAATCGAA
Lmo316          GGTATCTGTT CTTTTCTTAC TAAAATACCT TGTTTTGACT GTATCGCACT ATGTATCATT TAATAACCGA ATAGATCCCC TATCTTTGGT TCAAATCGAA
LacB11          GGTATCTGTT CTTTTCTTAC TAAAATACCT TGTTTTGACT GTATCGCACT ATGTATCATT TAATAACCGA ATAGATCCCC TATCTTTGGT TCAAATCGAA
Lar253          GGTATCTGTT CTTTTCTTAC TAAAATACCT TGTTTTGACT GTATCGCACT ATGTATCATT TAATAACCGA ATAGATCCCC TATCTTTGGT TCAAATCGAA
MLas11          GGTATCTGTT CTTTTCTTAC TAAAATACCT TGTTTTGACT GTATCGCACT ATGTATCATT TAATAACCGA ATAGATCCCC TATCTTTGGT TCAAATCGAA
MLma11          GGTATCTGTT CTTTTCTTAC TAAAATACCT TGTTTTGACT GTATCGCACT ATGTATCATT TAATAACCGA ATAGATCCCC TATCTTTGGT TCAAATCGAA
Lmu283          GGTATCTGTT ATTTTCTTAC TAAAATACCT TGTTTTGACT GTATCGCACT ATGTATCATT TAATAACCGA ATAGATCCCC TATCTTTGGT TCAAATCGAA
MLcr11          GGTATCTGTT CTTTTCTTAC TAAAATACCT TGTTTTGACT GTATCGCACT ATGTATCATT TAATAACCGA ATAGATCCCC TATCTTTGGT TCAAATCGAA
LpebM2          GGTATCTGTT ATTTTCTTAC TAAAATACCT TGTTTTGACT GTATCGCACT ATGTATCATT TAATAACCGA ATAGATCCCC TATCTTTGGT TCAAATCGAA
Mni674          GGTATCTGTT CTTTTCTTAC TAAAATACCT TGTTTTGACT GTATCGCACT ATGTATCATT TAATAACCGA ATAGATCCCC TATCTTTGGT TCAAATCGAA
Mpa603          GGTATCTGTT ATTTTCTTAC TAAAATACCT TGTTTTGACT GTATCGCACT ATGTATCATT TAATAACCGA ATAGATCCCC TATCTTTGGT TCAAATCGAA
Msy597          GGTATCTGTT CTTTTCTTAC TAAAATACCT TGTTTTGACT GTATCGCACT ATGTATCATT TAATAACCGA ATAGATCCCC TATCTTTGGT TCAAATCGAA
Mne795          GGTATCTGTT CTTTTCTTAC TAAAATACCT TGTTTTGACT GTATCGCACT ATGTATCATT TAATAACCGA ATAGATCCCC TATCTTTGGT TCAAATCGAA
Mve442          GGTATCTGTT ATTTTCTTAC TAAAATACCT TGTTTTGACT GTATCGCACT ATGTATCATT TAATAACCGA ATAGATCCCC TATCTTTGGT TCAAATCGAA
Mal338          GGTATCTGTT CTTTTCTTAC TAAAATACCT TGTTTTGACT GTATCGCACT ATGTATCATT TAATAACCGA ATAGATCCCC TATCTTTGGT TCAAATCGAA
Mto185          GGTATCTGTT CTTTTCTTAC TAAAATACCT TGTTTTGACT GTATCGCACT ATGTATCATT TAATAACCGA ATAGATCCCC TATCTTTGGT TCAAATCGAA
Mmo593          GGTATCTGTT CTTTTCTTAC TAAAATACCT TGTTTTGACT GTATCGCACT ATGTATCATT TAATAACCGA ATAGATCCCC TATCTTTGGT TCAAATCGAA
Mhi672          GGTATCTGTT CTTTTCTTAC TAAAATACCT TGTTTTGACT GTATCGCACT ATGTATCATT TAATAACCGA ATAGATCCCC TATCTTTGGT TCAAATCGAA
Ahi270          GGTATCTGTT CTTTTCTTAC TAAAATACCT TGTTTTGACT GTATCGCACT ATGTATCATT TAATAACCGA ATAGATCCCC TATCTTTGGT TCAAATCGAA
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Alo596        GGTATCTGTT CTTTTCTTAC TAAAATACCT TGTTTTGACT GTATCGCACT ATGTATCATT TAATAACCGA ATAGATCCCC TATCTTTGGT TCAAATCGAA
AluM53        GGTATCTGTT CTTTTCTTAC TAAAATACCT TGTTTTGACT GTATCGCACT ATGTATCATT TAATAACCGA ATAGATCCCC TATCTTTGGT TCAAATCGAA
Mca572        GGTATCTGTT CTTTTCTTAC TAAAATACCT TGTTTTGACT GTATCGCACT ATGTATCATT TAATAACCGA ATAGATCCCC TATCTTTGGT TCAAATCGAA
MMae11        ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Mtr683        ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Mma671        GGTATCTATT CTTTTCTTAC TAAAATACCT TGTTTTGACT GTATCGCACT ATGTATCATT TAATAACCGA ATAGATCCCC TATCTTTGGT TCAAATCGAA
Mtf502        GGTATCTATT CTTTTCTTAC TAAAATACCT TGTTTTGACT GTATCGCACT ATGTATCATT TAATAACCGA ATAGATCCCC TATCTTTGGT TCAAATCGAA
LphM81        GGTATCTGTT CTTTTCTTAC TAAAATACCT TGTTTTGACT GTATCGCACT ATGTATCATT TAATAACCGA ATAGATCCCC TATCTTTGGT TCAAATCGAA
AniM31        ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
MKvi11        GGTATCTATT CTTTTTTTAC TAAAATACCT TGTTTTGACT GTATCGCACT ATGTATCATT TAATAACCGA ATAGATCCCC TATCTTTGGT TCAAATCGAA
MAros1        GGTATCTATT CTTTTTTTAC TAAAATACCT TGTTTTGACT GTATCGCACT ATGTATCATT TAATAACCGA ATAGATCCCC TATCTTTGGT TCAAATCGAA
MshM21        GGTATCTATT CTTTTCTTAC TAAAATACCT TGTTTTGACT GTATCGCACT ATGTATCATT TAATAACCGA ATAGATCCCC TATCTTTGGT TCAAATCGAA


              ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     210        220        230        240        250        260        270        280        290        300
MAar11        TTTGAAATGG AGGAAGTTCA AGTCTATTTA GAACTAAATA GATCTCGCCG ACATGATTTC CTATACCCAC TTATTTTTCG GGAGTATATT TATGCACTTG
Aca594        TTTGAAATGG AGGAAGTTCA AGTCTATTTA GAACTAAATA GATCTCGCCG ACATGATTTC CTATACCCAC TTATTTTTCG GGAGTATATT TATGCACTTG
MAof11        TTTGAAATGG AGGAAGTTCA AGTCTATTTA GAACTAAATA GATCTCGCCG ACATGATTTC CTATACCCAC TTATTTTTCG GGAGTATATT TATGCACTTG
Lol451        TTTGAAATGG AGGAAGTTCA AGTATATTTA GAACTAAATA GATCTCGCCG ACATGATTTC CTATACCCAC TTATTTTTCG GGAGTATATT TATGCACTTG
Lob144        TTTGAAATGG AGGAAGTTCA AGTATATTTA GAACTAAATA GATCTCGCCG ACACGATTTC CTATACCCAC TTATTTTTCG GGAGTATATT TATGCACTTG
Lbr141        TTTGAAATGG AGGAAGTTCA AGTATATTTA GAACTAAATA GATCTCGCCG ACATGATTTC CTATACCCAC TTATTTTTCG GGAGTATATT TATGCACTTG
Lag308        TTTGAAATGG AGGAAGTTCA AGTATATTTA GAACTAAATA GATCTCGCCG ACATGATTTC CTATACCCAC TTATTTTTCG GGAGTATATT TATGCACTTG
MLtp11        TTTGAAATGG AGGAATTTCA AGTATATTTA GAACTAAATA GATCTCGCCG ACATGATTTC CTATACCCAC TTATTTTTCG GGAGTATATT TATGCACTTG
Ltr680        TTTGAAATGG AGGAAGTTCA AGTATATTTA GAACTAAATA GATCTCGCCG ACATGATTTC CTATACCCAC TTATTTTTCG GGAGTATATT TATGCACTTG
MLfl11        TTTGAAATGG AGGAAGTTCA AGTATATTTA GAACTAAATA GATCTCGCCG ACATGATTTC CTATACCCAC TTATTTTTCG GGAGTATATT TATGCACTTG
LplM57        TTTGAAATGG AGGAAGTTCA AGTATATTTA GAACTAAATA GATCTCGCCG ACATGATTTC CTATACCCAC TTATTTTTCG GGAGTATATT TATGCACTTG
Lti472        TTTGAAATGG AGGAAGTTCA AGTATATTTA GAACTAAATA GATCTCGCCG ACATGATTTC CTATACCCAC TTATTTTTCG GGAGTATATT TATGCACTTG
LthVie        TTTGAAATGG AGGAAGTTCA AGTATATTTA GAACTAAATA GATCTCGCCG ACATGATTTC CTATACCCAC TTATTTTTCG GGAGTATATT TATGCACTTG
MLpu11        TTTGAAATGG AGGAAGTTCA AGTATATTTA GAACTAAATA GATCTCGCCG ACATGATTTC CTATACCCAC TTATTTTTCG GGAGTATATT TATGCACTTG
Lmo316        TTTGAAATGG AGGAAGTTCA AGTATATTTA GAACTAAATA GATCTCGCCG ACACGATTTC CTATACCCAC TTATTTTTCG GGAGTATATT TATGCACTTG
LacB11        TTTGAAATGG AGGAAGTTCA AGTATATTTA GAACTAAATA GATCTCGCCG ACATGATTTC CTATACCCAC TTATTTTTCG GGAGTATATT TATGCACTTG
Lar253        TTTGAAATGG AGGAAGTTCA AGTATATTTA GAACTAAATA GATCTCGCCG ACATGATTTC CTATACCCAC TTATTTTTCG GGAGTATATT TATGCACTTG
MLas11        TTTGAAATGG AGGAAGTTCA AGTATATTTA GAACTAAATA GATCTCGCCG ACATGATTTC CTATACCCAC TTATTTTTCG GGAGTATATT TATGCACTTG
MLma11        TTTGAAATGG AGGAAGTTCA AGTATATTTA GAACTAAATA GATCTCGCCG ACATGATTTC CTATACCCAC TTATTTTTCG GGAGTATATT TATGCACTTG
Lmu283        TTTGAAATGG AGGAAGTTCA AGTATATTTA GAACTAAATA GATCTCGCCG ACATGATTTC CTATACCCAC TTATTTTTCG GGAGTATATT TATGCACTTG
MLcr11        TTTGAAATGG AGGAAGTTCA AGTATATTTA GAACTAAATA GATCTCGCCG ACATGATTTC CTATACCCAC TTATTTTTCG GGAGTATATT TATGCACTTG
LpebM2        TTTGAAATGG AGGAAGTTCA AGTATATTTA GAACTAAATA GATCTCGCCG ACATGATTTC CTATACCCAC TTATTTTTCG GGAGTATATT TATGCACTTG
Mni674        TTTGAAATGG AGGAAGTTCA AGTATATTTA GAACTAAATA GATCTCGCCG ACATGATTTC CTATACCCAC TTATTTTTCG GGAGTATATT TATGCACTTG
Mpa603        TTTGAAATGG AGGAAGTTCA AGTATATTTA GAACTAAATA GATCTCGCCG ACATGATTTC CTATACCCAC TTATTTTTCG GGAGTATATT TATGCACTTG
Msy597        TTTGAAATGG AGGAAGTTCA AGTATATTTA GAACTAAATA GATCTCGCCG ACATGATTTC CTATACCCAC TTATTTTTCG GGAGTATATT TATGCACTTG
Mne795        TTTGAAATGG AGGAAGTTCA AGTATATTTA GAACTAAATA GATCTCGCCG ACATGATTTC CTATACCCAC TTATTTTTCG GGAGTATATT TATGCACTTG
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Mve442      TTTGAAATGG AGGAAGTTCA AGTATATTTA GAACTAAATA GATCTCGCCG ACATGATTTC CTATACCCAC TTATTTTTCG GGAGTATATT TATGCACTTG
Mal338      TTTGAAATGG AGGAAGTTCA AGTATATTTA GAACTAAATA GATCTCGCCG ACATGATTTC CTATACCCAC TTATTTTTCG GGAGTATATT TATGCACTTG
Mto185      TTTGAAATGG AGGAAGTTCA AGTATATTTA GAACTAAATA GATCTCGCCG ACATGATTTC CTATACCCAC TTATTTTTCG GGAGTATATT TATGCACTTG
Mmo593      TTTGAAATGG AGGAAGTTCA AGTATATTTA GAACTAAATA GATCTCGCCG ACATGATTTC CTATACCCAC TTATTTTTCG GGAGTATATT TATGCACTTG
Mhi672      TTTGAAATGG AGGAAGTTCA AGTATATTTA GAACTGAATA GATCTCGCCG ACATGATTTC CTATACCCAC TTATTTTTCG GGAGTATATT TATGCACTTG
Ahi270      TTTGAAATGG AGGAAGTTCA AGTATATTTA GAACTAAATA GATCTCGCCG ACATGATTTC CTATACCCAC TTATTTTTCG GGAGTATATT TATGCACTTG
Alo596      TTTGAAATGG AGGAAGTTCA AGTATATTTA GAACTAAATA GATCTCGCCG ACATGATTTC CTATACCCAC TTATTTTTCG GGAGTATATT TATGCACTTG
AluM53      TTTGAAATGG AGGAAGTTCA AGTATATTTA GAACTAAATA AATCTCGCCG ACATGATTTC CTATACCCAC TTATTTTTCG GGAGTATATT TATGCACTTG
Mca572      TTTGAAATGG AGGAAGTTCA AGTATATTTA GAACTAAATA GATCTCGCCG ACATGATTTC CTATACCCAC TTATTTTTCG GGAGTATATT TATGCACTTG
MMae11      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Mtr683      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Mma671      TTTGAAATGG AGGAAGTTCA AGTATATTTA GAACTAAATA GATCTCGCCG ACATGATTTC CTATACCCAC TTATTTTTCG GGAGTATATT TATGCACTTG
Mtf502      TTTGAAATGG AGGAAGTTCA AGTATATTTA GAACTAAATA GATCTCGCCG ACATGATTTC CTATACCCAC TTATTTTTCG GGAGTATATT TATGCACTTG
LphM81      TTTGAAATGG AGGAAGTTCA AGTATATTTA GAACTAAATA GATCTCGCCG ACATGATTTC CTATACCCAC TTATTTTTCG GGAGTATATT TATGCACTTG
AniM31      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
MKvi11      TTTGAAATGG AGGAAGTTCA AGTCTATTTA GAACTAAATA GATCTCGCCG ACATGATTTC CTATACCCAC TTATTTTTCG GGAGTATATT TATGCACTTG
MAros1      TTTGAAATGG AGGAAGTTCA AGTCTATTTA GAACTAAATA GATCTCGCCG ACATGATTTC CTATACCCAC TTATTTTTCG GGAGTATATT TATGCACTTG
MshM21      TTTGAAATGG AGGAAGCTCA AGTCTATTTA GAACTAAATA GATCTCGCCG ACATGATTTC CTATACCCAC TTATTTTTCG GGAGTATATT TATGCACTTG


            ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   310        320        330        340        350        360        370        380        390        400
MAar11      CTCATGATCA TGGTTT-AAA TAAATCGATG ATTTTTTTGG AAAATCGGGG TTATGGTAAT AAATTTAGTT CACTAATTGT GAAACGCTTA ATTATTCGAA
Aca594      CTCATGATCA TGGTTT-AAA TAAATCGATG ATTTTTTTGG AAAATCGGGG TTATGGTAAT AAATTTAGTT CACTAATTGT GAAACGCTTA ATTATTCGAA
MAof11      CTCATGATCA TGGTTT-AAA TAAATCGATG ATTTTTTTGG AAAATCGGGG TTATGGTAAT AAATTTAGTT CACTAATTGT GAAACGCTTA ATTATTCGAA
Lol451      CTCATGATCA TGGTTT-AAA TAAATCGATG ATTTTTTTGG AAAATCGGGA TTATCGTAAT AAATTCAGTT CACTAATTGT GAAACGCTTA ATTATTCGAA
Lob144      CTCATGATCA TGGTTT-AAA TAAATCGATG ATTTTTTTGG AAAATCGGGA TTATCGTAAT AAATTCAGTT CACTAATTGT GAAACGCTTA ATTATTCGAA
Lbr141      CTCATGATCA TGGTTT-AAA TAAATCGATG ATTTTTTTGG AAAATCGGGA TTATCGTAAT AAATTCAGTT CACTAATTGT GAAACGCTTA ATTATTCGAA
Lag308      CTCATGATCA TGGTTT-AAA TAAATCGATG ATTTTTTTGG AAAATCGGGA TTATCGTAAT AAATTCAGTT CACTAATTGT GAAACGCTTA ATTATTCGAA
MLtp11      CTCATGATCA TGGTTT-AAA TAAATCGATG ATTTTTTTGG AAAATCGGGG TTGTGGTAAT AAATTCAGTT CACTAATTGT GAAACGCTTA ATTATTCGAA
Ltr680      CTCATGATCA TGGTTT-AAA TAAATCGATG ATTTTTTTGG AAAATCGGGA TTATCGTAAT AAATTCAGTT CACTAATTGT GAAACGCTTA ATTATTCGAA
MLfl11      CTCATGATCA TAGTTT-AAA TAAATCGATG ATTTTTTTGG AAAATCGGGA TTATCGTAAT AAATTCAGTT CACTAATTGT GAAACGCTTA ATTATTCGAA
LplM57      CTCATGATCA TGGTTT-AAA TAAATCGATG ATTTTTTTGG AAAATCGGGA TTATCGTAAT AAATTCAGTT CACTAATTGT GAAACGCTTA ATTATTCGAA
Lti472      CTCATGATCA TGGTTT-AAA TAAATCGATG ATTTTTTTGG AAAATCGGGA TTATCGTAAT AAATTCAGTT CACTAATTGT GAAACGCTTA ATTATTCGAA
LthVie      CTCATGA-CA TGGTAAAAAA TAAATCGATG ATTTTTTTGG AAAATCGGGA TTATCGTAAT AAATTCAGTT CACTAATTGT GAAACGCTTA ATTATTCGAA
MLpu11      CTCATGATCA TGGTTT-AAA TAAATCGATG ATTTTTTTGG AAAATCGGGA TTATCGTAAT AAATTCAGTT CACTAATTGT GAAACGCTTA ATTATTCGAA
Lmo316      CTCATGATCA TGGTTT-AAA TAAATCGATG ATTTTTTTGG AAAATCGGGA TTATCGTAAT AAATTCAGTT CACTAATTGT GAAACGCTTA ATTATTCGAA
LacB11      CTCATGATCA TGGTTT-AAA TAAATCGATG ATTTTTTTTG AAAATCGGGA TTATCGTAAT AAATTCAGTT CACTAATTGT GAAACGCTTA ATTATTCGAA
Lar253      CTCATGATCA TGGTTT-AAA TAAATCGATG ATTTTTTTGG AAAATCGGGA TTATCGTAAT AAATTCAGTT CACTAATTGT GAAACGCTTA ATTATTCGAA
MLas11      CTCATGATCA TGGTTT-AAA TAAATCGATG ATTTTTTTGG AAAATCGGGA TTATCGTAAT AAATTCAGTT CACTAATTGT GAAACGCTTA ATTATTCGAA
MLma11      CTCATGATCA TGGTTT-AAA TAAATCGATG ATTTTTTTGG AAAATCGGGA TTATCGTAAT AAATTCAGTT CACTAATTGT GAAACGCTTA ATTATTCGAA
Lmu283      CTCATGATCA TGGTTT-AAA TAAATCGATG ATTTTTTTGG AAAATCGGGA TTATCGTAAT AAATTCAGTT CACTAATTGT GAAACGCTTA ATTATTCGAA
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MLcr11          CTCATGATCA TGGTTT-AAA TAAATCGATG ATTTTTTTGG AAAATCGGGA TTATCGTAAT AAATTCAGTT CACTAATTGT GAAACGCTTA ATTATTCGAA
LpebM2          CTCATGATCA TGGTTT-AAA TAAATCGATG ATTTTTTTGG AAAATCGGGA TTATCGTAAT AAATTCAGTT CACTAATTGT GAAACGCTTA ATTATTCGAA
Mni674          CTCATGATCA TGGTTT-AAA TAAATCGACG ATTTATTTGG AAAATCGGGA TTATCGTAAT AAATTCAGTT CACTAATTGT GAAACGCTTA ATTATTCGAA
Mpa603          CTCATGATCA TGGTTT-AAA TAAATCGATG ATTTTTTTGG AAAATCGGGA TTATCGTAAT AAATTCAGTT CACTAATTGT GAAACGCTTA ATTATTCGAA
Msy597          CTCATGATCA TGGTTT-AAA TAAATCGATG ATTTTTTTGG AAAATCGGGA TTATCGTAAT AAATTCAGTT CACTAATTGT GAAACGCTTA ATTATTCGAA
Mne795          CTCATGATCA TGGTTT-AAA TAAATCGATG ATTTTTTTGG AAAATCGGGA TTATCGTAAT AAATTCAGTT CACTAATTGT GAAACGCTTA ATTATTCGAA
Mve442          CTCATGATCA TGGTTT-AAA TAAATCGATG ATTTTTTTGG AAAATCGGGA TTATCGTAAT AAATTCAGTT CACTAATTGT GAAACGCTTA ATTATTCGAA
Mal338          CTCATGATCA TGGTTT-AAA TAAATCGATG ATTTTTTTGG AAAATCGGGA TTATCGTAAT AAATTCAGTT CACTAATTGT GAAACGCTTA ATTATTCGAA
Mto185          CTCATGATCA TGGTTT-AAA TAAATCGATG ATTTTTTTGG AAAATCGGGA TTATCGTAAT AAATTCAGTT CACTAATTGT GAAACGCTTA ATTATTCGAA
Mmo593          CTCATGATCA TGGTTT-AAA TAAATCGATG ATTTTTTTGG AAAATCGGGA TTATCGTAAT AAATTCAGTT CACTAATTGT GAAACGCTTA ATTATTCGAA
Mhi672          CTCATGATCA TGGTTT-AAA TAAATCGATG ATTTTTTTGG AAAATCGGGA TTATCGTAAT AAATTCAGTT CACTAATTGT GAAACGCTTA ATTATTCGAA
Ahi270          CTCATGATCA TGGTTT-AAA TAAATCGATG GTTTTTTTGG AAAATAGGGA TTATCGTAAT AAATTCAGTT CACTAATTGT GAAACGCTTA ATTATTCGAA
Alo596          CTCATGATCA TGGTTT-AAA TAAATCGATG GTTTTTTTGG AAAATCGGGA TTATCGTAAT AAATTCAGTT CACTAATTGT GAAACGCTTA ATTATTCGAA
AluM53          CTCATGATCA TGGTTT-AAA TAAATCGATG GTTTTTTTGG AAAATCGGGA TTATCGTAAT AAATTCAGTT CACTAATTGT GAAACGCTTA ATTATTCGAA
Mca572          CTCATGATCA TGGTTT-AAA TAAATCGATG GTTTTTTTGG AAAATAGGGA TTATCGTAAT AAATTCAGTT CACTAATTGT GAAACGCTTA ATTATTCGAA
MMae11          ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- -----TCGAA
Mtr683          ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----TTCGAA
Mma671          CTCATGATCA TGGTTT-AAA TAAATCGATG ATTTTTTTGG AAAATCGGGG TTATCGTAAT AAATTCAGTT CACTAATTGT GAAACGCTTA ATTATTCGAA
Mtf502          CTCATGATCA TGGTTT-AAA TAAATCGATG ATTTTTTTGG AAAATCGGGG TTATCGTAAT AAATTCAGTT CACTAATTGT GAAACGCTTA ATTATTCGAA
LphM81          CTCATGATCA TGGTTT-AAA TAAATCGATG ATTTTTTTGG AAAATCGGGA TTATCGTAAT AAATTCAGTT CACTAATTGT GAAACGCTTA ATTATTCGAA
AniM31          ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
MKvi11          CTCATGATCA TGGTTT-AAA TAAATCGATG ATTTTTTTGG AAAATCGTGG TTATGGTAAT AAATTCAGTT CACTAATTGT GAAACGCTTA ATTATTCGAA
MAros1          CTCATGATCA TGGTTT-AAA TAAATCGATG ATTTTTTTGG AAAATCGGGG TTATGGTAAT AAATTCAGTT CACTAATTGT GAAACGCTTA ATTATTCGAA
MshM21          CTCATGATCA TGGTTT-AAA TAAATCGATG CTTTTTTTGG AAAATCGGGG TTATGGTAAT AAATTCAGTT CACTAATTGT GAAACGCTTA ATTATTGGAA


                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                       410        420        430        440        450        460        470        480        490        500
MAar11          TGGATCAACA GAATCATTTG AGTATTTCTG CTAATGATTC TAACCAAAAT CCATTTTTTG GGCACAACAA TAATTTGTAT TCTCAAATGA TATCGGCGGG
Aca594          TGGATCAACA GAATCATTTG AGTATTTCTG CTAATGATTC TAACCAAAAT CCATTTTTTG GGCACAACAA TAATTTGTAT TCTCAAATGA TATCGGCGGG
MAof11          TGGATCAACA GAATCATTTG AGTATTTCTG CTAATGATTC TAACCAAAAT CCATTTTTTG GGCACAACAA TAATTTGTAT TCTCAAATGA TATCGGCGGG
Lol451          TGGATCAACA GAATCATTTG AGTATTTCTG CTAATGATTC TAACCAAAAT CCATTTTTTG GGCACAACAA TAATTTGTAT TCTCAAATGA TATCGGCGGG
Lob144          TGGATCAACA GAATCATTTG AGTATTTCTG CTAATGATTC TAACCAAAAT CCATTTTTTG GGCACAACAA TAATTTGTAT TCTCAAATGA TATCGGCGGG
Lbr141          TGGATCAACA GAATCATTTG AGTATTTCTG CTAATGATTC TAACCAAAAT CCATTTTTTG GGCACAACAA TAATTTGTAT TCTCAAATGA TATCGGCGGG
Lag308          TGGATCAACA GAATCATTTG AGTATTTCTG CTAATGATTC TAACCAAAAT CCATTTTTTG GGCACAACAA TAATTTGTAT TCTCAAATGA TATCGGCGGG
MLtp11          TGGATCAACA GAATCATTTG ATTATTTCTG CTAATGATTC TAACCAAAAT CCATTTTTTG GGCACAACAA TCATTTGTAT TCTCAAATGA TATCGGCGGG
Ltr680          TGGATCAACA GAATCATTTG AGTATTTCTG CTAATGATTC TAACCAAAAT CCATTTTTTG GGCACAACAA TAATTTGTAT TCTCAAATGA TATCGGCGGG
MLfl11          TGGATCAACA GAATCATTTG AGTATTTCTG CTAATGATTC TAACCAAAAT CCATTTTTTG GGCACAACAA TAATTTGTAT TCTCAAATGA TATCGGCGGG
LplM57          TGGATCAACA GAATCATTTG AGTATTTCTG CTAATGATTC TAACCAAAAT CCATTTTTTG GGCACAACAA TAATTTGTAT TCTCAAATGA TATCGGCGGG
Lti472          TGGATCAACA GAATCATTTG AGTATTTCTG CTAATGATTC TAACCAAAAT CCATTTTTTG GGCACAACAA TAATTTGTAT TCTCAAATGA TATCGGCGGG
LthVie          TGGATCAACA GAATCATTTG AGTATTTCTG CTAATGATTC TAACCAAAAT CCATTTTTTG GGCACAACAA TAATTTGTAT TCTCAAATGA TATCGGCGGG
MLpu11          TGGATCAACA GAATCATTTG AGTATTTCTG CTAATGATTC TAACCAAAAT CCATTTTTTG GGCACAACAA TAATTTGTAT TCTCAAATGA TATCGGCGGG
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Lmo316      TGGATCAACA GAATCATTTG AGTATTTCTG CTAATGATTC TAACCAAAAT CCATTTTTTG GGCACAACAA TAATTTGTAT TCTCAAATGA TATCGGCGGG
LacB11      TGGATCAACA GAATCATTTG AGTATTTCTG CTAATGATTC TAACCAAAAT CCATTTTTTG GGCACAACAA TAATTTGTAT TCTCAAATGA TATCGGCGGG
Lar253      TGGATCAACA GAATCATTTG AGTATTTCTG CTAATGATTC TAACCAAAAT CCATTTTTTG GGCACAACAA TAATTTGTAT TCTCAAATGA TATCGGCGGG
MLas11      TGGATCAACA GAATCATTTG AGTATTTCTG CTAATGATTC TAACCAAAAT CCATTTTTTG GGCACAACAA TAATTTGTAT TCTCAAATGA TATCGGCGGG
MLma11      TGGATCAACA GAATCATTTG AGTATTTCTG CTAATGATTC TAACCAAAAT CCATTTTTTG GGCACAACAA TAATTTGTAT TCTCAAATGA TATCGGCGGG
Lmu283      TGGATCAACA GAATCATTTG AGTATTTCTG CTAATGATTC TAACCAAAAT CCATTTTTTG GGCACAACAA TAATTTGTAT TCTCAAATGA TATCGGCGGG
MLcr11      TGGATCAACA GAATCATTTG AGTATTTCTG CTAATGATTC TAACCAAAAT CCATTTTTTG GGCACAACAA TAATTTGTAT TCTCAAATGA TATCGGCGGG
LpebM2      TGGATCAACA GAATCATTTG AGTATTTCTG CTAATGATTC TAACCAAAAT CCATTTTTTG GGCACAACAA TAATTTGTAT TCTCAAATGA TATCGGCGGG
Mni674      TGGATCAACA GAATCATTTG AGTATTTCTG CTAATGATTC TAACCAAAAT CCATTTTTTG GGCACAACAA TAATTTGTAT TCTCAAATGA TATCGGCGGG
Mpa603      TGGATCAACA GAATCATTTG AGTATTTCTG CTAATGATTC TAACCAAAAT CCATTTTTTG GGCACAACAA TAATTTGTAT TCTCAAATGA TATCGGCGGG
Msy597      TGGATCAACA GAATCATTTG AGTATTTCTG CTAATGATTC TAACCAAAAT CCATTTTTTG GGCACAACAA TAATTTGTAT TCTCAAATGA TATCGGCGGG
Mne795      TGGATCAACA GAATCATTTG AGTATTTCTG CTAATGATTC TAACCAAAAT CCATTTTTTG GGCACAACAA TAATTTGTAT TCTCAAATGA TATCGGCGGG
Mve442      TGGATCAACA GAATCATTTG AGTATTTCTG CTAATGATTC TAACCAAAAT CCATTTTTTG GGCACAACAA TAATTTGTAT TCTCAAATGA TATCGGCGGG
Mal338      TGGATCAACA GAATCATTTG AGTATTTCTG CTAATGATTC TAACCAAAAT CCATTTTTTG GGCACAACAA TAATTTGTAT TCTCAAATGA TATCGGCGGG
Mto185      TGGATCAACA GAATCATTTG AGTATTTCTG CTAATGATTC TAACCAAAAT CCATTTTTTG GGCACAACAA TAATTTGTAT TCTCAAATGA TATCGGCGGG
Mmo593      TGGATCAACA GAATCATTTG AGTATTTCTG CTAATGATTC TAACCAAAAT CCATTTTTTG GGCACAACAA TAATTTGTAT TCTCAAATGA TATCGGCGGG
Mhi672      TGGATCAACA GAATCATTTG AGTATTTCTG CTAATGATTC TAACCAAAAT CCATTTTTTG GGCACAACAA TAATTTGTAT TCTCAAATGA TATCGGCGGG
Ahi270      TGGATCAACA GAATCATTTG AGTATTTCTG CTAATGATTC TAACCAAAAT CCATTTTTTG GGCACAACAA TAATTTGTAT TCTCAAATGA TATCGGCGGG
Alo596      TGGATCAACA GAATCATTTG AGTATTTCTG CTAATGATTC TAACCAAAAT CCATTTTTGG GGCACAACAA TAATTTGTAT TCTCAAATGA TATCGGCGGG
AluM53      TGGATCAACA GAATCATTTG AGTATTTCTG CTAATGATTC GAACCAAAAT CCATTTTTTG GGCACAACAA TAATTTGTAT TCTCAAATGA TATCGGCGGG
Mca572      TGGATCAACA GAATCATTTG AGTATTTCTG CTAATGATTC TAACCAAAAT CCATTTTTTG GGCACAACAA TAATTTGTAT TCTCAAATGA TATCGGCGGG
MMae11      TGGATCAACA GAATCATTTG AGTATTTCTG CTAATGATTC TAACCAAAAT CCATTTTTTG GGCACAACAA TAATTTGTAT TCTCAAATGA TATCGGCGGG
Mtr683      TGGATCAACA GAATCATTTG AGTATTTCTG CTAATGATTC TAACCAAAAT CCATTTTTTG GGCACAACAA TAATTTGTAT TCTCAAATGA TATCGGCGGG
Mma671      TGGATCAACA GAATCATTTG AGTATTTCTG CTAATGATTC TAACCAAAAT CCATTTTTTG GACACaAGAa tAATTTGTAT TCTCAAATGA TATCGGCGGG
Mtf502      TGGATCAACA GCATCATTTG AGTATTTCTG CTAATGATTC TAACCAAAAT CCATTTTTTG GACACAAGAA TaatTTGTAT TCTCAAATGA TATCGGCGGG
LphM81      TGGATCAACA GAATCATTTG AGTATTTCTG CTAATGATTC TAACCAAAAT CCATTTTTTG GGCACAACAA TAATTTGTAT TCTCAAATGA TATCGGCGGG
AniM31      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
MKvi11      TGGATCAACA GAATCATTTG AGTATTTCTG CTAATGATTC TAACCAAAAT CCATTTTTTG GGCACAACAA TAATTTGTAT TCTCAAATGA TATCGGCGGG
MAros1      TGGATCAACA GAATCATTTG AGTATTTCTG CTAATGATTC TAACCAAAAT CCATTTTTTG GGCACAACAA TAATTTGTAT TCTCAAATGA TATCGGCGGG
MshM21      TGGATCAACA GAATCATTTG AGTATTTCTG CTAATGATTC TAACCAAAAT CCATTTTTTG GGCACAACAA TAATTTGTAT TCTCAAATGA TATCGGCGGG


            ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   510        520        530        540        550        560        570        580        590        600
MAar11      ATTTGGAGTC ATTGTGGAAA TTCCATTTTC CTTACGATTA GTATCTTACT CACAAGGGGA AGAAGTCGCA AAATCTCAAA ATTTACAATC AATTCATTCA
Aca594      ATTTGGAGTC ATTGTGGAAA TTCCATTTTC CTTACGATTA GTATCTTACT CACAAGGGGA AGAAGTCGCA AAATCTCAAA ATTTACAATC AATTCATTCA
MAof11      ATTTGGAGTC ATTGTGGAAA TTCCATTTTC CTTACGATTA GTATCTTACT CACAAGGGGA AGAAGTCGCA AAATCTCAAA ATTTACAATC AATTCATTCA
Lol451      ATTTGGAGTC ATTGTGGAAA TTCCATTTTC CTTACGATTA GTATCTTACT CACAAGAGGA AGAAGTCGCA AAATCTCATA ATTTACAATC AATTCATTCA
Lob144      ATTTGGAGTC ATTGTGGAAA TTCCATTTTC CTTACGATTA GTATCTTACT CACAAGAGGA AGAAGTCGCA AAATCTCATA ATTTACAATC AATTCATTCA
Lbr141      ATTTGGAGTC ATTGTGGAAA TTCCATTTTC CTTACGATTA GTATCTTACT CACAAGAGGA AGAAGTCGCA AAATCTCATA ATTTACAATC AATTCATTCA
Lag308      ATTTGGAGTC ATTGTGGAAA TTCCATTTTC CTTACGATTA GTATCTTACT CACAAGAGGA AGAAGTCGCA AAATCTCATA ATTTACAATC AATTCATTCA
MLtp11      ATTTGGAGTC GTTGTGGAAA TTCCATTTTC CTTGCGATTA GTATCTTACT CACAAGGGGA AGAAGTCGCA AAATCTCATA ATTTACAATC AATTCATTCA
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Ltr680          ATTTGGAGTC ATTGTGGAAA TTCCATTTTC CTTACGATTA GTATCTTACT CACAAGAGGA AGAAGTCGCA AAATCTCATA ATTTACAATC AATTCATTCA
MLfl11          ATTTGGAGTC ATTGTGGAAA TTCCATTTTC CTTACGATTA GTATCTTACT CACAAGGGGA AGAAGTCGCA AAATCTCATA ATTTACAATC AATTCATTCA
LplM57          ATTTGGAGTC ATTGTGGAAA TTCCATTTTC CTTACGATTA GTATCTTACT CACAAGAGGA AGAAGTCGCA AAATCTCATA ATTTACAATC AATTCATTCA
Lti472          ATTTGGAGTC ATTGTGGAAA TTCCATTTTC CTTACGATTA GTATCTTACT CACAAGGGGA AGAAGTCGCA AAATCTCATA ATTTACAATC AATTCATTCA
LthVie          ATTTGGAGTC ATTGTGGAAA TTCCATTTTC CTTACGATTA GTATCTTACT CACAAGAGGA AGAAGTCGCA AAATCTCATA ATTTACAATC AATTCATTCA
MLpu11          ATTTGGAGTC ATTGTGGAAA TTCCATTTTC CTTACGATTA GTATCTTACT CACAAGGGGA AGCAGTCGCA AAATCTCATA ATTTACAATC AATTCATTCA
Lmo316          ATTTGGAGTC ATTGTGGAAA TTCCATTTTC CTTACGATTA GTATCTTACT CACAAGGGGA AGAAGTCGCA AAATCTCATA ATTTACAATC AATTCATTCA
LacB11          ATTTGGAGTC ATTGTGGAAA TTCCATTTTC CTTACGATTA GTATCTTACT CACAAGGGGA AGAAGTCGCA AAATCTCATA ATTTACAATC AATTCATTCA
Lar253          ATTTGGAGTC ATTGTGGAAA TTCCATTTTC CTTACGATTA GTATCTTACT CACAAGGGGA AGAAGTCGCA AAATCTCATA ATTTACAATC AATTCATTCA
MLas11          ATTTGGAGTC ATTGTGGAAA TTCCATTTTC CTTACGATTA GTATCTTACT CACAAGGGGA AGAAGTCGCA AAATCTCATA ATTTACAATC AATTCATTCA
MLma11          ATTTGGAGTC ATTGTGGAAA TTCCATTTTC CTTACGATTA GTATCTTACT CACAAGGGGA AGAAGTCGCA AAATCTCATA ATTTACAATC AATTCATTCA
Lmu283          ATTTGGAGTC ATTGTGGAAA TTCCATTTTC CTTACGATTA GTATCTTACT CACAAGGGGA AGAAGTCGCA AAATCTCATA ATTTACAATC AATTCATTCA
MLcr11          ATTTGGAGTC ATTGTGGAAA TTCCATTTTC CTTACGATTA GTATCTTACT CACAAGGGGA AGAAGTCGCA AAATCTCATA ATTTACAATC AATTCATTCA
LpebM2          ATTTGGAGTC ATTGTGGAAA TTCCATTTTC CTTACGATTA GTATCTTACT CACAAGGGGA AGAAGTCGCA AAATCTCATA ATTTACAATC AATTCATTCA
Mni674          ATTTGGAGTC ATTGTGGAAA TTCCATTTTC CTTACGATTA GTATCTTACT CACAAGGGGA AGAAGTCGCA AAATCTCATA ATTTACAATC AATTCATTCA
Mpa603          ATTTGGAGTC ATTGTGGAAA TTCCATTTTC CTTACGATTA GTATCTTACT CACAAGGGGA AGAAGTCGCA AAATCTCATA ATTTACAATC AATTCATTCA
Msy597          ATTTGGAGTC ATTGTGGAAA TTCCATTTTC CTTAAGATTA GTATCTTACT CACAAGGGGA AGAAGTCGCA AAATCTCATA ATTTACAATC AATTCATTCA
Mne795          ATTTGGAGTC ATTGTGGAAA TTCCATTTTC CTTAAGATTA GTATCTTACT CACAAGGGGA AGAAGTCGCA AAATCTCATA ATTTACAATC AATTCATTCA
Mve442          ATTTGGAGTC ATTGTGGAAA TTCCATTTTC CTTACGATTA GTATCTTACT CACAAGGGGA AGAAGTCGCA AAATCTCATA ATTTACAATC AATTCATTCA
Mal338          ATTTGGAGTC ATTGTGGAAA TTCCATTTTC CTTACGATTA GTATCTTACT CACAAGGGGA AGAAGTCGCA AAATCTCATA ATTTACAATC AATTCATTCA
Mto185          ATTTGGAGTC ATTGTGGAAA TTCCATTTTC CTTACGATTA GTATCTTACT CACAAGGGGA AGAAGTCGCA AAATCTCATA ATTTACAATC AATTCATTCA
Mmo593          ATTTGGAGTC ATTGTGGAAA TTCCATTTTC CTTACGATTA GTATCTTACT CACAAGGGGA AGAAGTCGCA AAATCTCATA ATTTACAATC AATTCATTCA
Mhi672          ATTTGGAGTC ATTGTGGAAA TTCCATTTTC CTTACGATTA GTATCTTACT CACAAGGGGA AGAAGTCGCA AAATCTCATA ATTTACAATC AATTCATTCA
Ahi270          ATTTGGAGTC ATTGTGGAAA TTCCATTTTC CTTACGATTA GTATCTTACT CACAAGGGGA AGAAGTCGCA AAATCTCATA ATTTACAATC AATTCATTCA
Alo596          ATTTGGAGTC ATTGTGGAAA TTCCATTTTC CTTACGATTA GTATCTTACT CACAAGGGGA AGAAGTCGCA AAATCTCATA ATTTACAATC AATTCATTCA
AluM53          ATTTGGAGTC ATTGTGGAAA TTCCATTTTC CTTACGATTA GTATCTTACT CACAAGGGGA AGAAGTCGCA AAATCTCATA ATTTACAATC AATTCATTCA
Mca572          ATTTGGAGTC ATTGTGGAAA TTCCATTTTC CTTACGATTA GTATCTTACT CACAAGGGGA AGAAGTCGCA AAATCTCATA ATTTACAATC AATTCATTCA
MMae11          ATTTGGAGTC ATTGTGGAAA TTCCATTTTC CTTACGATTA GTATCTTACT CACAAGGGGA AGAAGTCGCA AAATCTCATA ATTTACAATC AATTCATTCA
Mtr683          ATTTGGAGTC ATTGTGGAAA TTCCATTTTC CTTACGATTA GTATCTTACT CACAAGGGGA AGAAGTCGCA AAATCTCATA ATTTACAATC AATTCATTCA
Mma671          ATTTGGAGTC ATTGTGGAAA TTCCATTTTC CTTACGATTA GTATCTTACT CACAAGGGGA AGAAGTCGCA AAATCTCATA ATTTACAATC AATTCATTCA
Mtf502          ATTTGGAGTC ATTGTGGAAA TTCCATTTTC CTTACGATTA GTATCTTACT CACAAGGGGA AGAAGTCGCA AAATCTCATA ATTTACAATC AATTCATTCA
LphM81          ATTTGGAGTC ATTGTGGAAA TTCCATTTTC CTTACGATTA GTATCTTACT CACAAGGGGA AGAAGTCGCA AAATCTCATA ATTTACAATC AATTCATTCA
AniM31          ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
MKvi11          ATTTGGAGTC ATTGTGGAAA TTCCATTTTC CTTACGATTA GTATCTTACT CACAAGGGGA AGAAGTCGCA AAATCTCATA ATTTACAATC AATTCATTCA
MAros1          ATTTGGAGTC ATTGTGGAAA TTCCATTTTC CTTACGATTA GTATCTTACT CACAAGGGGA AGAAGTCGCA AAATCTCATA ATTTACAATC AATTCATTCA
MshM21          ATTTGGAGTC ATTGTGGAAA TTCCATTTTC CTTACGATTA GTATCTTACT CACAAGGGGA AGAAGTCGCA AAATCTCATA ATTTACAATC AATTCATTCA


                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                       610        620        630        640        650        660        670        680        690        700
MAar11          ATATTTCCTT TTTTCGAGGA CAAATTCTCG CATTTAAATT ATGTGTTAGA GGTACTAATA CCTCATCCCA TCCATCTAGA AATCTTAGTT CAAGCCCTTC
Aca594          ATATTTCCTT TTTTCGAGGA CAAATTCTCG CATTTAAATT ATGTGTTAGA GGTACTAATA CCTCATCCCA TCCATCTAGA AATCTTAGTT CAAGCCCTTC
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MAof11          ATATTTCCTT TTTTCGAGGA CAAATTCTCG CATTTAAATT ATGTGTTAGA GGTACTAATA CCTCATCCCA TCCATCTAGA AATCTTAGTT CAAGCCCTTC
Lol451          ATATTTCCTT TTTTCGAGGA CAAATTCTCG CATTTAAATT ATGTGTTAGA GGTACTAATA CCTCATCCCA TCCATCTAGA AATCTTAGTT CAAGCCCTTC
Lob144          ATATTTCCTT TTTTCGAGGA CAAATTCTCG CATTTAAATT ATGTGTTAGA GGTACTAATA CCTCATCCCA TCCATCTAGA AATCTTAGTT CAAGCCCTTC
Lbr141          ATATTTCCTT TTTTCGAGGA CAAATTCTCG CATTTAAATT ATGTGTTAGA GGTACTAATA CCTCATCCCA TCCATCTAGA AATCTTAGTT CAAGCCCTTC
Lag308          ATATTTCCTT TTTTCGAGGA CAAATTCTCG CATTTAAATT ATGTGTTAGA GGTACTAATA CCTCATCCCA TCCATCTAGA AATCTTAGTT CAAGCCCTTC
MLtp11          ATATTTCCTT TTTTAGAGGA CAAATTCTCA CATTTAAATT ATGTGTTAGA GGTACTAATA CCTCATCCCA TCCATCTAGA AATCTTAGTT CAAGCCCTTC
Ltr680          ATATTTCCTT TTTTCGAGGA CAAATTCTCG CATTTAAATT ATGTGTTAGA GGTACTAATA CCTCATCCCA TCCATCTAGA AATCTTAGTT CAAGCCCTTC
MLfl11          ATATTTCCTT TTTTCGAGGA CAAATTCTCG CATTTAAATT ATGTGTTAGA GGTACTAATA CCTCATCCCA TCCATCTAGA AATCTTAGTT CAAGCCCTTC
LplM57          ATATTTCCTT TTTTCGAGGA CAAATTCTCG CATTTAAATT ATGTGTTAGA GGTACTAATA CCTCATCCCA TCCATCTAGA AATCTTAGTT CAAGCCCTTC
Lti472          ATATTTCCTT TTTTCGAGGA CAAATTATCG CATTTAAATT ATGTGTTAGA GGTACTAATA CCTCATCCCA TCCATCTAGA AATCTTAGTT CAAGCCCTTC
LthVie          ATATTTCCTT TTTTCGAGGA CAAATTCTCG CATTTAAATT ATGTGTTAGA GGTACTAATA CCTCATCCCA TCCATCTAGA AATCTTAGTT CAAGCCCTTC
MLpu11          ATATTTCCTT TTTTCGAGGA CAAATTCTCG CATTTAAATT ATGTGTTAGA GGTACTAATA CCTCATCCCA TCCATCTAGA AATCTTAGTT CAAGCCCTTC
Lmo316          ATATTTCCTT TTTTCGAGGA CAAATTCTCG CATTTAAATT ATGTGTTAGA GGTACTAATA CCTCATCCCA TCCATCTAGA AATCTTAGTT CAAGCCCTTC
LacB11          ATATTTCCTT TTTTCGAGGA CAAATTCTCG CATTTAAATT ATGTGTTAGA GGTACTAATA CCTCATCCCA TCCATCTAGA AATCTTAGTT CAAGCCCTTC
Lar253          ATATTTCCTT TTTTCGAGGA CAAATTATCG CATTTAAATT ATGTGTTAGA GGTACTAATA CCTCATCCCA TCCATCTAGA AATCTTAGTT CAAGCCCTTC
MLas11          ATATTTCCTT TTTTCGAGGA CAAATTATCG CATTTAAATT ATGTGTTAGA GGTACTAATA CCTCATCCCA TCCATCTAGA AATCTTAGTT CAAGCCCTTC
MLma11          ATATTTCCTT TTTTCGAGGA CAAATTCTCG CATTTAAATT ATGTGTTAGA GGTACTAATA CCTCATCCCA TCCATCTAGA AATCTTAGTT CAAGCCCTTC
Lmu283          ATATTTCCTT TTTTCGAGGA CAAATTATCG CATTTAAATT ATGTGTTAGA GGTACTAATA CCTCATCCCA TCCATCTAGA AATCTTAGTT CAAGCCCTTC
MLcr11          ATATTTCCTT TTTTCGAGGA CAAATTATCG CATTTAAATT ATGTGTTAGA GGTACTAATA CCTCATCCCA TCCATCTAGA AATCTTAGTT CAAGCCCTTC
LpebM2          ATATTTCCTT TTTTCGAGGA CAAATTATCG CATTTAAATT ATGTGTTAGA GGTACTAATA CCTCATCCCA TCCATCTAGA AATCTTAGTT CAAGCCCTTC
Mni674          ATATTTCCTT TTTTCGAGGA CAAATTATCG CATTTAAATT ATGTGTTAGA GGTACTAATA CCTCATCCCA TCCATCTAGA AATCTTAGTT CAAGCCCTTC
Mpa603          ATATTTCCTT TTTTCGAGGA CAAATTATCG CATTTAAATT ATGTGTTAGA GGTACTAATA CCTCATCCCA TCCATCTAGA AATCTTAGTT CAAGCCCTTC
Msy597          ATATTTCCTT TTTTCGAGGA CAAATTATCG CATTTAAATT ATGTGTTAGA GGTACTAATA CCTCATCCCA TCCATCTAGA AATCTTAGTT CAAGCCCTTC
Mne795          ATATTTCCTT TTTTCGAGGA CAAATTATCG CATTTAAATT ATGTGTTAGA GGTACTAATA CCTCATCCCA TCCATCTAGA AATCTTAGTT CAAGCCCTTC
Mve442          ATATTTCCTT TTTTCGAGGA CAAATTATCG CATTTAAATT ATGTGTTAGA GGTACTAATA CCTCATCCCA TCCATCTAGA AATCTTAGTT CAAGCCCTTC
Mal338          ATATTTCCTT TTTTCGAGGA CAAATTCTCG CATTTAAATT ATGTGTTAGA GGTACTAATA CCTCATCCCA TCCATCTAGA AATCTTAGTT CAAGCCCTTC
Mto185          ATATTTCCTT TTTTCGAGGA CAAATTCTCG CATTTAAATT ATGTGTTAGA GGTACTAATA CCTCATCCCA TCCATCTAGA AATCTTAGTT CAAGCCCTTC
Mmo593          ATATTTCCTT TTTTCGAGGA CAAATTCTCG CATTTAAATT ATGTGTTAGA GGTACTAATA CCTCATCCCA TCCATCTAGA AATCTTAGTT CAAGCCCTTC
Mhi672          ATATTTCCTT TTTTCGAGGA CAAATTCTCG CATTTAAATT ATGTGTTAGA GGTACTAATA CCTCATCCCA TCCATCTAGA AATCTTAGTT CAAGCCCTTC
Ahi270          ATATTTCCTT TTTTCGAGGA CAAATTCTCG CATTTAAATT ATGTGTTAGA GGTACTAATA CCTCATCCCA TCCATCTAGA AATCTTAGTT CAAGCCCTTC
Alo596          ATATTTCCTT TTTTCGAGGA CAAATTCTCG CATTTAAATT ATGTGTTAGA GGTACTAATA CCTCATCCCA TCCATCTAGA AATCTTAGTT CAAGCCCTTC
AluM53          ATATTTCCTT TTTTCGAGGA CAAATTCTCG CATTTAAATT ATGTGTTAGA GGTACTAATA CCTCATCCCA TCCATCTAGA AATCTTAGTT CAAGCCCTTC
Mca572          ATATTTCCTT TTTTCGAGGA CAAATTCTCG CATTTAAATT ATGTGTTAGA GGTACTAATA CCTCATCCCA TCCATCTAGA AATCTTAGTT CAAGCCCTTC
MMae11          ATATTTCCTT TTTTCGAGGA CAAATTCTCG CATTTAAATT ATGTGTTAGA GGTACTAATA CCTCATCCCA TCCATCTAGA AATCTTAGTT CAAGCCCTTC
Mtr683          ATATTTCCTT TTTTCGAGGA CAAATTCTCG CATTTAAATT ATGTGTTAGA GGTACTAATA CCTCATCCCA TCCATCTAGA AATCTTAGTT CAAGCCCTTC
Mma671          ATATTTCCTT TTTTCGAGGA CAAATTCTCG CATTTAAATT ATGTGTTAGA GGTACTAATA CCTCATCCCA TCCATCTAGA AATCTTAGTT CAAGCCCTTC
Mtf502          ATATTTCCTT TTTTCGAGGA CAAATTCTCG CATTTAAATT ATGTGTTAGA GGTACTAATA CCTCATCCCA TCCATCTAGA AATCTTAGTT CAAGCCCTTC
LphM81          ATATTTCCTT TTTTCGAGGA CAAATTCTCG CATTTAAATT ATGTGTTAGA GGTACTAATA CCTCATCCCA TCCATCTAGA AATCTTAGTT CAAGCCCTTC
AniM31          ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
MKvi11          ATATTTCCTT TTTTCGAGGA CAAATTCTCG CATTTAAATT ATGTGTTAGA GGTACTAATA CCTCATCCCA TCCATCTAGA AATCTTAGTT CAAGCCCTTC
MAros1          ATATTTCCTT TTTTCGAGGA CAAATTCTCG CATTTAAATT ATGTGTTAGA GGTACTAATA CCTCATCCCA TCCATCTAGA AATCTTAGTT CAAGCCCTTC
MshM21          ATATTTCCTT TTTTCGAGGA CAAATTCTCG CATTTAAATT ATGTGTTAGA GGTACTAATA CCTCATCCCA TCCATCTAGA AATCTTAGTT CAAGCCCTTC
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                       710        720        730        740        750        760        770        780        790        800
MAar11          GCTACTGGGT AAAAGATGCT TCTTCTTTGC ATTTATTACG GTTCTCTCTC TACGAGTATT GTAATTCGAA GAGTTTTATT ACTCCAAAGA AATCTATTTC
Aca594          GCTACTGGGT AAAAGATGCT TCTTCTTTGC ATTTATTACG GTTCTCTCTC TACGAGTATT GTAATTCGAA GAGTTTTATT ACTCCAAAGA AATCTATTTC
MAof11          GCTACTGGGT AAAAGATGCT TCTTCTTTGC ATTTATTACG GTTCTCTCTC TACGAGTATT GTAATTCGAA GAGTTTTATT ACTCCAAAGA AATCTATTTC
Lol451          GCTACTGGGT AAAAGATGCT TCTTCTTTGC ATTTATTACG GTTCTCTCTC TACGAGTATT GTAATTCGAA GAGTTTTATT ACTCCAAAGA AATCTATTTC
Lob144          GCTACTGGGT AAAAGATGCT TCTTCTTTGC ATTTATTACG GTTCTCTCTC TACGAGTATT GTAATTCGAA GAGTTTTATT ACTCCAAAGA AATCTATTTC
Lbr141          GCTACTGGGT AAAAGATGCT TCTTCTTTGC ATTTATTACG GTTCTCTCTC TACGAGTATT GTAATTCGAA GAGTTTTATT ACTCCAAAGA AATCTATTTC
Lag308          GCTACTGGGT AAAAGATGCT TCTTCTTTGC ATTTATTACG GTTCTCTCTC TACGAGTATT GTAATTCGAA GAGTTTTATT ACTCCAAAGA AATCTATTTC
MLtp11          GCTACTGGGT AAAAGATGCT TCTTCTTTGC ATTTATTACG GTTCTCTCTC TACGAGTATT GTAATTCGAA GAGTTTTATT ACTCCACAGA AATCTATTTC
Ltr680          GCTACTGGGT AAAAGATGCT TCTTCTTTGC ATTTATTACG GTTCTCTCTC TACGAGTATT GTAATTCGAA GAGTTTTATT ACTCCAAAGA AATCTATTTC
MLfl11          GCTACTGGGT AAAAGATGCT TCTTCTTTGC ATTTATTACG GTTCTCTCTC TACGAGTATT GTAATTCGAA GAGTTTTATT ACTCCAAAGA AATCTATTTC
LplM57          GCTACTGGGT AAAAGATGCT TCTTCTTTGC ATTTATTACG GTTCTCTCTC TACGAGTATT GTAATTCGAA GAGTTTTATT ACTCCAAAGA AATCTATTTC
Lti472          GCTACTGGGT AAAAGATGCT TCTTCTTTGC ATTTATTACG GTTCTCTCTC TACGAGTATT GTAATTCGAA GAGTTTTATT ACTCCAAAGA AATCTATTTC
LthVie          GCTACTGGGT AAAAGATGCT TCTTCTTTGC ATTTATTACG GTTCTCTCTC TACGAGTATT GTAATTCGAA GAGTTTTATT ACTCCAAAGA AATCTATTTC
MLpu11          GCTACTGGGT AAAAGATGCT TCTTCTTTGC ATTTATTACG GTTCTCTCTC TACGAGTATT GTAATTCGAA GAGTTTTATT ACTCCAAAGA AATCTATTTC
Lmo316          GCTACTGGGT AAAAGATGCT TCTTCTTTGC ATTTATTACG GTTCTCTCTC TACGAGTATT GTAATTCGAA GAGTTTTATT ACTCCAAAGA AATCTATTTC
LacB11          GCTACTGGGT AAAAGATGCT TCTTCTTTGC ATTTATTACG GTTCTCTCTC TACGAGTATT GTAATTCGAA GAGTTTTATT ACTCCAAAGA AATCTATTTC
Lar253          GCTACTGGGT AAAAGATGCT TCTTCTTTGC ATTTATTACG GTTCTCTCTC TACGAGTATT GTAATTCGAA GAGTTTTATT ACTCCAAAGA AATCTATTTC
MLas11          GCTACTGGGT AAAAGATGCT TCTTCTTTGC ATTTATTACG GTTCTCTCTC TACGAGTATT GTAATTCGAA GAGTTTTATT ACTCCAAAGA AATCTATTTC
MLma11          GCTACTGGGT AAAAGATGCT TCTTCTTTGC ATTTATTACG GTTCTCTCTC TACGAGTATT GTAATTCGAA GAGTTTTATT ACTCCAAAGA AATCTATTTC
Lmu283          GCTACTGGGT AAAAGATGCT TCTTCTTTGC ATTTATTACG GTTCTCTCTC TACGAGTATT GTAATTCGAA GAGTTTTATT ACTCCAAAGA AATCTATTTC
MLcr11          GCTACTGGGT AAAAGATGCT TCTTCTTTGC ATTTATTACG GTTCTCTCTC TACGAGTAGT GTAATTCGAA GAGTTTTATT ACTCCAAAGA AATCTATTTC
LpebM2          GCTACTGGGT AAAAGATGCT TCTTCTTTGC ATTTATTACG GTTCTCTCTC TACGAGTATT GTAATTCGAA GAGTTTTATT ACTCCAAAGA AATCTATTTC
Mni674          GCTACTGGGT AAAAGATGCT TCTTCTTTGC ATTTATTACG GTTCTCTCTC TACGAGTATT GTAATTCGAA GAGTTTTATT ACTCCAAAGA AATCTATTTC
Mpa603          GCTACTGGGT AAAAGATGCT TCTTCTTTGC ATTTATTACG GTTCTCTCTC TACGAGTATT GTAATTCGAA GAGTTTTATT ACTCCAAAGA AATCTATTTC
Msy597          GCTACTGGGT AAAAGATGCT TCTTCTTTGC ATTTATTACG GTTCTCTCTC TACGAGTATT GTAATTCGAA GAGTTTTATT ACTCCAAAGA AATCTATTTC
Mne795          GCTACTGGGT AAAAGATGCT TCTTCTTTGC ATTTATTACG GTTCTCTCTC TACGAGTATT GTAATTCGAA GAGTTTTATT ACTCCAAAGA AATCTATTTC
Mve442          GCTACTGGGT AAAAGATGCT TCTTCTTTGC ATTTATTACG GTTCTCTCTC TACGAGTATT GTAATTCGAA GAGTTTTATT ACTCCAAAGA AATCTATTTC
Mal338          GCTACTGGGT AAAAGATGCT TCTTCTTTGC ATTTATTACG GTTCTCTCTC TACGAGTATT GTAATTCGAA GAGTTTTATT ACTCCAAAGA AATCTATTTC
Mto185          GCTACTGGGT AAAAGATGCT TCTTCTTTGC ATTTATTACG GTTCTCTCTC TACGAGTATT GTAATTCGAA GAGTTTTATT ACTCCAAAGA AATCTATTTC
Mmo593          GCTACTGGGT AAAAGATGCT TCTTCTTTGC ATTTATTACG GTTCTCTCTC TACGAGTATT GTAATTCGAA GAGTTTTATT ACTCCAAAGA AATCTATTTC
Mhi672          GCTACTGGGT AAAAGATGCT TCTTCTTTGC ATTTATTACG GTTCTCTCTC TACGAGTATT GTAATTCGAA GAGTTTTATT ATTCCAAAGA AATCTATTTC
Ahi270          GCTACTGGGT AAAAGATGCT TCTTCTTTGC ATTTATTACG GTTCTCTCTC TACGAGTATT GTAATTCGAA GAGTTTTATT ACTCCAAAGA AATCTATTTC
Alo596          GCTACTGGGT AAAAGATGCT TCTTCTTTGC ATTTATTACG GTTCTCTCTC TACGAGTATT GTAATTCGAA GAGTTTTATT ACTCCAAAGA AATCTATTTC
AluM53          GCTACTGGGT AAAAGATGCT TCTTCTTTGC ATTTATTACG GTTCTCTCTC TACGAGTATT GTAATTCGAA GAGTTTTATT ACTCCAAAGA AATCTATTTC
Mca572          GCTACTGGGT AAAAGATGCT TCTTCTTTGC ATTTATTACG GTTCTCTCTC TACGAGTATT GTAATTCGAA GAGTTTTATT ACTCCAAAGA AATCTATTTC
MMae11          GCTACTGGGT AAAAGATGCT TCTTCTTTGC ATTTATTACG GTTCTCTCTC TACGAGTATT GTAATTCGAA GAGTTTTATT ACTCCAAAGA AATCTATTTC
Mtr683          GCTACTGGGT AAAAGATGCT TCTTCTTTGC ATTTATTACG GTTCTCTCTC TACGAGTATT GTAATTCGAA GAGTTTTATT ACTCCAAAGA AATCTATTTC
Mma671          GCTACTGGGT AAAAGATGCT TCTTCTTTGC ATTTATTACG GTTCTCTCTC TACGAGTATT GTAATTCGAA GAGTTTTATT ACTCCAAAAA AATCTATTTC
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Mtf502          GCTACTGGGT AAAAGATGCT TCTTCTTTGC ATTTATTACG GTTCTCTCTC TACGAGTATT GTAATTCGAA GAGTTTTATT ACTCCAAAGA AATCTATTTC
LphM81          GCTACTGGGT AAAAGATGCT TCTTCTTTGC ATTTATTACG GTTCTCTCTC TACGAGTATT GTAATTCGAA GAGTTTTATT ACTCCAAAGA AATCTATTTC
AniM31          ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
MKvi11          GCTACTGGGT AAAAGATGCT TCTTCTTTGC ATTTATTACG GTTCTCTCTC TACGAGTATT GTAATTCGAA GAGTTTTATT ACTCCAAAGA AATCTATTTC
MAros1          GCTACTGGGT AAAAGATGCT TCTTCTTTGC ATTTATTACG GTTCTCTCTC TACCAGTATT GTAATTCGAA GAGTTTTATT ACTCCAAAGA AATCTATTTC
MshM21          GCTACTGGGT AAAAGATGCT TCTTCTTTGC ATTTATTACG GTTCTCTCTC TACGAGTATT GTAATTCGAA GAGTTTTATT ACTCCAAAGA AATCTATTTC


                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                       810        820        830        840        850        860        870        880        890        900
MAar11          GATTTTGAAT CCAAGATTAT TCTTGTTCCT -ATATAATTC TCATGCATGT GAATACGAGT CCATTTTCCT TTTT-CTCCG TAATCAATCT TCTCATTT-A
Aca594          GATTTTGAAT CCAAGATTAT TCTTGTTCCT -ATATAATTC TCATGCATGT GAATACGAGT CCATTTTCCT TTTT-CTCCG TAATCAATCT TCTCATTT-A
MAof11          GATTTTGAAT CCAAGATTAT TCTTGTTCCT -ATATAATTC TCATGCATGT GAATACGAGT CCATTTTCCT TTTT-CTCCG TAATCAATCT TCTCATTT-A
Lol451          GATTTTTAAT CCAAGATTAT TCTTGTTCCT -ATATAATTC TCATGCATGT GAATACGAGT CCATTTTCCT TTTT-CTCCG TAATCAATCT TCTCATTT-A
Lob144          GATTTTTAAT CCAAGATTAT TCTTGTTCCT -ATATAATTC TCATGCATGT GAATACGAGT CC-TTTTCCT TTT--CTCCG TAATCAATCT TCTCATTT-A
Lbr141          GATTTTTAAT CCAAGATTAT TCTTGTTCCT -ATATAATTC TCATGCATGT GAATACGAGT CCATTTTCCT TTTT-CTCCG TAATCAATCT TCTCATTT-A
Lag308          GATTTTTAAT CCAAGATTAT TCTTGTTCCT -ATATAATTC TCATGCATGT GAATACGAGT CCATTTTCCT TTTT-CTCCG TAATCAATCT TCTCATTT-A
MLtp11          GATTTTTAAT CCAAGATTTT TCTTGTTCCT -ATATAATTC TCATGCATGT GAATACGAGT CCATTTTCCT TTTT-CTCCG TAATCAATCT TGTCATTT-A
Ltr680          GATTTTTAAT CCAAGATTAT TCTTGTTCCT -ATATAATTC TCATGCATGT GAATACGAGT CCATTTTCCT TTTT-CTCCG TAATCAATCT TCTCATTT-A
MLfl11          GATTTTTAAT CCAAGATTAT TCTTGTTCCT -ATATAATTC TCATGCATGT GAATACGAGT CCATTTTCCT TTTT-CTCCG TAATCAATCT TCTCATTT-A
LplM57          GATTTTTAAT CCAAGATTAT TCTTGTTCCT -ATATAATTC TCATGCATGT GAATACGAGT CCATTTTCCT TTTT-CTCCG TAATCAATCT TCTCATTT-A
Lti472          GATTTTTAAT CCAAGATTAT TCTTGTTCCT -ATATAATTC TCATGCATGT GAATACGAGT CCATTTTCCT TTTT-CTCCG TAATCAATCT TCTCATTT-A
LthVie          GATTTTTAAT CCAAGATTAT TCTTGTTCCT -ATATAATTC TCATGCATGT GAATACGAGT CCATTTTCCT TTTTTCTCCG TAATCAATCT TCTCATTTTA
MLpu11          GATTTTTAAT CCAAGATTAT TCTTGTTCCT -ATATAATTC TCATGCATGT GAATACGAGT CCATTTTCCT TTTT-CTCCG TAATCAATCT TCTCATTT-A
Lmo316          GATTTTTAAT CCAAGATTAT TCTTGTTCCT TATATAATTC TCATGCATGT GAATACGAGT CCATTTTCCT TTTT-CTCCG TAATCAATCT TCTCATTT-A
LacB11          GATTTTTAAT CCAAGATTAT TCTTGTTCCT -ATATAATTC TCATGCATGT GAATACGAGT CCATTTTCCT TTTT-CTCCG TAATCAATCT TCTCATTT-A
Lar253          GATTTTTAAT CCAAGATTAT TCTTGTTCCT -ATATAATTC TCATGCATGT GAATACGAGT CCATTTTCCT TTTT-CTCCG TAATCAATCT TCTCATTT-A
MLas11          GATTTTTAAT CCAAGATTAT TCTTGTTCCT -ATATAATTC TCATGCATGT GAATACGAGT CCATTTTCCT TTTT-CTCCG TAATCAATCT TCTCATTT-A
MLma11          GATTTTTAAT CCAAGATTAT TCTTGTTCCT -ATATAATTC TCATGCATGT GAATACGAGT CCATTTTCCT TTTT-CTCCG TAATCAATCT TCTCATTT-A
Lmu283          GATTTTTAAT CCAAGATTAT TCTTGTTCCT -ATATAATTC TCATGCATGT GAATACGAGT CCATTTTCCT TTTT-CTCCG TAATCAATCT TCTCATTT-A
MLcr11          GATTTTTAAT CCAAGATTAT TCTTGTTCCT -ATATAATTC TCATGCATGT GAATACGAGT CCATTTTCCT TTTT-CTCCG TAATCAATCT TCTCATTT-A
LpebM2          GATTTTTAAT CCAAGATTAT TCTTGTTCCT -ATATAATTC TCATGCATGT GAATACGAGT CCATTTTCCT TTTT-CTCCG TAATCAATCT TCTCATTT-A
Mni674          GATTTTTAAT CCAAGATTAT TCTTGTTCCT -ATATAATTC TCATGCATGT GAATACGAGT CCATTTTCCT TTTT-CTCCG TAATCAATCT TCTCATTT-A
Mpa603          GATTTTTAAT CCAAGATTAT TCTTGTTCCT -ATATAATTC TCATGCATGT GAATACGAGT CCATTTTCCT TTTT-CTCCG TAATCAATCT TCTCATTT-A
Msy597          GATTTTTAAT CCAAGATTAT TCTTGTTCCT -ATATAATTC TCATGCATGT GAATACGAGT CCATTTTCCT TTTT-CTCCG TAATCAATCT TCTCATTT-A
Mne795          GATTTTTAAT CCAAGATTAT TCTTGTTCCT -ATATAATTC TCATGCATGT GAATACGAGT CCATTTTCCT TTTT-CTCCG TAATCAATCT TCTCATTT-A
Mve442          GATTTTTAAT CCAAGATTAT TCTTGTTCCT -ATATAATTC TCATGCATGT GAATACGAGT CCATTTTCCT TTTT-CTCCG TAATCAATCT TCTCATTT-A
Mal338          GATTTTTAAT CCAAGATTAT TCTTGTTCCT -ATATAATTC TCATGCATGT GAATACGAGT CCATTTTCCT TTTT-CTCCG TAATCAATCT TCTCATTT-A
Mto185          GATTTTTAAT CCAAGATTAT TCTTGTTCCT -ATATAATTC TCATGCATGT GAATACGAGT CCATTTTCCT TTTT-CTCCG TAATCAATCT TCTCATTT-A
Mmo593          GATTTTTAAT CCAAGATTAT TCTTGTTCCT -ATATAATTC TCATGCATGT GAATACGAGT CCATTTTCCT TTTT-CTCCG TAATCAATCT TCTCATTT-A
Mhi672          GATTTTTAAT CCAAGATTAT TCTTGTTCCT -ATATAATTC TCATGCATGT GAATACGAGT CCATTTTCCT TTTT-CTCCG TAATCAATCT TCTCATTT-A
Ahi270          GATTTTTAAT CCAAGATTAT TCTTGTTCCT -ATATAATTC TCATGCATGT GAATACGAGT CCATTTTTCT TTTT-CTCCG TAATCAATCT TCTCATTT-A
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Alo596          GATTTTTAAT CCAAGATTAT TCTTGTTCCT -ATATAATTC TCATGCATGT GAATACGAGT CCATTTTCCT TTTT-CTCCG TAATCAATCT TCTCATTT-A
AluM53          CATTTTTAAC CCAAGATTAT TCTTGTTCCT -ATATAATTC TCATGCATGT GAATACGAGT CCATTTTCCT TTTT-CTCCG TAATCAATCT TCTCATTT-A
Mca572          GATTTTTAAT CCAAGATTAT TCTTGTTCCT -ATATAATTC TCATGCATGT GAATACGAGT CCATTTTTCT TTTT-CTCCG TAATCAATCT TCTCATTT-A
MMae11          GATTTTTAAT CCAAGATTAT TCTTGTTCCT -ATATAATTC TCATGCATGT GAATACGAGT CCATTTTCCT TTTT-CTCCG TAATCAATCT TCTCATTT-A
Mtr683          GATTTTTAAT CCAAGATTAT TCTTGTTCCT -ATATAATTC TCATGCATGT GAATACGAGT CCATTTTCCT TTTT-CTCCG TAATCAATCT TCTCATTT-A
Mma671          GATTTTTAAT CCAAGATTCT TCTTGTTCCT -ATATAATTC TCATGCATGT GAATACGAGT CCATTTTCCT TTTT-CTCCG TAATCAATCT TCTCATTT-A
Mtf502          GATTTTTAAT CCACGATTCT TCTTGTTCCT -ATATAATTC TCATGCATGG GAATACGAGT CCATTTTCCT TTTT-CTCCG TAATCAATCT TCTCATTT-A
LphM81          GATTTTGAAT CCAAGATTAT TCTTGTTCCT -ATATAATTC TCATGCATGT GAATACGAGT CCATTTTCCT TTTT-CTCCG TAATCAATCT TCTCATTT-A
AniM31          ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
MKvi11          GATTTTTAAT CCAAGATTAT TCTTGTTCCT -ATATAATTC TCATGCATGT GAATACGAGT CCATTTTCCT TTTT-CTCCG TAATCAATCT TCTCATTT-A
MAros1          GATTTTTAAT CCAAGATTAT TCTTGTTCCT -ATATAATTC TCATGCATGT GAATACGAGT CCATTTTCCT TTTT-CTCCG TAATCAATCT TCTCATTT-A
MshM21          GATTTTTAAT CCAAGATTAT TCTTGTTCCT -ATATAATTC TCATGCATTT GAATACGAGT CCATTTTCCT TTTT-CTCCG TAATCAATCT TCTCATTT-A


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                       910        920        930        940        950        960        970        980        990       1000
MAar11          CGATCAACAT CTTCtGGAGT TTTTCTTGAA CGAATTCATT TCTATGGAAA AATAGAGTAT CTTGTAGAAG TCTTTTATAA TGATTTTCAG ACCAACCTAT
Aca594          CGATCAACAT CTTCTGGAGT TTTTCTTGAA CGAATTCATT TCTATGGAAA AATAGAGTAT CTTGTAGAAG TCTTTTATAA TGATTTTCAG ACCAACCTAT
MAof11          CGATCAACAT CTTCTGGAGT TTTTCTTGAA CGAATTCATT TCTATGGAAA AATAGAGTAT CTTGTAGAAG TCTTTTATAA TGATTTTCAG ACCAACCTAT
Lol451          CGATCAACAT CTTCTGGAGT TTTTCTTGAA CGAATTCATT TCTATGGAAA AATAGAGTAT CTTGTAGAAG TCTTTTATAA TGATTTTCAG ACCAACCTAT
Lob144          CGATCAACAT CT-CTGGAG- TTTTCTTGAA CGAATTCATT TCTATGGAAA A-TAGAGTAT CTTGTAGAAG TCTTTTATAA TGATTTTCAG ACCAACCTAT
Lbr141          CGATCAACAT CTTCTGGAGT TTTTCTTGAA CGAATTCATT TCTATGGAAA AATAGAGTAT CTTGTAGAAG TCTTTTATAA TGATTTTCAG ACCAACCTAT
Lag308          CGATCAACAT CTTCTGGAGT TTTTCTTGAA CGAATTCATT TCTATGGAAA AATAGAGTAT CTTGTAGAAG TCTTTTATAA TGATTTTCAG ACCAACCTAT
MLtp11          CGATCAACAT CTTCTGGAGT CTTTCTTGAA CGAATTCATT TCTATGGAAA AATAGAGTAT CTTGTAGAAG TCTTTTATAA TGATTTTCAG ACCAACCTAT
Ltr680          CGATCAACAT CTTCTGGAGT TTTTCTTGAA CGAATTCATT TCTATGGAAA AATAGAGTAT CTTGTAGAAG TCTTTTATAA TGATTTTCAG ACCAACCTAT
MLfl11          CGATCAACAT CTTCTGGAGT TTTTCTTGAA CGAATTCATT TCTATGGAAA AATAGAGTAT CTTGTAGAAG TCTTTTATAA TGATTTTCAG ACCAACCTAT
LplM57          CGATCAACAT CTTCTGGAGT TTTTCTTGAA CGAATTCATT TCTATGGAAA AATAGAGTAT CTTGTAGAAG TCTTTTATAA TGATTTTCAG ACCAACCTAT
Lti472          CGATCAACAT CTTCTGGAGT TTTTCTTGAA CGAATTCATT TCTATGGAAA AATAGAGTAT CTTGTAGAAG TCTTTTATAA TGATTTTCAG ACCAACCTAT
LthVie          CGATCAACAT CTTCTGGAGT TTTTCTTGAA CGAATTCATT TCTATGGAAA AATAGAGTAT CTTGTAGAAG TCTTTTATAA TGATTTTCAG ACCAACCTAT
MLpu11          CGATCAACAT CTTCTGGAGT TTTTCTTGAA CGAATTCATT TCTATGGAAA AATAGAGTAT CTTGTAGAAG TCTTTTATAA TGATTTTCAG ACCAACCTAT
Lmo316          CGATCAACAT CTTCTGGAGT TTTTCTTGAA CGAATTCATT TCTATGGAAA AATAGAGTAT CTTGTAGAAG TCTTTTATAA TGATTTTCAG ACCAACCTAT
LacB11          CGATCAACAT CTTCTGGAGT TTTTCTTGAA CGAATTCATT TCTATGGAAA AATAGAGTAT CTTGTAGAAG TCTTTTATAA TGATTTTCAG ACCAACCTAT
Lar253          CGATCAACAT CTTCTGGAGT TTTTCTTGAA CGAATTCATT TCTATGGAAA AATAGAGTAT CTTGTAGAAG TCTTTTATAA TGATTTTCAG ACCAACCTAT
MLas11          CGATCAACAT CTTCTGGAGT TTTTCTTGAA CGAATTCATT TCTATGGAAA AATAGAGTAT CTTGTAGAAG TCTTTTATAA TGATTTTCAG ACCAACCTAT
MLma11          CGATCAACAT CTTCTGGAGT TTTTCTTGAA CGAATTCATT TCTATGGAAA AATAGAGTAT CTTGTAGAAG TCTTTTATAA TGATTTTCAG ACCAACCTAT
Lmu283          CGATCAACAT CTTCTGGAGT TTTTCTTGAA CGAATTCATT TCTATGGAAA AATAGAGTAT CTTGTAGAAG TCTTTTATAA TGATTTTCAG ACCAACCTAT
MLcr11          CGATCAACAT CTTCTGGAGT TTTTCTTGAA CGAATTCATT TCTATGGAAA AATAGAGTAT CTTGTAGAAG TCTTTTATAA TGATTTTCAG ACCAACCTAT
LpebM2          CGATCAACAT CTTCTGGAGT TTTTCTTGAA CGAATTCATT TCTATGGAAA AATAGAGTAT CTTGTAGAAG TCTTTtATAA TGATTTtCaG ACcAaC----
Mni674          CGATCAACAT CTTCTGGAGT TTTTCTTGAA CGAATTCATT TCTATGGAAA AATAGAGTAT CTTGTAGAAG TCTTTTATAA TGATTTTCAG ACCAACCTAT
Mpa603          CGATCAACAT CTTCTGGAGT TTTTCTTGAA CGAATTCATT TCTATGGAAA AATAGAGTAT CTTGTAGAAG TCTTTTATAA TGATTTTCAG ACCAACCTAT
Msy597          CGATCAACAT CTTCTGGAGT TTTTCTTGAA CGAATTCATT TCTATGGAAA AATAGAGTAT CTTGTAGAAG TCTTTTATAA TGATTTTCAG ACCAACCTAT
Mne795          CGATCAACAT CTTCTGGAGT TTTTCTTGAA CGAATTCATT TCTATGGAAA AATAGAGTAT CTTGTAGAAG TCTTTTATAA TGATTTTCAG ACCAACCTAT
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Mve442      CGATCAACAT CTTCTGGAGT TTTTCTTGAA CGAATTCATT TCTATGGAAA AATAGAGTAT CTTGTAGAAG TCTTTTATAA TgATTTTCAG ACCAACCTAT
Mal338      CGATCAACAT CTTCTGGAGT TTTTCTTGAA CGAATTCATT TCTATGGAAA AATAGAGTAT CTTGTAGAAG TCTTTTATAA TGATTTTCAG ACCAACCTAT
Mto185      CGATCAACAT CTTCTGGAGT TTTTCTTGAA CGAATTCATT TCTATGGAAA AATAGAGTAT CTTGTAGAAG TCTTTTATAA TGATTTTCAG ACCAACCTAT
Mmo593      CGATCAACAT CTTCTGGAGT TTTTCTTGAA CGAATTCATT TCTATGTAAA AATAGAGTAT CTTGTAGAAG TCTTTTATAA TGATTTTCAG ACCAACCTAT
Mhi672      CGATCAACAT CTTCTGGAGT TTTTCTTGAA CGAATTCATT TCTATGGAAA AATAGAGTAT CTTGTAGAAG TCTTTTATAA TGATTTTCAG ACCAACCTAT
Ahi270      CGATCAACAT CTTCTGGAGT TTTTCTTGAA CGAATTCATT TCTATGGAAA AATAGAGTAT CTTGTAGAAG TCTTTTATAA TGATTTTCAG ACCAACCTAT
Alo596      CGATCAACAT CTTCTGGAGT TTTTCTTGAA CGAATTCATT TCTATGGAAA AATAGAGTAT CTTGTAGAAG TCTTTTATAA TGATTTTCAG ACCAACCTAT
AluM53      CgAtCaaCAT CTTCTGgAGt TTTtCtTGAA CGAATTCATT TCTATGGAAA AATAGAGTAT CTtGtAGAAG TCTt------ ---------- ----------
Mca572      CGATCAACAT CTTCTGGAGT TTTTCTTGAA CGAATTCATT TCTATGGAAA AATAGAGTAT CTTGTAGAAG TCTTTTATAA TGATTTTCAG ACCAACCTAT
MMae11      CGATCAACAT CTTCTGGAGT TTTTCTTGAA CGAATTCATT TCTATGGAAA AATAGAGTAT CTTGTAGAAG TCATTTATAA TGATTTTCAG ACCAACCTAT
Mtr683      CGATCAACAT CTTCTGGAGT TTTTCTTGAA CGAATTCATT TCTATGGAAA AATAGAGTAT CTTGTAGAAG TCATTTATAA TGATTTTCAG ACCAACCTAT
Mma671      CGATCAACAT CTTCTGGAAT TTTTATTGAA CGAATTCATT TCTATGGAAA AATAGAGTAT CTTGTAGAAG TCTTTTATAA TAATTTTCAG ACTAACCTAT
Mtf502      CGATCAACAT CTTCTGGAAT TTTTATTGAA CGAATTCATT TCTATGGAAA AATAGAGTAT CTTCTAGAAG TCTTTTATAA TAATTTTCAG ACTAACCTAT
LphM81      CGATCAACAT CTTCTGGAGT TTTTCTTGAA CGAATTCATT TCTATGGAAA AATAGAGTAT CTTGTAGAAG TCTTTTATAA TGATTTTCAG ACCAACCTAT
AniM31      ---------- ---------- ---------- --AATTCATT TCTATGGAAA AaTAGAGTAT CTTGTAGAAG TCTTTTATAA TGATTTTCAG ACCAACCTAT
MKvi11      CGATCAACAT CTTCTGGAGT TTTTCTTGAA CGAATTCATT TCTATGGAAA AATAGAGTAT CTTGTAGAAG TCTTTTATAA TGATTTTCAG ACCAACCTAT
MAros1      CGATCAACAT CTTCTGGAGT TTTTCTTGAA CGAATTCATT TCTATGGAAA AATAGAGTAT CTTGTAGAAG TCTTTTATAA TGATTTTCAG ACCAACCTAT
MshM21      CGATCAATAT CTTCTGGAGT TTTTCTTGAA CGAATTCATT TCTATGGAAA AATAGAGTAT CTTGTAGAAG TCTTTTATAA TGATTTTCAG ACCAACCTAT


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                  1010       1020       1030       1040       1050       1060       1070       1080       1090       1100
MAar11      GGTTGTTCAA AGACCCTTTG ATCCATTTTA TTAGGTATCA AGGAAAGTCA ATTTTGGCCT CAAAAGATAC GTCTCTTCTG ATGAATAAGT GGAAATATTA
Aca594      GGTTGTTCAA AGACCCTTTG ATCCATTTTA TTAGGTATCA AGGAAAGTCA ATTTTGGCCT CAAAAGATAC GTCTCTTCTG ATGAATAAGT GGAAATATTA
MAof11      GGTTGTTCAA AGACCCTTTG ATCCATTTTA TTAGGTATCA AGGAAAGTCA ATTTTGGCCT CAAAAGATAC GTCTCTTCTG ATGAATAAGT GGAAATATTA
Lol451      GGTTGTTCAA AGACCCTTTG ATCCATTTTA TTAGGTATCA AGGAAAGTCA ATTTTGGCCT CAAAAGATAC GTCTCTTCTG ATGAATAAGT GGAAATATTA
Lob144      GGTTGTTCAA AGACCCTTTG ATCCATTTTA TTAGGTATCA AGGAAAGTCA ATTTTGGCCT CAAAAGATAC GTCTCTTCTG ATGAATAAGT GGAAATATTA
Lbr141      GGTTGTTCAA AGACCCTTTG ATCCATTTTA TTAGGTATCA AGGAAAGTCA ATTTTGGCCT CAAAAGATAC GTCTCTTCTG ATGAATAAGT GGAAATATTA
Lag308      GGTTGTTCAA AGACCCTTTG ATCCATTTTA TTAGGTATCA AGGAAAGTCA ATTTTGGCCT CAAAAGATAC GTCTCTTCTG ATGAATAAGT GGAAATATTA
MLtp11      GGTTGTTCAA AGACCCTTTG ATCCATTTTA TTAGGTATCA AGGAAAGTCA ATTTTGGCCT CAAAAGATAC GTCTCTTCTG ATGAATAAGT GGAAATATTA
Ltr680      GGTTGTTCAA AGACCCTTTG ATCCATTTTA TTAGGTATCA AGGAAAGTCA ATTTTGGCCT CAAAAGATAC GTCTCTTCTG ATGAATAAGT GGAAATATTA
MLfl11      GGTTGTTCAA AGACCCTTTG ATCCATTTTA TTAGGTATCA AGGAAAGTCA ATTTTGGCCT CAAAAGATAC GTCTCTTCTG ATGAATAAGT GGAAATATTA
LplM57      GGTTGTTCAA AGACCCTTTG ATCCATTTTA TTAGGTATCA AGGAAAGTCA ATTTTGGCCT CAAAAGATAC GTCTCTTCTG ATGAATAAGT GGAAATATTA
Lti472      GGTTGTTCAA AGACCCTTTG ATCCATTTTA TTAGGTATCA AGGAAAGTCA ATTTTGGCCT CAAAAGATAC GTCTCTTCTG ATGAATAAGT GGAAATATTA
LthVie      GGTTGTTCAA AGACCCTTTG ATCCATTTTA TTAGGTATCA AGGAAAGTCA ATTTTGGCCT CAAAAGATAC GTCTCTTCTG ATGAATAAGT GGAAATATTA
MLpu11      GGTTGTTCAA AGACCCTTTG ATCCATTTTA TTAGGTATCA AGGAAAGTCA ATTTTGGCCT CAAAAGATAC GTCTCTTCTG ATGAATAAGT GGAAATATTA
Lmo316      GGTTGTTCAA AGACCCTTTG ATCCATTTTA TTAGGTATCA AGGAAAGTCA ATTTTGGCCT CAAAAGATAC GTCTCTTCTG ATGAATAAGT GGAAATATTA
LacB11      GGTTGTTCAA AGACCCTTTG ATCCATTTTA TTAGGTATCA AGGAAAGTCA ATTTTGGCCT CAAAAGATAC GTCTCTTCTG ATGAATAAGT GGAAATATTA
Lar253      GGTTGTTCAA AGACCCTTTG ATCCATTTTA TTAGGTATCA AGGAAAGTCA ATTTTGGCCT CAAAAGATAC GTCTCTTCTG ATGAATAAGT GGAAATATTA
MLas11      GGTTGTTCAA AGACCCTTTG ATCCATTTTA TTAGGTATCA AGGAAAGTCA ATTTTGGCCT CAAAAGATAC GTCTCTTCTG ATGAATAAGT GGAAATATTA
MLma11      GGTTGTTCAA AGACCCTTTG ATCCATTTTA TTAGGTATCA AGGAAAGTCA ATTTTGGCCT CAAAAGATAC GTCTCTTCTG ATGAATAAGT GGAAATATTA
Lmu283      GGTTGTTCAA AGACCCTTTG ATCCATTTTA TTAGGTATCA AGGAAAGTCA ATTTTGGCCT CAAAAGATAC GTCTCTTCTG ATGAATAAGT GGAAATATTA
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MLcr11        GGTTGTTCAA AGACCCTTTG ATCCATTTTA TTAGGTATCA AGGAAAGTCA ATTTTGGCCT CAAAAGATAC GTCTCTTCTG ATGAATAAGT GGAAATATTA
LpebM2        ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Mni674        GGTTGTTCAA AGACCCTTTG ATCCATTTTA TTAGGTATCA AGGAAAGTCA ATTTTGGCCT CAAAAGATAC GTCTCTTCTG ATGAATAAGT GGAAATATTA
Mpa603        GGTTGTTCAA AGACCCTTTG ATCCATTTTA TTAGGTATCA AGGAAAGTCA ATTTTGGCCT CAAAAGATAC GTCTCTTCTG ATGAATAAGT GGAAATATTA
Msy597        GGTTGTTCAA AGACCCTTTG ATCCATTTTA TTAGGTATCA AGGAAAGTCA ATTTTGGCCT CAAAAGATAC GTCTCTTCTG ATGAATAAGT GGAAATATTA
Mne795        GGTTGTTCAA AGACCCTTTG ATCCATTTTA TTAGGTATCA AGGAAAGTCA ATTTTGGCCT CAAAAGATAC GTCTCTTCTG ATGAATAAGT GGAAATATTA
Mve442        GGTTGTTCAA AGACCCTTTG ATCCATTTTA TTAGGTATCA AGGAAAGTCA ATTTTGGCCT CAAAAGATAC GTCTCTTCTG ATGAATAAGT GGAAATATTA
Mal338        GGTTGGTCAA AGACCCTTTG ATCCATTTTA TTAGGTATCA AGGAAAGTCA ATTTTGGCCT CAAAAGATAC GTCTCTTCTG ATGAATAAGT GGAAATATTA
Mto185        GGTTGTTCAA AGACCCTTTG ATCCATTTTA TTAGGTATCA AGGAAAGTCA ATTTTGGCCT CAAAAGATAC GTCTCTTCTG ATGAATAAGT GGAAATATTA
Mmo593        GGTTGTTCAA AGACCCTTTG ATCCATTTTA TTAGGTATCA AGGAAAGTCA ATTTTGGCCT CAAAAGATAC GTCTCTTCTG ATGAATAAGT GGAAATATTA
Mhi672        GGTTGTTCAA AGACCCTTTG ATCCATTTTA TTAGGTATCA AGGAAAGTCA ATTTTGGCCT CAAAAGATAC GTCTCTTCTG ATGAATAAGT GGAAATATTA
Ahi270        GGTTGTTCAA AGACCCTTTG ATCCATTTTA TTAGGTATCA AGGAAAGTCA ATTTTGGCCT CAAAAGATAC GTCTCTTCTG ATGAATAAGT GGAAATATTA
Alo596        GGTTGTTCAA AGACCCTTTG ATCCATTTTA TTAGGTATCA AGGAAAGTCA ATTTTGGCCT CAAAAGATAC GTCTCTTCTG ATGAATAAGT GGAAATATTA
AluM53        ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Mca572        GGTTGTTCAA AGACCCTTTG ATCCATTTTA TTAGGTATCA AGGAAAGTCA ATTTTGGCCT CAAAAGATAC GTCTCTTCTG ATGAATAAGT GGAAATATTA
MMae11        GGTTGTTCAA AGACCCTTTG ATCCATTTTA TTAGGTATCA AGGAAAGTCA ATTTTGGCCT CAAAAGATAC GTCTCTTCTG ATGAATAAGT GGAAATATTA
Mtr683        GGATGTTCAA AGACCCATTG ATCCATTTTA TTAGGTATCA AGGAAAGTCA ATTTTGGCCT CAAAAGATAC GTCTCTTCTG ATGAATAAGT GGAAATATTA
Mma671        GGTTGTTCAA AGACCCTTTG ATCCATTTTA TTAGGTATCA AGGAAAGTCA ATTTTGGCCT CAAAAGATAC GTCTCTTCTG ATGAATAAGT GGAAATATTA
Mtf502        GGTTGTTCAA AGACCCTTTG ATCCATTTTA TTAGGTATCA AGGAAAGTCA ATTTTGGCCT CAAAAGATAC GTCTCTTCTG ATGAATAAGT GGAAATATTA
LphM81        GGTTGTTCAA AGACCCTTTG ATCCATTTTA TTAGGTATCA AGGAAAGTCA ATTTTGGCCT CAAAAGATAC GTCTCTTCTG ATGAATAAGT GGAAATATTA
AniM31        GGTTGTTCAA AGACCCTTTG ATCCATTTTA TTAGGTATCA AGGAAAGTCC ATTTTGGCCT CAAAGGATAC GTCTCTTCTG ATGAATAAGT GGAAATATTA
MKvi11        GGTTGTTCAA AGACCCTTTG ATCCATTTTA TTAGGTATCA AGGAAAGTCA ATTTTGGCCT CAAAAGATAC GTCTCTTCTG ATGAATAAGT GGAAATATTA
MAros1        GGTTGTTCAA AGACCCTTTG ATCCATTTTA TTAGGTATCA AGGAAAGTCC ATTTTGGCCT CAAAAGATAC GTCTCTTCTG ATGAATAAGT GGAAATATTA
MshM21        GGTTGTTCAA AGACCCTTTA ATCCATTTTA TTAGGTATCA AGGAAAGTCA ATTTTGGCCT CAAAGGATAC GTCTCTTCTG ATGAATAAGT GGAAATATTA


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                    1110       1120       1130       1140       1150       1160       1170       1180       1190       1200
MAar11        CTTTGTCGAT TTATGGCAAT ATTATTTTTA CATGTGGACT CAATCAGGAA GAGTCCGTAT AAATCAATTA TCTAAATATT CTCTCGACTT TCTGGGCTAT
Aca594        CTTTGTCGAT TTATGGCAAT ATTATTTTTA CATGTGGACT CAATCAGGAA GAGTCCGTAT AAATCAATTA TCTAAATATT CTCTCGACTT TCTGGGCTAT
MAof11        CTTTGTCGAT TTATGGCAAT ATTATTTTTA CATGTGGACT CAATCAGGAA GAGTCCGTAT AAATCAATTA TCTAAATATT CTCTCGACTT TCTGGGCTAT
Lol451        CTTTGTCGAT TTATGGCAAT ATTATTTTTA CATGTGGACT CAATCAGGAA GAGTCCGTAT AAATCAATTA TCTAAATATT CTCTCGACTT TCTGGGCTAT
Lob144        CTTTGTCGAT TTATGGCAAT ATTATTTTTA CATGTGGACT CAATCAGGAA GAGTCCGTAT AAATCAATTA TCTAAATATT CTCTCGACTT TCTGGGCTAT
Lbr141        CTTTGTCGAT TTATGGCAAT ATTATTTTTA CATGTGGACT CAATCAGGAA GAGTCCGTAT AAATCAATTA TCTAAATATT CTCTCGACTT TCTGGGCTAT
Lag308        CTTTGTCGAT TTATGGCAAT ATTATTTTTA CATGTGGACT CAATCAGGAA GAGTCCGTAT AAATCAATTA TCTAAATATT CTCTCGACTT TCTGGGCTAT
MLtp11        CTTTGTCGAT TTATGGCAAT ATTATTTTTA CATGTGGACT CAATCAGGAA GAGTCCGTAT AAATCAATTA TCTAAATATT CTCTCGACTT TCTGGGCTAT
Ltr680        CTTTGTCGAT TTATGGCAAT ATTATTTTTA CATGTGGACT CAATCAGGAA GAGTCCGTAT AAATCAATTA TCTAAATATT CTCTCGACTT TCTGGGCTAT
MLfl11        CTTTGTCGAT TTATGGCAAT ATTATTTTTA CATGTGGACT CAATCAGGAA GAGTCCGTAT AAATCAATTA TCTAAATATT CTCTCGACTT TCTGGGCTAT
LplM57        CTTTGTCGAT TTATGGCAAT ATTATTTTTA CATGTGGACT CAATCAGGAA GAGTCCGTAT AAATCAATTA TCTAAATATT CTCTCGACTT TCTGGGCTAT
Lti472        CTTTGTCGAT TTATGGCAAT ATTATTTTTA CATGTGGACT CAATCAGGAA GAGTCCGTAT AAATCAATTA TCTAAATATT CTCTCGACTT TCTGGGCTAT
LthVie        CTTTGTCGAT TTATGGCAAT ATTATTTTTA CATGTGGACT CAATCAGGAA GAGTCCGTAT AAATCAATTA TCTAAATATT CTCTCGACTT TCTGGGCTAT
MLpu11        CTTTGTCGAT TTATGGCAAT ATTATTTTTA CATGTGGACT CAATCAGGAA GAGTCCGTAT AAATCAATTA TCTAAATATT CTCTCGACTT TCTGGGCTAT
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Lmo316          CTTTGTCGAT TTATGGCAAT ATTATTTTTA CATGTGGACT CAATCAGGAA GAGTCCGTAT AAATCAATTA TCTAAATATT CTTTCGACTT TCTGGGCTAT
LacB11          CTTTGTCGAT TTATGGCAAT ATTATTTTTA CATGTGGACT CAATCAGGAA GAGTCCGTAT AAATCAATTA TCTAAATATT CTCTCGACTT TCTGGGCTAT
Lar253          CTTTGTCGAT TTATGGCAAT ATTATTTTTA CATGTGGACT CAATCAGGAA GAGTCCGTAT AAATCAATTA TCTAAATATT CTCTCGACTT TCTGGGCTAT
MLas11          CTTTGTCGAT TTATGGCAAT ATTATTTTTA CATGTGGACT CAATCAGGAA GAGTCCGTAT AAATCAATTA TCTAAATATT CTCTCGACTT TCTGGGCTAT
MLma11          CTTTGTCGAT TTATGGCAAT ATTATTTTTA CATGTGGACT CAATCAGGAA GAGTCCGTAT AAATCAATTA TCTAAATATT CTCTCGACTT TCTGGGCTAT
Lmu283          CTTTGTCGAT TTATGGCAAT ATTATTTTTA CATGTGGACT CAATCAGGAA GAGTCCGTAT AAATCAATTA TCTAAATATT CTCTCGACTT TCTGGGCTAT
MLcr11          CTTTGTCGAT TTATGGCAAT ATTATTTTTA CATGTGGACT CAATCAGGAA GAGTCCGTAT AAATCAATTA TCTAAATATT CTCTCGACTT TCTGGGCTAT
LpebM2          ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Mni674          CTTTGTCGAT TTATGGCAAT ATTATTTTTA CATGTGGACT CAATCAGGAA GAGTCCGTAT AAATCAATTA TCTAAATATT CTCTCGACTT TCTGGGCTAT
Mpa603          CTTTGTCGAT TTATGGCAAT ATTATTTTTA CATGTGGACT CAATCAGGAA GAGTCCGTAT AAATCAATTA TCTAAATATT CTCTCGACTT TCTGGGCTAT
Msy597          CTTTGTCGAT TTATGGCAAT ATTATTTTTA CATGTGGACT CAATCAGGAA GAGTCCGTAT AAATCAATTA TCTAAATATT CTCTCGACTT TCTGGGCTAT
Mne795          CTTTGTCGAT TTATGGCAAT ATTATTTTTA CATGTGGACT CAATCAGGAA GAGTCCGTAT AAATCAATTA TCTAAATATT CTCTCGACTT TCTGGGCTAT
Mve442          CTTTGTCGAT TTATGGCAAT ATTATTTTTA CATGTGGACT CAATCAGGAA GAGTCCGTAT AAATCAATTA TCTAAATATT CTCTCGACTT TCTGGGCTAT
Mal338          CTTTGTCGAT TTATGGCAAT ATTATTTTTA CATGTGGACT CAATCAGGAA GAGTCCGTAT AAATCAATTA TCTAAATATT CTCTCGACTT TCTGGGCTAT
Mto185          CTTTGTCGAT TTATGGCAAT ATTATTTTTA CATGTGGACT CAATCAGGAA GAGTCCGTAT AAATCAATTA TCTAAATATT CTCTCGACTT TCTGGGCTAT
Mmo593          CTTTGTCGAT TTATGGCAAT ATTATTTTTA CATGTGGACT CAATCAGGAA GAGTCCGTAT AAATCAATTA TCTAAATATT CTCTCGACTT TCTGGGCTAT
Mhi672          CTTTGTCGAT TTATGGCAAT ATTATTTTTA CATGTGGACT CAATCAGGAA GAGTCCGTAT AAATCAATTA TCTAAATATT CTCTCGACTT TCTGGGCTAT
Ahi270          CTTTGTCGAT TTATGGCAAT ATTATTTTTA CATGTGGACT CAATCAGGAA GAGTCCGTAT AAATCAATTA TCTAAATATT CTCTCGACTT TCTGGGCTAT
Alo596          CTTTGTCGAT TTATGGCAAT ATTATTTTTA CATGTGGACT CAATCAGGAA GAGTCCGTAT AAATCAATTA TCTAAATATT CTCTCGACTT TCTGGGCTAT
AluM53          ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Mca572          CTTTGTCGAT TTATGGCAAT ATTATTTTTA CATGTGGACT CAATCAGGAA GAGTCCGTAT AAATCAATTA TCTAAATATT CTCTCGACTT TCTGGGCTAT
MMae11          TTTTGTCGAT TTATGGCAAT ATTATTTTTA CATGTGGACT CAATCAGGAA GAGTCCGTAT AAATCAATTA TCTAAATATT CTCTCGACTT TCTGGGCTAT
Mtr683          TTTTGTCGAT TTATGGCAAT ATTATTTTTA CATGTGGACT CAATCAGGAA GAGTCCGTAT AAATCAATTA TCTAAATATT CTCTCGACTT TCTGGGCTAT
Mma671          CTTTGTCGAT TTATGGCAAT ATTATTTTTA CATGTGGACT CAATCAGGAA GAGTCCGTAT AAATCAATTA TCTAAATATT CTCTCGACTT TCTGGGCTAT
Mtf502          CTTTGTCGAT TTATGGCAAT ATTATTTTTA CATGTGGACT CAATCAGGAA GAGTCCATAT AAATCAATTA TCTAAATATT CTCTCGACTT TCTGGGCTAT
LphM81          CTTTGTCGAT TTATGGCAAT ATTATTTTTA CATGTGGACT CAATCAGGAA GAGTCCGTAT AAATCAATTA TCTAAATATT CTCTCGACTT TCTGGGCTAT
AniM31          CTTTGTCGAT TTATGGCAAT ATTATTTTTA CATGTGGACT CAATCAGGAA GAGTCCGTAT AAATCAATTA TCTAAATATT CTCTCGACTT TCTGGGCTAT
MKvi11          CTTTGTCGAT TTATGGCAAT ATTATTTTTA CATGTGGACT CAATCAGGAA GAGTCCGTAT AAATCAATTA TCTAAATATT CTCTCGACTT TCTGGGCTAT
MAros1          CTTTGTCGAT TTATGGCAAT ATTATTTTTA CATGTGGACT CAATCAGGGA GAGTCCGTAT AAATAAATTA TCTAAATATT CTCTCGACTT TCTGGGCTAT
MshM21          CTTTGTCGAT TTATGGCAAT ATTATTTTTA CATGTGGTCT CAGTCAGGAA GAGTCCGTAT AAATCAATTA TCTAAATATT CTCTCGACTT TCTGGGCTAT

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                      1210       1220       1230       1240       1250       1260       1270       1280       1290       1300
MAar11          CTTTCAAGTG TGCGATTAAA TCCTTCAGTG GTACGGAGTC AAATGCTAGA AAATTCATTT ATAATAGATA ATGCTATGAA GACGTTGGAT ACAAGAATTC
Aca594          CTTTCAAGTG TGCGATTAAA TCCTTCAGTG GTACGGAGTC AAATGCTAGA AAATTCATTT ATAATAGATA ATGCTATGAA GACGTTGGAT ACAAGAATTC
MAof11          CTTTCAAGTG TGCGATTAAA TCCTTCAGTG GTACGGAGTC AAATGCTAGA AAATTCATTT ATAATAGATA ATGCTATGAA GACGTTGGAT ACAAGAATTC
Lol451          CTTTCAAGTG TGCGATTAAA TCCTTCAGTG GTACGGAGTC AAATGCTAGA AAATTCATTT ATAATAGATA ATCCTATGAA GACGTTGGAT ACAAGAATTC
Lob144          CTTTCAAGTG TGCGATTAAA TCCTTCAGTG GTACGGAGTC AAATGCTAGA AAATTCATTT ATAATAGATA ATCCTATGAA GACGTTGGAT ACAAGAATTC
Lbr141          CTTTCAAGTG TGCGATTAAA TCCTTCAGTG GTACGGAGTC AAATGCTAGA AAATTCATTT ATAATAGATA ATCCTATGAA GACGTTGGAT ACAAGAATTC
Lag308          CTTTCAAGTG TGCGATTAAA TCCTTCAGTG GTACGGAGTC AAATGCTAGA AAATTCATTT ATAATAGATA ATCCTATGAA GACGTTGGAT ACAAGAATTC
MLtp11          CTTTCAAGTG TGCGATTAAA TCCTTCAGTG GTACGGAGTC AAATGCTAGA AAATTCATTT ATAATAGATA ATCCTATGAA GACGTTGGCT ACAAGAATTC
Ltr680          CTTTCAAGTG TGCGATTAAA TCCTTCAGTG GTACGGAGTC AAATGCTAGA AAATTCATTT ATAATAGATA ATCCTATGAA GACGTTGGAT ACAAGAATTC
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MLfl11       CTTTCAAGTG TGCGATTAAA TCCTTCAGTG GTACGGAGTC AAATGCTAGA AAATTCATTT ATAATAGATA ATCCTATGAA GACGTTGGAT ACAAGAATTC
LplM57       CTTTCAGGTG TGCGATTAAA TCCTTCAGTG GTACGGAGTC AAATGCTAGA AAATTCATTT ATAATAGATA ATCCTATGAA GACGTTGGAT ACAAGAATTC
Lti472       CTTTCAAGTG TGCGATTAAA TCCTTCAGTG GTACGGAGCT AAATGCTAGA AAATTCATTT ATAATAGATA ATCCTACGAA GACGTTGGAT ACAAGAATTC
LthVie       CTTTCAAGTG TGCGATTAAA TCCTTCAGTG GTACGGAG-C AAATGCTAGA AAATTCATTT ATAATAGATA ATCCTATGAA GACGTTGGAT ACAAGAATTC
MLpu11       CTTTCAAGTG TGCGATTAAA TCCTTCAGTG GTACGGAGTC AAATGCTAGA AAATTCATTT ATAATAGATA ATCCTATGAA GACGTTGGAT ACAAGAATTC
Lmo316       CTTTCAAGTG TGCGATTAAA TCCTTCAGTG GTACGGAGTC AAATGCTAGA AAATTCATTT ATAATAGATA ATCCTATGAA GACGTTGGAT ACAAGAATTC
LacB11       CTTTCAAGTG TGCGATTAAA TCCTTCAGTG GTACGGAGTC AAATGCTAGA AAATTCATTT ATAATAGATA ATCCTATGAA GACGTTGGAT ACAAGAATTC
Lar253       CTTTCAGGTG TGCGATTAAA TCCTTCAGTG GTACGGAGTC AAATGCTAGA AAATTCATTT ATAATAGATA ATCCTATGAA GACGTTGGAT ACAAGAATTC
MLas11       CTTTCAGGTG TGCGATTAAA TCCTTCAGTG GTACGGAGTC AAATGCTAGA AAATTCATTT ATAATAGATA ATCCTATGAA GACGTTGGAT ACAAGAATTC
MLma11       CTTTCAAGTG TGCGATTAAA TCCTTCAGTG GTACGGAGTC AAATGCTAGA AAATTCATTT ATAATAGATA ATCCTATGAA GACGTTGGAT ACAAGAATTC
Lmu283       CTTTCAGGTG TGCGATTAAA TCCTTCAGTG GTACGGAGTC AAATGCTAGA AAATGCATTT ATAATAGATA ATCCTATGAA GACGTTGGAT ACAAGAATTC
MLcr11       CTTTCAGGTG TGCGATTAAA TCCTTCAGTG GTACGGAGTC AAATGCTAGA AAATTCATTT ATAATAGATA ATCCTATGAA GACGTTGGAT ACAAGAATTC
LpebM2       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Mni674       CTTTCAGGTG TGCGATTAAA TCCTTCAGTG GTACGGAGTC AAATGCTAGA AAATTCATTT ATAATAGATA ATCCTATGAA GACGTTGGAT ACAAGAATTC
Mpa603       CTTTCAGGTG TGCGATTAAA TCCTTCAGTG GTACGGAGTC AAATGCTAGA AAATGCATTT ATAATAGATA ATCCTATGAA GACGTTGGAT ACAAGAATTC
Msy597       CTTTCAGGTG TGCGATTAAA TCCTTCAGTG GTACGGAGTC AAATGCTAGA AAATTCATTT ATAATAGATA ATCCTATGAA GACGTTGGAT ACAAGAATTC
Mne795       CTTTCAGGTG TGCGATTAAA TCCTTCAGTG GTACGGAGTC AAATGCTAGA AAATTCATTT ATAATAGATA ATCCTATGAA GACGTTGGAT ACAAGAATTC
Mve442       CTTTCAAGTG TGCGATTAAA TCCTTCAGTG GTACGGAGTC AAATGCTAGA AAATTCATTT ATAATAGATA ATCCTATGAA GACGTTGGAT ACAAGAATTC
Mal338       CTTTCAAGTG TGCGATTAAA TCCTTCAGTG GTACGGAGTC AAATGCTAGA AAATTCATTT ATAATAGATA ATCCTATGAA GACGTTGGAT ACAAGAATTC
Mto185       CTTTCAAGTG TGCGATTAAA TCCTTCAGTG GTACGGAGTC AAATGCTAGA AAATTCATTT ATAATAGATA ATCCTATGAA GACGTTGGAT ACAAGAATTC
Mmo593       CTTTCAAGTG TGCGATTAAA TCCTTCAGTG GTACGGAGTC AAATGCTAGA AAATTCATTT ATAATAGATA ATCCTATGAA GACGTTGGAT ACAAGAATTC
Mhi672       CTTTCAAGTG TGCGATTAAA TCCTTCAGTG GTACGGAGTC AAATGCTAGA AAATTCATTT ATAATAGATA ATCCTATGAA GACGTTGGAT ACAAGAATTC
Ahi270       TTTTCAAGGG TGCGATTAAA TCCTTCAGTG GTACGGAGTC AAATGCTAGA AAATTCATTT ATAATAGATA ATCCTATGAA GACGTTGGAT ACAAGAATTC
Alo596       CTTTCAAGTG TGCGATTAAA TCCTTCAGTG GTACGGAGTC AAATGCTAGA AAATTCATTT ATAATAGATA ATCCTATGAA GACGTTGGAT ACAAGAATTC
AluM53       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Mca572       TTTTCAAGGG TGCGATTAAA TCCTTCAGTG GTACGGAGTC AAATGCTAGA AAATTCATTT ATAATAGATA ATCCTATGAA GACGTTGGAT ACAAGAATTC
MMae11       CTTTCAAGTG TGCGATTAAA TCCTTCAGTG GTACGGAGTC AAATGCTAGA AAATTCATTT ATAATAGATA ATCCTATGAA GACGTTGGAT ACAAGAATTC
Mtr683       CTTTCAAGTG TGCGATTAAA TCCTTCAGTG GTACGGAGTC AAATGCTAGA AAATTCATTT ATAATAGATA ATCCTATGAA GACGTTGGAT ACAAGAATTC
Mma671       CTTTCAAGTG TGCGATTAAA TCCTTCAGTG GTGCGGAGTC AAATGCTAGA AAATTCATTT ATAATAGATA ATGCTATGAA GACGCTGGAT ACAAGAATTC
Mtf502       CTTTCAAGTG TGCGATTAAA TCCTTCAGTG GTACGGAGTC AAATGCTAGA AAATTCATTT ATAATAGATA ATGCTATGAA GACGCTGGAT ACAAGAATTC
LphM81       CTTTCAAGTG TGCGATTAAA TCCTTCAGTG GTACGGAGTC AAATGCTAGA AAATTCATTT ATAATAGATA ATCCTATGAA GACGTTGGAT ACAAGAATTC
AniM31       CTTTCAAGTG TGCGATTAAA TCCTTCAGTG GTACGGAGTC AAATGCTAGA AAATTCATTT ATAATAGATA ATGCTATGAA GACGTTGGAT ACAAGAATTC
MKvi11       CTTTCAAGTG TGCGATTAAA TCCTTCAGTG GTACGGAGTC AAATGCTAGA AAATTCATTT ATAATAGATA ATGCTATGAA GACGTTGGAT ACAAGAATTC
MAros1       CTTTCAAGTG TGCGATTAAA GCCTTCAGTG GTACGGAGTC AAATGCTAGA AAATTCATTT ATAATAGATA ATGCTATGAA GACGTTGGAT ACAAGAATTC
MshM21       CTTTCAAGTG TGCGATTAAA TCCTTCAGTG GTACGGAGTC AAATGCTAGA AAATTCATTT ATAATAGATA ATGCTATGAA GACGTTGGAT ACAAGAATTC


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                   1310       1320       1330       1340       1350       1360       1370       1380       1390       1400
MAar11       CAATTATTTC TCTTATTGGA TCATTGTCTA AGGCAAAATT TTGTAACACA TT-AGGGCAT CCCATT-AGT AA-GCCGACG TGGGCCGATT CTTCCGATTC
Aca594       CAATTATTTC TCTTATTGGA TCATTGTCTA AGGCAAAATT TTGTAACACA TT-AGGGCAT CCCATT-AGT AA-GCCGACG TGGGCCGATT CTTCCGATTC
MAof11       CAATTATTTC TCTTATTGGA TCATTGTCTA AGGCAAAATT TTGTAACACA TT-AGGGCAT CCCATT-AGT AA-GCCGACG TGGGCCGATT CTTCCGATTC
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Lol451        CAATTATTTC TCTTATTGGA TCATTGTCTA AGGCAAAATT TTGTAACACC TT-AGGGCAT CCCATT-ACT AA-GCCGACG TGTGCGGATT CCTCCGATTC
Lob144        CAATTATTTC TCTTATTGGA TCATTGTCTA AGGCAAAATT TTGTAACACC TT-AGGGCAT CCCATT-ACT AA-GCCGACG TGGGCGGATT CCTCCGATTC
Lbr141        CAATTATTTC TCTTATTGGA TCATTGTCTA AGGCAAAATT TTGTAACACC TT-AGGGCAT CCCATT-ACT AA-GCCGACG TGGGCGGATT CCTCCGATTC
Lag308        CAATTATTTC TCTTATTGGA TCATTGTCTA AGGCAAAATT TTGTAACACC TT-AGGGCAT CCCATT-ACT AA-GCCGACG TGGGCGGATT CCTCCGATTC
MLtp11        CAATTATTTC TCTTATTGGA TCATTGTCTA AGGCAAAATT TTGTAACACC TT-AGGGCAT CCCATT-ACT AA-GCCGACG TGGGCGGATT CCTCCGATTC
Ltr680        CAATTATTTC TCTTATTGGA TCATTGTCTA AGGCAAAATT TTGTAACACC TT-AGGGCAT CCCATT-ACT AA-GCCGACG TGGGCGGATT CCTCCGATTC
MLfl11        CAATTATTTC TCTTATTGGA TCATTGTCTA AGGCAAAATT TTGTAACACC TT-AGGGCAT CCCATT-ACT AA-GCCGACG TGGGCGGATT CCTCCGATTC
LplM57        CAATTATTTC TCTTATTGGA TCATTGTCTA AGGCAAAATT TTGTAACACA TT-AGGGCAT CCCATT-ACT AA-GCCGACG TGGGCGGATT CCTCCGATTC
Lti472        CAATTATTTC TCTTATTGGA TCATTGTCTA AGGCAAAATT TTGTAACACA TT-AGGGCAT CCCATT-ACT AAAGCCGACG -GGGCGGATT CCTCCGATTC
LthVie        CAATTATTTC TCTTACTGGA TCATTGTCTA AGGCAAAATT TTGTAACACC TTTAGGGCAT CCCATTTACT AA-GCCGACG TGGGCGGATT CCTCCGATTC
MLpu11        CAATTATTTC TCTTATTGGA TCATTGTCTA AGGCAAAATT TTGTAACACA TT-AGGGCAT CCCATT-ACT AA-GCCGACG TGGGCGGATT CCTCCGATTC
Lmo316        CAATTATTTC TCTTATTGGA TCATTGTCTA AGGCAAAATT TTGTAACACA TT-AGGGCAT CCCATT-ACT AA-GCCGACG TGGGCGGATT CCTCCGATTC
LacB11        CAATTATTTC TCTTATTGGC TCATTGTCTA AGGCAAAATT TTGTAACACA TT-AGGGCAT CCCATT-ACT AA-GCCGACG TGGGCGGATT CCTCCGATTC
Lar253        CAATTATTTC TCTTATTGGA TCATTGTCTA AGGCAAAATT TTGTAACACA TT-AGGGCAT CCCATT-ACT AA-GCCGACG TGGGCGGATT CCTCCGATTC
MLas11        CAATTATTTC TCTTATTGGA TCATTGTCTA AGGCAAAATT TTGTAACACA TT-AGGGCAT CCCATT-ACT AA-GCCGACG TGGGCGGATT CCTCCGATTC
MLma11        CAATTATTTC TCTTATTGGC TCATTGTCTA AGGCAAAATT TTGTAACACA TT-AGGGCAT CCCATT-ACT AA-GCCGACG TGGGCGGATT CCTCCGATTC
Lmu283        CAATTATTTC TCTTATTGGA TCATTGTCTA AGGCAAAATT TTGTAACACA TT-AGGGCAT CCCATT-ACT AA-GCCGACG TGGGCGGATT CCTCCGATTC
MLcr11        CAATTATTTC TCTTATTGGA TCATTGTCTA AGGCAAAATT TTGTAACACA TT-AGGGCAT CCCATT-ACT AA-GCCGACG TGGGCGGATT CCTCCGATTC
LpebM2        ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Mni674        CAATTATTTC TCTTATTGGA TCATTGTCTA AGgCAAAATT TTGTAACACA TT-AGGGCAT CCCATT-ACT AA-GCCGACG TGGGCGGATT CCTCCGATTC
Mpa603        CAATTATTTC TCTTATTGGA TCATTGTCTA AGGCAAAATT TTGTAACACA TT-AGGGCAT CCCATT-ACT AA-GCCGACG TGGGCGGATT CCTCCGATTC
Msy597        CAATTATTTC TCTTATTGGA TCATTGTCTA AGGCAAAATT TTGTAACACA TT-AGGGCAT CCCATT-ACT AA-GCCGACG TGGGCGGATT CCTCCGATTC
Mne795        CAATTATTTC TCTTATTGGA TCATTGTCTA AGGCAAAATT TTGTAACACA TT-AGGGCAT CCCATT-ACT AA-GCCGACG TGGGCGGATT CCTCCGATTC
Mve442        CAATTATTTC TCTTATTGGA TCATTGTCTA AGGCAAAATT TTGTAACACA TT-AGGGCAT CCCATT-ACT AA-GCCGACG TGGGCGGATT CCTCCGATTC
Mal338        CAATTATTTC TCTTATTGGA TCATTGTCTA AGGCAAAATT TTGTAACACA TT-AGGGCAT CCCATT-ACT AA-GCCGACG TGGGCGGATT CCTCCGATTC
Mto185        CAATTATTTC TCTTATTGGA TCATTGTCTA AGGCAAAATT TTGTAACACA TT-AGGGCAT CCCATT-ACT AA-GCCGACG TGGGCGGATT CCTCCGATTC
Mmo593        CAATTATTTC TCTTATTGGA TCATTGTCTA AGGCAAAATT TTGTAACACA TT-AGGGCAT CCCATT-ACT AA-GCCGACG TGGGCGGATT CCTCCGATTC
Mhi672        CAATTATTTC TCTTATTGGA TCATTGTCTA AGGCAAAATT TTGTAACACA TT-AGGGCAT CCCATT-ACT AA-GCCGACG TGGGCGGATT CCTCCGATTC
Ahi270        CAATCATTTC TCTTATTGGA TCATTGTCTA AGGCAAAATT TTGTAACACA TT-AGGGCAT CCCATT-ACT AA-GCCGACG TGGGCGGATT CCTCCGATTC
Alo596        CAATTATTTC TCTTATTGGA TCATTGTCTA AGGCAAAATT TTGTAACACA TT-AGGGCAT CCCATT-ACT AA-GCCGACG TGGGCGGATT CCTCCGATTC
AluM53        ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Mca572        CAATCATTTC TCTTATTGGA TCATTGTCTA AGGCAAAATT TTGTAACACA TT-AGGGCAT CCCATT-ACT AA-GCCGACG TGGGCGGATT CCTCCGATTC
MMae11        CAATTATTTC TCTTATTGGA TCATTGTCTA AGGCAAAATT TTGTAACACA TT-AGGGCAT CCCATT-ACT AA-GCCGACG TGGGCGGATT CCTCCGATTC
Mtr683        CAATTATTTC TCTTATTGGA TCATTGTCTA AGGCAAAATT TTGTAACACA TT-AGGGCAT CCCATT-ACT AA-GCCGACG TGGGCGGATT CCTCCGATTC
Mma671        CAATTATTTA TCTTATTGGA TCATTGTCTA AGGCAAAATT TTGTAACACA TT-AGGGCAT CCCATT-AGT AA-GCCGACG TGGGCCGATT CCTCCGATTC
Mtf502        CAATTATTTC TCTTATTGGA TCATTGTCTA AGGCAAAATT TTGTAACACA TT-AGGGCAT CCCATT-AGT AA-GCCGACG TGGGCCGATT CCTCCGATTC
LphM81        CAATTATTTC TCTTATTGGA TCATTGTCTA AGGCAAAATT TTGTAACACA TT-AGGGCAT CCCATT-ACT AA-GCCGACG TGGGCGGATT CCTCCGATTC
AniM31        CAATTATTTC TCTTATTGGA TCGTTGTCTA AGGCAAAATT TTGTAACACA TT-AGGGCAT CCCATT-AGT AA-GCCGACG TGGGCCGATT CCTCCGATTC
MKvi11        CAATTATTTC TCTTATTGGA TCATTGTCTA AGGCAAAATT TTGTAACACA TT-AGGGCAT CCCATT-AGT AA-GCCGACG TGGGCCGATT CCTCCGATTC
MAros1        CAATTATTTC TCTTATTGGA TCATTGTCTA AGGCAAAATT TTGTAACACA TT-AGGGCAT CCCATT-AGT AA-GCCGACG TGGGCCGATT CCTCCGATTC
MshM21        CAATTATTTC TCTTATTGGC TCATTGTCTA AGGCGAAATT TTGTAACACA TT-AGGGCAT CCCATT-AGT AA-GCCGACG TGGGCCGATT CCTCCGATTC
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                  1410       1420       1430       1440       1450       1460       1470       1480       1490       1500
MAar11      TGATATTATT GACCGATTTG TGCGTATATG CAGAAATCTT TCTCATTACC ACAGTGGATC TTCAAAAAAA AAGAGTTTGT ATCGAATAAA ATATATACTT
Aca594      TGATATTATT GACCGATTTG TGCGTATATG CAGAAATCTT TCTCATTACC ACAGTGGATC TTCAAAAAAA AAGAGTTTGT ATCGAATAAA ATATATACTT
MAof11      TGATATTATT GACCGATTTG TGCGTATATG CAGAAATCTT TCTCATTACC ACAGTGGATC TTCAAAAAAA AAGAGTTTGT ATCGAATAAA ATATATACTT
Lol451      TGATATTATT GACCGATTTG TGCGTATATG CAGAAATCTT TCTCATTATC ACAGTGGATC TTCAAAAAAA AAGAGTTTGT ATCGAATAAA ATATATACTT
Lob144      TGATATTATT GACCGATTTG TGCGTATATG CAGAAATCTT TCTCATTATC ACAGTGGATC TTCAAAAAAA AAGAGTTTGT ATCGAATAAA ATATATACTT
Lbr141      TGATATTATT GACCGATTTG TGCGTATATG CAGAAATCTT TCTCATTATC ACAGTGGATC TTCAAAAAAA AAGAGTTTGT ATCGAATAAA ATATATACTT
Lag308      TGATATTATT GACCGATTTG TGCGTATATG CAGAAATCTT TCTCATTATC ACAGTGGATC TTCAAAAAAA AAGAGTTTGT ATCGAATAAA ATATATACTT
MLtp11      TGATATTATT GACCGATTTG TGCGTATATG CAGAAATCTT TCTCATTATC ACAGTGGATC TTCAAAAAAA AAGAGTTTGT ATCGAATAAA ATATATACTT
Ltr680      TGATATTATT GACCGATTTG TGCGTATATG CAGAAATCTT TCTCATTATC ACAGTGGATC TTCAAAAAAA AAGAGTTTGT ATCGAATAAA ATATATACTT
MLfl11      TGATATTATT GACCGATTTG TGCGTATATG CAGAAATCTT TCTCATTATC ACAGTGGATC TTCAAAAAAA AAGAGTTTGT ATCGAATAAA ATATATACTT
LplM57      TGATATTATT GACCGATTTG TGCGTATATG CAGAAATCTT TCTCATTATC ACAGCGGATC TTCAAAAAAA AAGAGTTTGT ATCGAATAAA ATATATCCTT
Lti472      TGATATTATT GACCGATTTG TGCGTATATG CAGAAATCTT TCTCATTATC ACAGTGGATC TTCAAAAAAA AAGAGTTTGT ATCGAATAAA ATATATACTT
LthVie      TGATATTATT GACCGATTTG TGCGTATATG CAGAAATCTT TCTCATTATC ACAGTGGATC TTCAAAAAAA AAGAGTTTGT ATCGAATAAA ATATATACTT
MLpu11      TGATATTATT GACCGATTTG TGCGTATATG CAGAAATCTT TCTCATTATC ACAGTGGATC TTCAAAAAAA AAGAGTTTGT ATCGAATAAA ATATATACTT
Lmo316      TGATATTATT GACCGATTTG TGCKTATATG CAGAAATCTT TCTCATTATC ACAGTGGATC TTCAAAAAAA AAGAGTTTGT ATCGAATAAA ATATATACTT
LacB11      TGATATTATT GACCGATTTG TGCGTATATG CAGAAATCTT TCTCATTATC ACAGTGGATC TTCAAAAAAA AAGAGTTTGT ATCGAATAAA ATATATACTT
Lar253      TGATATTATT GACCGATTTG TGCGTATATG CAGAAATCTT TCTCATTATC ACAGCGGATC TTCAAAAAAA AAGAGTTTGT ATCGAATAAA ATATATCCTT
MLas11      TGATATTATT GACCGATTTG TGCGTATATG CAGAAATCTT TCTCATTATC ACAGCGGATC TTCAAAAAAA AAGAGTTTGT ATCGAATAAA ATATATCCTT
MLma11      TGATATTATT GACCGATTTG TGCGTATATG CAGAAATCTT TCTCATTATC ACAGTGGATC TTCAAAAAAA AAGAGTTTGT ATCGAATAAA ATATATACTT
Lmu283      TGATATTATT GACCGATTTG TGCGTATATG CAGAAATCTT TCTCATTATC ACAGCGGATC TTCAAAAAAA AAGAGTTTGT ATCGAATAAA ATATATCCTT
MLcr11      TGATATTATT GACCGATTTG TGCGTATATG CAGAAATCTT TCTCATTATC ACAGCGGATC TTCAAAAAAA AAGAGTTTGT ATCGAATAAA ATATATCCTT
LpebM2      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Mni674      TGATATTATT GACCGATTTG TGCGTATATG CAGAAATCTT TCTCATTATC ACAGCGGATC TTCAAAAAAA AAAAGTTTGT ATCGAATAAA ATATATCCTT
Mpa603      TGATATTATT GACCGATTTG TGCGTATATG CAGAAATCTT TCTCATTATC ACAGCGGATC TTCAAAAAAA AAGAGTTTGT ATCGAATAAA ATATATCCTT
Msy597      TGATATTATT GACCGATTTG TGCGTATATG CAGAAATCTT TCTCATTATC ACAGCGGATC TTCAAAAAAA AAGAGTTTGT ATCGAATAAA ATATATCCTT
Mne795      TGATATTATT GACCGATTTG TGCGTATATG CAGAAATCTT TCTCATTATC ACAGCGGATC TTCAAAAAAA AAGAGTTTGT ATCGAATAAA ATATATCCTT
Mve442      TGATATTATT GACCGATTTG TGCGTATATG CAGAAATCTT TCTCATTATC ACAGCGGATC TTCAAAAAAA AAGAGTTTGT ATCGAATAAA ATATATCCTT
Mal338      TGATATTATT GACCGATTTG TGCGTATATG CAGAAATCTT TCTCATTATC ACAGTGGATC TTCAAAAAAA AAGAGTTTGT ATCGAATAAA ATATATACTT
Mto185      TGATATTATT GACCGATTTG TGCGTATATG CAGAAATCTT TCTCATTATC ACAGTGGATC TTCAAAAAAA AAGAGTTTGT ATCGAATAAA ATATATACTT
Mmo593      TGATATTATT GACCGATTTG TGCGTATATG CAGAAATCTT TCTCATTATC ACAGTGGATC TTCAAAAAAA AAGAGTTTGT ATCGAATAAA ATATATACTT
Mhi672      TGATATTATT GACCGATTTG TGCGTATATG CAGAAATCTT TCTCATTATC ACAGTGGATC TTCAAAAAAA AAGAGTTTGT ATCGAATAAA ATATATACTT
Ahi270      TGATATTATT GACCGATTTG TGCGTATATG CAGAAATCTT TCTCATTATC ACAGTGGATC TTCAAAAAAA AAGAGTTTGT ATCGAATAAA ATATATACTT
Alo596      TGATATTATT TACCGATTTG TGCGTATATG CAGAAATCTT TCTCATTATC ACAGTGGATC TTCAAAAAAA AAGAGTTTGT ATCGAATAAA ATATATACTT
AluM53      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Mca572      TGATATTATT GACCGATTTG TGCGTATATG CAGAAATCTT TCTCATTATC ACAGTGGATC TTCAAAAAAA AAGAGTTTGT ATCGAATAAA ATATATACTT
MMae11      TGATATTATT GACCGATTTG TGCGTATATG CAGAAATCTT TCTCATTATC ACAGTGGATC TTCAAAAAAA AAGAGTTTGT ATCGAATAAA ATATATACTT
Mtr683      TGATATTATT GACCGATTTG TGCGTATATG CAGAAATCTT TCTCATTATC ACAGTGGATC TTCAAAAAAA AAGAGTTTGT ATCGAATAAA ATATATACTT
Mma671      TGATATTATT GACCGATTTG CGCGTATATG CAGAAATCTT TCTCATTATC ACAGTGGATC TTCAAAAAAA AAGAGTTTGT ATCGAATAAA ATATATACTT
Mtf502      TGATATTATT GACCGATTTG CGCGTATATG CAGAAATCTT TCTCATTATC ACAGTGGATC TTCAAAAAAA AAGAGTTTGT ATCGAATAAA ATATATACTT
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LphM81        TGATATTATT GACCGATTTG TGCGTATATG CAGAAATCTT TCTCATTATC ACAGTGGATC TTCAAAAAAA AAGAGTTTGT ATCGAATAAA ATATATACTT
AniM31        TGATATTATT GACCGATTTG TGCGTATATG CAGAAATCTT TCTCATTATC ACAGTGGATC TTCAAAAAAA AAGAGTTTGT ATCGAATAAA ATATATACTT
MKvi11        TGATATTATT GACCGATTTG TGCGTATATG CAGAAATCTT TCTCATTATC ACAGTGGATC TTCAAAAAAA AAAAGTTTGT ATCGAATAAA ATATATACTT
MAros1        TGATATTATT GAACGATTTG TGCGTATATG CAGAAATCTT TCTCATTATC ACAGTGGATC TTCAAAAAAA AAGAGTTTGT ATCGAATAAA ATATATACTT
MshM21        TGATATTATT GACCGATTTG TGCGTATATG CAGAAATCTT TCTCATTATC ACAGTGGATC TTCAAAAAAA AAGAGTTTGT ATCGAGTAAA ATATATACTT


              ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    1510       1520       1530       1540       1550       1560       1570       1580       1590       1600
MAar11        CGGTTTTCTT GTGTTAAAAC TTTGGCCCGT AAACACAAAA GTACTGTACG TGCTTTTTTG AAAAGATTAG GTTCGGGATT TTTGGAAGAA TTCTTTACGG
Aca594        CGGTTTTCTT GTGTTAAAAC TTTGGCCCGT AAACACAAAA GTACTGTACG TGCTTTTTTG AAAAGATTAG GTTCGGGATT TTTGGAAGAA TTCTTTACGG
MAof11        CGGTTTTCTT GTGTTAAAAC TTTGGCCCGT AAACACAAAA GTACTGTACG TGCTTTTTTG AAAAGATTAG GTTCGGGATT TTTGGAAGAA TTCTTTACGG
Lol451        CGGTTTTCTT GTGTTAAAAC TTTGGCCCGT AAACACAAAA GTACTGTACG TGCTTTTTTG AAAAGATTAG GTTCGGAATT TTTGGAAGAA TTCTTTACGG
Lob144        CGGTTTTCTT GTGTTAAAAC TTTGGCCCGT AAACACAAAA GTACTGTACG TGCTTTTTTG AAAAGATTAG GTTCGGAATT TTTGGAAGAA TTCTTTACGG
Lbr141        CGGTTTTCTT GTGTTAAAAC TTTGGCCCGT AAACACAAAA GTACTGTACG TGCTTTTTTG AAAAGATTAG GTTCGGAATT TTTGGAAGAA TTCTTTACGG
Lag308        CGATTTTCTT GTGTTAAAAC TTTGGCCCGT AAACACAAAA GTACTGTACG TGCTTTTTTG AAAAGATTAG GTTCGGAATT TTTGGAAGAA TTCTTTACGG
MLtp11        CGGTTTTCTT GTGTTAAAAC TTTGGCCCGT AAACACAAAA GTACTGTACG TGCTTTTTTG AAAAGATTAG GTTCGGAATT TTTGGAAGAA TTCTTTACGG
Ltr680        CGGTTTTCTT GTGTTAAAAC TTTGGCCCGT AAACACAAAA GTACTGTACG TGCTTTTTTG AAAAGATTAG GTTCGGAATT TTTGGAAGAA TTCTTTACGG
MLfl11        CGGTTTTCTT GTGTTAAAAC TTTGGCCCGT AAACACAAAA GTACTGTACG TGCTTTTTTG AAAAGATTAG GTTCGGAATT TTTGGAAGAA TTCTTTACGG
LplM57        CGGTTTTCTT GTGTTAAAAC TTTGGCCCGT AAACACAAAA GTACTGTACG TGCTTTTTTG AAAAGATTAG GTTCGGAATT TTTGGAAGAA TTCTTTACGG
Lti472        CGGTTTTCTT GTGTTAAAAC TTTGGCCCGT AAACACAAAA GTACTGTACG TGCTTTTTTG AAAAGATTAG GTTCGGAATT TTTGGAAGAA TTCTTTACGG
LthVie        CGGTTTTCTT GTGTTAAAAC TTTGGCCCGT AAACACAAAA GTACTGTACG TGCTTTTTTG AAAAGATTAG GTTCGGAATT TTTGGAAGAA TTCTTTACGG
MLpu11        CGGTTTTCTT GTGTTAAAAC TTTGGCCCGT AAACACAAAA GTACTGTACG TGCTTTTTTG AAAAGATTAG GTTCGGAATT TTTGGAAGAA TTCTTTACGG
Lmo316        CGGTTTTCTT GTGTTAAAAC TTTGGCCCGT AAACACAAAA GTACTGTACG TGCTTTTTTG AAAAGATTAG GTTCGGAATT TTTGGAAGAA TTCTTTACGG
LacB11        CGGTTTTCTT GTGTTAAAAC TTTGGCCCGT AAACACAAAA GTACTGTACG TGCTTTTTTG AAAAGATTAG GTTCGGAATT TTTGGAAGAA TTCTTTACGG
Lar253        CGGTTTTCTT GTGTTAAAAC TTTGGCCCGT AAACACAAAA GTACTGTACG TGCTTTTTTG AAAAGATTAG GTTCGGAATT TTTGGAAGAA TTCTTTACGG
MLas11        CGGTTTTCTT GTGTTAAAAC TTTGGCCCGT AAACACAAAA GTACTGTACG TGCTTTTTTG AAAAGATTAG GTTCGGAATT TTTGGAAGAA TTCTTTACGG
MLma11        CGGTTTTCTT GTGTTAAAAC TTTGGCCCGT AAACACAAAA GTACTGTACG TGCTTTTTTG AAAAGATTAG GTTCGGAATT TTTGGAAGAA TTCTTTACGG
Lmu283        CGGTTTTCTT GTGTTAAAAC TTTGGCCCGT AAACACAAAA GTACTGTACG TGCTTTTTTG AAAAGATTAG GTTCGGAATT TTTGGAAGAA TTCTTTACGG
MLcr11        CGGTTTTCTT GTGTTAAAAC TTTGGCCCGT AAACACAAAA GTACTGTACG TGCTTTTTTG AAAAGATTAG GTTCGGAATT TTTGGAAGAA TTCTTTACGG
LpebM2        ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Mni674        CGGTTTTCTT GTGTTAAAAC TTTGGCCCGT AAACACAAAA GTACTGTACG TGCTTTTTTG AAAAGATTAG GTTCGGAATT TTTGGAAGAA TTCTTTACGG
Mpa603        CGGTTTTCTT GTGTTAAAAC TTTGGCCCGT AAACACAAAA GTACTGTACG TGCTTTTTTG AAAAGATTAG GTTCGGAATT TTTGGAAGAA TTCTTTACGG
Msy597        CGGTTTTCTT GTGTTAAAAC TTTGGCCCGT AAACACAAAA GTACTGTACG TGCTTTTTTG AAAAGATTAG GTTCGGAATT TTTGGAAGAA TTCTTTACGG
Mne795        CGGTTTTCTT GTGTTAAAAC TTTGGCCCGT AAACACAAAA GTACTGTACG TGCTTTTTTG AAAAGATTAG GTTCGGAATT TTTGGAAGAA TTCTTTACGG
Mve442        CGGTTTTCTT GTGTTAAAAC TTTGGCCCGT AAACACAAAA GTACTGTACG TGCTTTTTTG AAAAGATTAG GTTCGGAATT TTTGGAAGAA TTCTTTACGG
Mal338        CGGTTTTCTT GTGTTAAAAC TTTGGCCCGT AAACACAAAA GTACTGTACG TGCTTTTTTG AAAAGATTAG GTTCGGAATT TTTGGAAGAA TTCTTTACGG
Mto185        CGGTTTTCTT GTGTTAAAAC TTTGGCCCGT AAACACAAAA GTACTGTACG TGCTTTTTTG AAAAGATTAG GTTCGGAATT TTTGGAAGAA TTCTTTACGG
Mmo593        CGGTTTTCTT GTGTTAAAAC TTTGGCCCGT AAACACAAAA GTACTGTACG TGCTTTTTTG AAAAGATTAG GTTCGGAATT TTTGGAAGAA TTCTTTACGG
Mhi672        CGGTTTTCTT GTGTTAAAAC TTTGGCCCGT AAACACAAAA GTACTGTACG TGCTTTTTTG AAAAGATTAG GTTCGGAATT TTTGGAAGAA TTCTTTACGG
Ahi270        CGGTTTTCTT GTGTTAAAAC TTTGGCCCGT AAACACAAAA GTACTGTACG TGCTTTTTTG AAAAGATTAG GTTCGGAATT TTTGGAAGAA TTCTTTACGG
Alo596        CGGTTTTCTT GTGTTAAAAC TTTGGCCCGT AAACACAAAA GTACTGTACG TGCTTTTTTG AAAAGATTAG GTTCGGAATT TTTGGAAGAA TTCTTTACGG
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AluM53       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Mca572       CGGTTTTCTT GTGTTAAAAC TTTGGCCCGT AAACACAAAA GTACTGTACG TGCTTTTTTG AAAAGATTAG GTTCGGAATT TTTGGAAGAA TTCTTTACGG
MMae11       CGGTTTTCTT GTGTTAAAAC TTTGGCCCGT AAACACAAAA GTACTGTACG TGCTTTTTTG AAAAGATTAG GTTCGGAATT TTTGGAAGAA TTCTTTACGG
Mtr683       CGGTTTTCTT GTGTTAAAAC TTTGGCCCGT AAACACAAAA GTACTGTACG TGCTTTTTTG AAAAGATTAG GTTCGGAATT TTTGGAAGAA TTCTTTACGG
Mma671       CGGTTTTCTT GTGTTAAAAC TTTGGCCCGT AAACACAAAA GTACTGTACG TGCTTTTTTG AAAAGATTAG GTTCGGAATT TTTGGAAGAA TTCTTTACGG
Mtf502       CGGTTTTCTT GTGTTAAAAC TTTGGCCCGT AAACACAAAA GTACTGTACG TGCTTTTTTG AAAAGATTAG GTTCGGAATT TTTGGAAGAA TTCTTTACGG
LphM81       CGGTTTTCTT GTGTTAAAAC TTTGGCCCGT AAACACAAAA GTACTGTACG TGCTTTTTTG AAAAGATTAG GTTCGGAATT TTTGGAAGAA TTCTTTACGG
AniM31       CGGTTTTCTT GTGTTAAAAC TTTGGCCCGT AAACACAAAA GTACTGTACG TGCTTTTTTG AAAAGATTAG GTTCGGAATT TTTGGAAGAA TTCTTTACGG
MKvi11       CGGTTTTCTT GTGTTAAAAC GTTGGCCCGT AAACACAAAA GTACTGTACG TGCTTTTTTG AAAAGATTAG GTTCGGAATT TTTGGAAGAA TTCTTTACGG
MAros1       CGGTTTTCTT GTGTTAAAAC TTTGGCCCGT AAACACAAAA GTACTGTACG TGCTTTTTTG AAAAGATTAG GTTCGGAATT TTTGGAAGAA TTCTTTACGG
MshM21       CGGTTTTCTT GTGTTAAAAC TTTGGCCCGT AAACACAAAA GTACTGTACG TGCTTTTTTG AAAAGATTAG GTTCCGGATT TTTGGAAGAA TTCTTTACGG


             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   1610       1620       1630       1640       1650       1660       1670       1680       1690       1700
MAar11       AAACGGAAGA AGACCATGTT TTTTCTTTGA TTTTCCCAAA AGGTTTTTTT ACTTTGCGAA AGTTCTATCG GGGACGAATT TGGTATTTGG ATATTATTTG
Aca594       AAACGGAAGA AGACCATGTT TTTTCTTTGA TTTTCCCAAA AGGTTTTTTT ACTTTGCGAA AGTTCTATCG GGGACGAATT TGGTATTTGG ATATTATTTG
MAof11       AAACGGAAGA AGACCATGTT TTTTCTTTGA TTTTCCCAAA AGGTTTTTTT ACTTTGCGAA AGTTCTATCG GGGACGAATT TGGTATTTGG ATATTATTTG
Lol451       AAACGGAAGA AGACCATGTT TTTTCTTTGA TCTTTCCAAA AGGTTTTTTT ACTTTGCGAA AGTTCTATCG GGGACGAATT TGGTATTTGG ATATTATTTG
Lob144       AAACGGAAGA AGACCATGTT TTTTCTTTGA TCTTTCCAAA AGGTTTTTTT ACTTTGCGAA AGTTCTATCG GGGACGAATT TGGTATTTGG ATATTATTTG
Lbr141       AAACGGAAGA AGACCATGTT TTTTCTTTGA TCTTTCCAAA AGGTTTTTTT ACTTTGCGAA AGTGCTATCG GGGACGAATT TGGTATTTGG ATATTATTTG
Lag308       AAACGGAAGA AGACCATATT TTTTCTTTGA TCTTTCCAAA AGGTTTTTTT ACTTTGCGAA AGTTCTATCG GGGACGAATT TGGTATTTGG ATATTATTTG
MLtp11       AAACGGAAGA AGACCATGTT TTTTCTTTGA TCTTTCCAAA AGGTTTTTTT ACTTTGCGAA AGTTCTATCG GGGACGAATT TGGTATTTGG ATATTATTTG
Ltr680       AAACGGAAGA AGACCATGTT TTTTCTTTGA TCTTTCCAAA AGGTTTTTTT ACTTTGCGAA AGTTCTATCG GGGACGAATT TGGTATTTGG ATATTATTTG
MLfl11       AAACGGAAGA AGACCATATT TTTTCTTTGA TCTTTCCAAA AGGTTTTTTT ACTTTGCGAA AGTTCTATCG GGGACGAATT TGGTATTTGG ATATTATTTG
LplM57       AAACGGAAGA AGACCATGTT TTTTCTTTGA TCTTTCCAAA AGGTTTTTTT ACTTTGCGAA AGTTCTATCG GGGACGAATT TGGTATTTGG ATATTATTTG
Lti472       AAACGGAAGA AGACCATGTT TTTTCTTTGA TCTTTCCAAA AGGTTTTTTT ACTTTGCGAA AGTTCTATCG GGGACGAATT TGGTATTTGG ATATTATTTG
LthVie       AAACGGAAGA AGACCATGTT TTTTCTTTGA TCTTTCCAAA AGGTTTTTTT ACTTTGCGAA AGTTCTATCG GGGACGAATT TGGTATTTGG ATATTATTTG
MLpu11       AAACGGAAGA AGACCATGTT TTTTCTTTGA TCTTTCCAAA AGGTTTTTTT ACTTTGCGAA AGTTCTATCG GGGACGAATT TGGTATTTGG ATATTATTTG
Lmo316       AAACGGAAGA AGACCATGTT TTTTCTTTGA TCTTTCCAAA AGGTTTTTTT ACTTTGCGAA AGTTCTATCG GGGACGAATT TGGTATTTGG ATATTATTTG
LacB11       AAACGGAAGA AGACCATGTT TTTTCTTTGA TCTTTCCAAA AGGTTTTTTT ACTTTGCGAA AGTTCTATCG GGGACGAATT TGGTATTTGG ATATTATTTG
Lar253       AAACGGAAGA AGACCATGTT TTTTCTTTGA TCTTTCCAAA AGGTTTTTTT ACTTTGCGAA AGTTCTATCG GGGACGAATT TGGTATTTGG ATATTATTTG
MLas11       AAACGGAAGA AGACCATGTT TTTTCTTTGA TCTTTCCAAA AGGTTTTTTT ACTTTGCGAA AGTTCTATCG GGGACGAATT TGGTATTTGG ATATTATTTG
MLma11       AAACGGAAGA AGACCATGTT TTTTCTTTGA TCTTTCCAAA AGGTTTTTTT ACTTTGCGAA AGTTCTATCG GGGACGAATT TGGTATTTGG ATATTATTTG
Lmu283       AAACGGAAGA AGACCATGTT TTTTCTTTGA TCTTTCCAAA AGGTTTTTTT ACTTTGCGAA AGTTCTATCG GGGACGAATT TGGTATTTGG ATATTATTTT
MLcr11       AAACGGAAGA AGACCATGTT TTTTCTTTGA TCTTTCCAAA AGGTTTTTTT ACTTTGCGAA AGTTCTATCG GGGACGAATT TGGTATTTGG ATATTATTTG
LpebM2       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Mni674       AAACGGAAGA AGACCATGTT TTTTCTTTGA TCTTTCCAAA AGGTTTTTTT ACTTTGCGAA AGTTCTATCG GGGACGAATT TGGTATTTGG ATATTATTTG
Mpa603       AAACGGAAGA AGACCATGTT TTTTCTTTGA TCTTTCCAAA AGGTTTTTTT ACTTTGCGAA AGTTCTATCG GGGACGAATT TGGTATTTGG ATATTATTTG
Msy597       AAACGGAAGA AGACCATGTT TTTTCTTTGA TCTTTCCAAA AGGTTTTTTT ACTTTGCGAA AGTTCTATCG GGGACGAATT TGGTATTTGG ATATTATTTG
Mne795       AAACGGAAGA AGACCATGTT TTTTCTTTGA TCTTTCCAAA AGGTTTTTTT ACTTTGCGAA AGTTCTATCG GGGACGAATT TGGTATTTGG ATATTATTTG
Mve442       AAACGGAAGA AGACCATGTT TTTTCTTTGA TCTTTCCAAA AGGTTTTTTT ACTTTGCGAA AGTTCTATCG GGGACGAATT TGGTATTTGG ATATTATTTG
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Mal338          AAACGGAAGA AGACCATGTT TTTTCTTTGA TCTTTCCAAA AGGTTTTTTT ACTTTGCGAA AGTTCTATCG GGGACGAATT TGGTATTTGG ATATTATTTG
Mto185          AAACGGAAGA AGACCATGTT TTTTCTTTGA TCTTTCCAAA AGGTTTTTTT ACTTTGCGAA AGTTCTATCG GGGACGAATT TGGTATTTGG ATATTATTTG
Mmo593          AAACGGAAGA AGACCATGTT TTTTCTTTGA TCTTTCCAAA AGGTTTTTTT ACTTTGCGAA AGTTCTATCG GGGACGAATT TGGTATTTGG ATATTATTTG
Mhi672          AAACGGAAGA AGACCATGTT TTTTCTTTGA TCTTTCCAAA AGGTTTTTTT ACTTTGCGAA AGTTCTATCG GGGACGAATT TGGTATTTGG ATATTATTTG
Ahi270          AAACGGAAGA AGACCATGTT TTTTCTTTGA TCTTTCCAAA AGGTTTTTTT ACTTTGCGAA AGTTCTATCG GGGACGAATT TGGTATTTGG ATATTATTTG
Alo596          AAACCGAAGA AGACCATGTT TTTTCTTTGA TCTTTCCAAA AGGTTTTTTT ACTTTGCGAA AGTTCTATCG GGGACGAATT TGGTATTTGG ATATTATTTG
AluM53          ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Mca572          AAACGGAAGA AGACCATGTT TTTTCTTTGA TCTTTCCAAA AGGTTTTTTT ACTTTGCGAA AGTTCTATCG GGGACGAATT TGGTATTTGG ATATTATTTG
MMae11          AAACGGAAGA AGACCATGTT TTTTCTTTGA TCTTTCCAAA AGGTTTTTTT ACTTTGCGAA AGTTCTATCG GGGACGAATT TGGTATTTGG ATATTATTTG
Mtr683          AAACGGAAGA AGACCATGTT TTTTCTTTGA TCTTTCCAAA AGGTTTTTTT ACTTTGCGAA AGTTCTATCG GGGACGAATT TGGTATTTGG ATATTATTTG
Mma671          AAACGGAAGA AGACCATGTT TTTTCTTTGA TCTTCCCAAA AGGTTTTTTT ACTTTGCGAA AGTTCTATCG GGGACGAATT TGGTATTTGG ATATTATTTG
Mtf502          AAACGGAAGA AGACCATGTT TTTTCTTTGA TCTTCCCAAA AGGTTTTTTT ACTTTGCGAA AGTTCTATCG GGGACGAATT TGGTATTTGG ATATTATTTG
LphM81          AAACGGAAGA AGACCATGTT TTTTCTTTGA TCTTTCCAAA AGGTTTTTTT ACTTTGCGAA AGTTCTATCG GGGACGCATT TGGTATTTGG ATATTATTTG
AniM31          AAACGGAAGA AGACCATGTT TTTTCTTTGA TCTTCCCAAA AGGTTTTTTT ACTTTGCGAA AGTTCTATCG GGGACGAATT TGGTATTTGG ATATTATTTG
MKvi11          AAACGGAAGA AGACCATGTT TTTTCTTTGA TCTTCCCAAA AGGTTTTTTT ACTTTGCGAA AGTTCTATCG GGGACGAATT TGGTATTTGG ATATTATTTG
MAros1          AAACGGAAGA AGACCATGTT TTTTCTTTGA TCTTCCCAAA AGGTTTTTTT ACTTTGCGAA AGTTCTATCG GGGACGAATT TGGTATTTGG ATATTATTTG
MshM21          AAACGGAAGA AGAGCATGTT TTTTCTTTGA TCTTCCCAAG AGGTTTTTTT ACTTTGCGAA AGTCCTATCG GGGACGAATT TGGTATTTGG ATATTATTTG


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                      1710       1720       1730       1740       1750       1760       1770       1780       1790       1800
MAar11          -TATCAATAC TCTGGTCAAT CATGACTGAT TGGTTATGAA ATTATGTAAA TTCAATTAAA ATAATAAAA- ---------- ---TCAAAAT GAGAATTTTT
Aca594          -TATCAATAC TCTGGTCAAT CATGACTGAT TGGTTATGAA ATTATGTAAA TTCAATTAAA ATAATAAAA- ---------- ---TCAAAAT GAGAATTTTT
MAof11          -TATCAATAC TCTGGTCAAT CATGACTGAT TGGTTATGAA ATTATGTAAA TTCAATTAAA ATAATAAAA- ---------- ---TCAAAAT GAGAATTTTT
Lol451          -TATCAATGC TCTGGTCAAT CATGATTGAT TGGTTATGAA ATTATGTAAA TTTTATTAAA ATAATAAAAT TAAAATAATA AAATCAAAAT GATAATTTTT
Lob144          -TATCAATGC TCTGGTCAAT CATGATTGAT TGGTTATGAA ATTATGTAAA TTTTATTAAA ATAATAAAAT TAAAATAATA AAATCAAAAT GATGATTTTT
Lbr141          -TATCAATGC TCTGGTCAAT CATGATTGAT TGGTTATGAA ATTATTTTAA TAAAATTAAA ATAATAAAA- ---------- ---TCAAAAT GATAATTTTT
Lag308          -TATCAATGC TCTGGTCAAT CATGATTGAT TGGTTATGAA ATTATGTAAA TTTTATTATT TTAATTTTAT TAAAATAATA AAATCAAAAT GATAATTTTT
MLtp11          -TATCAATGC TCTGGTCAAT CATGATTGAT TGGTTATGAA ATTATGTAAA TTTTATTAAA ATAATAAAAT TAAAATAATA AAATCAAAAT GATAATTTTT
Ltr680          -TATCAATGC TCTGGTCAAT CATGATTGAT TGGTTATGAA ATTATTTTAA TAAAATTAAA ATAATAAAAT TAAAATAATA AAATCAAAAT GATAATTTTT
MLfl11          -TATCAATGC TCTGGTCAAT CATGATTGAT TGGTTATGAA ATTATGTAAA TTTTATTATT TTAATTTTAT TAAAATAATA AAATCAAAAT GATAATTTTT
LplM57          -TATCAATGC TCTGGTCAAT CATGACTGAT TGGTTATGAA ATTTTGTAAA TTTTTTAAAA ATAATAAAA- ---------- AAATAAAAAT GATAATTTTT
Lti472          -TATCAATGC TCTGGTCAAT CATGACTGAT TGGTTATGAA ATTATGTAAA TTTTTAAAAA ATAATAAAAT TAAAATAATA AAATCAAAAT GATAATTTTT
LthVie          -TATCAATGC TCTGGTCAAT CATGATTGAT TGGTTATGAA ATTATGTAAA TTTTATTAAA ATAATAAAAT TAAAATAATA ATATCAAAAT GATGATTTTT
MLpu11          -TATCAATGC TCTGGTCAAT CATGATTGAT TGGTTATGAA ATTATGTAAA TTTTATTAAA ATAATAAAAT TAAAATAATA AAATCAAAAT GATAATTTTT
Lmo316          -TATCAATGC TCTGGTCAAT CATGATTGAT TGGTTATGAA ATTATGTAAA TTTTATTAAA ATAATAAAAT TAAAATAATA AAATCAAAAT GATA-TTTTT
LacB11          -TATCAATGC TCTGGTCAAT CATGACTGAT TGGTTATGAA ATTCTGTAAA TTTTATTAAA ATAATAAAA- ---------- ---TCAAAAT GATAATTTTT
Lar253          -TATCAATGC TCTGGTCAAT CATGACTGAT TGGTTATGAA ATTTTGTAAA TTTATTAAAA ATAATAAA-- --------TA AAATAAAAAT GATAATTTTT
MLas11          -TATCAATGC TCTGGTCAAT CATGACTGAT TGGTTATGAA ATTTTGTAAA TTTTTTTAAA ATAATAAAAA AAA------- -----AAAAT GATAATTTTT
MLma11          -TATCAATGC TCTGGTCAAT CATGACTGAT TGGTTATGAA ATTCTGTAAA TTTTATTAAA ATAATAAAA- ---------- ---TCAAAAT GATAATTTTT
Lmu283          GTATCAATGC TCTGGTCAAT CATGACTGAT TGGTTATGAA ATTATGTAAA TTTTTTCAAA ATAATAAAA- ---------- ----AAAAAT GATAATTTTT
MLcr11          -TATCAATGC TCTGGTCAAT CATGACTGAT TGGTTATGAA ATTATGTAAA TTTTTTAAAA ATAATAAAAA A--------- -----AAAAT GATAATTTTT
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LpebM2          ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Mni674          -TATCAATGC TCTGGTCAAT CATGACTGAT TGGTTATGAA ATTATGTAAA TTTATTAAAA ATAATAAAA- ---------- ----AAAAAT GATAATTTTT
Mpa603          -TATCAATGC TCTGGTCAAT CATGACTGAT TGGTTATGAA ATTATGTAAA TTTTTTCAAA ATAATAAAA- ---------- ----AAAAAT GATAATTTTT
Msy597          -TATCAATGC TCTGGTCAAT CATGACTGAT TGGTTATGAA ATTATGTAAA TTTATTAAAA ATAATAAAA- ---------- -----AAAAT GATAATTTTT
Mne795          -TATCAATGC TCTGGTCAAT CATGACTGAT TGGTTATGAA ATTATGTAAA TTTATTAAAA ATAATAAAA- ---------- -----AAAAT GATAATTTTT
Mve442          -TATCAATGC TCTGGTCAAT CATGACTGAT TGGTTATGAA ATTATGTAAA TTTTTTCAAA ATAATAAAAA ---------- -----AAAAT GATAATTTTT
Mal338          -TATCAATGC TCTGGTCAAT CATGATTGAT TGGTTATGAA ATTATTTTAA TTTTATTATT TTAATAAAAT TAAAATAATA AAATCAAAAT GATAATTTTT
Mto185          -TATCAATGC TCTGGTCAAT CATGATTGAT TGGTTATGAA ATTATTTTAA TTTTATTATT TTAATTTTAT TAAAATAATA AAATCAAAAT GATAATTTTT
Mmo593          -TATCAATGC TCTGGTCAAT CATGATTGAT TGGTTATGAA ATTATTTTAA TTTTATTATT TTAATAAAAT TAAAATAATA AAATCAAAAT GATAATTTTT
Mhi672          -TATCAATGC TCTGGTCAAT CATGATTGAT TGGTTATGAA ATTATGTAAA TTTTATTATT TTAATAAAAT TAAAATAATA AAATCAAAAT GATAATTTTT
Ahi270          -TATCAATGC TCTGGTCAAT CATGACTGAT TGGTTATGAA ATTATGTAAA TTTTATTAAA ATAATAAAAT TCAAATAATA AAATCAAAAT GATAATTTTT
Alo596          -TATCAATGC TCTGGTCAAT CATGACTGAT TGGTTATGAA ATTATGTAAA TTTTTTTAAA ATAATAAAAT TCAAATAATA AAATCAAAAT GATAATTTTT
AluM53          ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Mca572          -TATCAATGC TCTGGTCAAT CATGACTGAT TGGTTATGAA ATTATGTAAA TTTTATTAAA ATAATAAAAT TCAAATAATA AAATCAAAAT GATAATTTTT
MMae11          -TATCAATGC TCTGGTCAAT CATGACTGAT TGGTTATGAA ATTATGTAAA TTTTATTAAA ATAATAAAAT TAAAATAATA AAATCAAAAT GATAATTTTT
Mtr683          -TATCAATGC TCTGGTCAAT CATGACTGAT TGGTTATGAA ATTATGTAAA TTTTATTAAA ATAATAAAAT TAAAATAATA AAATCAAAAT GATAATTTTT
Mma671          -TATCAATGC TCTGGTCAAT CATGACTGAT TGGTTATGAA ATTATGTAAA TTCAATTAAA ATAATAAAA- ---------- ---------- -AGAATTTTT
Mtf502          -TATCAATGC TCTGGTCAAT CATGACTGAT TGGTTATGAA ATTATGTAAA TTCAATTAAA ATAATAAAA- ---------- ---------- -AGAATTTTT
LphM81          -TATCAATGC TCTGGTCAAT CATGACTGAT TGGTTATGAA ATTATGTAAA TTTTATTAAA ATAAGAAAA- ---------- ---TCAAAAT GATAATTTTT
AniM31          -TATCAATGC TCTGGTCAAT CATGACTGAT TGGTTATGAA ATTATGTAAA TTCAATTAAA ATAATAAAA- ---------- ---TCAAAAT GAGAATTTTT
MKvi11          -TATCAATAC TCTGGTCAAT CATGACTGAT TGGTTATGAA ATTATGTAAA TTCAATTAAA ATAATAAAA- ---------- ---TCAAAAT GAGAATTTTT
MAros1          -TATCAATAC TCTGGTCAAT CATGACTGAT TGGTTATGAA ATTATGTAAA TTAAATTAAA ATAATAAAA- ---------- ---TCAAAAT GATAATTTTT
MshM21          -TATCAATGC TCTGGTCAAT CATGAATGAT TGGTTATGAC ATTATGTAAA TTCAATTAAA ATAATAAAA- ---------- ---TAAAAAT GAGAATTTTT


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                      1810       1820       1830       1840       1850       1860       1870       1880       1890       1900
MAar11          -CCGAAATGA TGAAGAGATA ACAAACGAAT TT----CGTT CTAGTATTAA ATGTTCATGC A-----GTAA GAATAAGAGG GGATTGGCCG AGTATTCCAC
Aca594          -CCGAAATGA TGAAGAGATA ACAAACGAAT TT----CGTT CTAGTATTAA ATGTTCATGC A-----GTAA GAATAAGAGG GGATTGGCCG AGTATTCCAC
MAof11          -CCGAAATGA TGAAGAGATA ACAAACGAAT TT----CGTT CTAGTATTAA ATGTTCATGC A-----GTAA GAATAAGAGG GGATTGGCCG AGTATTCCAC
Lol451          -CCGAAATGA TGAAGAGATA ACAAACGAAT TT----ATTT CTAGTATTAA ATGTTCATGC A-----GTAA GAATAAGAGG GGATTGGCCG AGTATTCCAC
Lob144          -CCGAAATGA TGAAGAGATA ACAAACGAAT TT----ATTT CTAGTATTAA ATGTTCATGC A-----GTAA GAATAAGAGG GGATTGGCCG AGTATTCCAC
Lbr141          -CCGAAATGA TGAAGAGATA ACAAACGAAT TT----ATTT CTAGTATTAA ATGTTCATGC A-----GTAA GAATAAGAGG GGATTGGCCG AgTATTCCAC
Lag308          -CCGAAATGA TGAAGAGATA ACAAACGAAT TT----ATTT CTAGTATTAA ATGTTCATGC A-----GTAA GAATAAGAGG GGATTGGCCG AGTATTCCAC
MLtp11          -CCGAAATGA TGAAGAGATA ACAAACGAAT TT----ATTT CTAGTATTAA ATGTTCATGC A-----GTAA GAATAAGAGG GGATTGGCCG AGTATTCCAC
Ltr680          -CCGAAATGA TGAAGAGATA ACAAACGAAT TT----ATTT CTAGTATTAA ATGTTCATGC A-----GTAA GAATAAGAGG GGATTGGCCG AGTATTCCAC
MLfl11          CCCGAAATGA TGAAGAGATA ACAAACGAAT TT----ATTT CTAGTATTAA ATGTTCATGC A-----GTAA gAAtAAGAGG GGATtGGCCG AGTATtCCaC
LplM57          -CCGAAATGA TGAAGAGATA ACAAACGAAT TT----ATTT CTAGTATTAA ATGTTCATGC A-----GTAA GAATAAGAGG GGATTGGCCG AGTATTCCAC
Lti472          -CCGAAATGA TGAAGAGATA ACAAACGAAT TT----ATTT CTAGTATTAA ATGTTCATGC A-----GTAA GAATAAGAGG GGATTGGCCG AGTATTCCAC
LthVie          -CCGAAATGA TGAAGAGATA ACAAACGAAT TT----ATTT CTAGTATTAA ATGTTCATGC A-----GTAA GAATAAGAGG GGATTGGCCG AGTATTCCAC
MLpu11          -CCGAAATGA TGAAGAGATA ACAAACGAAT TT----ATTT CTAGTATTAA ATGTTCATGC A-----GTAA GAATAAGAGG GGATTGGCCG AGTATTCCAC
Lmo316          -CCGAAATGA TGAAGAGATA ACAAACGAAT TT----ATTT CTAGTATTAA ATGTTCATGC A-----GTAA GAATAAGAGG GGATTGGCCG AGTATTCCAC
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LacB11       -CCGAAATGA TGAAGAGATA ACAAACGAAT TT----ATTT CTAGTATTAA ATGTTCATGC A-----GTAA GAATAAGAGG GGATTGGCCG AGTATTCCAC
Lar253       -CCGAAATGA TGAAGAGATA ACAAACGAAT TT----ATTT CTAGTATTAA ATGTTCATGC A-----GTAA GAATAAGAGG GGATTGGCCG AGTATTCCAC
MLas11       -CCGAAATGA TGAAGAGATA ACAAACGAAT TT----ATTT CTAGTATTAA ATGTTCATGC A-----GTAA GAATAAGAGG GGATTGGCCG AGTATTCCAC
MLma11       -CCGAAATGA TGAAGAGATA ACAAACGAAT TT----ATTT CTAGTATTAA ATGTTCATGC A-----GTAA GAATAAGAGG GGATTGGCCG AGTATTCCAC
Lmu283       TCCGAAATGA TGAAGAGATA ACAAACGAAT TT----ATTT CTAGTATTAA ATGTTCATGC A-----GTAA GAATAAGAGG GGATTGGCCG AGTATTCCAC
MLcr11       -CCGAAATGA TGAAGAGATA ACAAACGAAT TT----ATTT CTAGTATTAA ATGTTCATGC A-----GTAA GAATAAGAGG GGATTGGCCG AGTATTCCAC
LpebM2       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Mni674       -CCGAAATGA TGAAGAGATA ACAAACGCAT TT----TTTT CTAGTATTAA ATGTTCATGC A-----GTAA GAATAAGAGG GGATTGGCCG AGTATTCCAC
Mpa603       -CCGAAATGA TGAAGAGATA ACAAACGAAT TT----ATTT CTAGTATTAA ATGTTCATGC A-----GTAA GAATAAGAGG GGATTGGCCG AGTATTCCAC
Msy597       -CCGAAATGA TGAAGAGATA ACAAACGAAT TT----ATTT CTAGTATTAA ATGTTCATGC A-----GTAA GAATAAGAGG GGATTGGCCG AGTATTCCAC
Mne795       -CCGAAATGA TGAAGAGATA ACAAACGAAT TT----ATTT CTAGTATTAA ATGTTCATGC A-----GTAA GAATAAGAGG GGATTGGCCG AGTATTCCAC
Mve442       -CCGAAATGA TGAAGAGATA ACAAACGAAT TT----ATTT CTAGTATTAA ATGTTCATGC A-----GTAA GAATAAGAGG GGATTGGCCG AGTATTCCAC
Mal338       -CCGAAATGA TGAAGAGATA ACAAACGAAT TT----ATTT CTAGTATTAA ATGTTCATGC A-----GTAA GAATAAGAGG GGATTGGCCG AGTATTCCAC
Mto185       -CCGAAATGA TGAAGAGATA ACAAACGAAT TT----ATTT CTAGTATTAA ATGTTCATGC A-----GTAA GAATAAGAGG GGATTGGCCG AGTATTCCAC
Mmo593       -CCGAAATGA TGAAGAGATA ACAAACGAAT TT----ATTT CTAGTATTAA ATGTTCATGC A-----GTAA GAATAAGAGG GGATTGGCCG AGTATTCCAC
Mhi672       -CCGAAATGA TGAAGAGATA ACAAACGAAT TT----ATTT CTAGTATTAA ATGTTCATGC A-----GTAA GAATAAGAGG GGATTGGCCG AGTATTCCAC
Ahi270       -CCGAAATGA TGAAGAGATA ACAAACGAAT TC----ATTT CTAGTATTAA ATGTTCATGC A-----GTAA GAATAAGAGG GGATTGGCCG AGTATTCCAC
Alo596       -CCGAAATGA TGACGAGATA ACAAACGAAT TT----ATTT CTAGTATTAA ATGTTCATGC AATGCAGTAA GAATAAGAGG GGATTGGCCG AGTATTCCAC
AluM53       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Mca572       -CCGAAATGA TGAAGAGATA ACAAACKAAT TC----ATTT CTAGTATTAA ATGTTCATGC A-----GTAA GAATAAGAGG GGATTGGCCG AGTATTCCAC
MMae11       -CCGAAATGT TGAAGAGATA ACAAACGAAT TT----ATTT CTAGTATTAA ATGTTCATGC A-----GTAA GAATAAGAGG GGATTGGCCG AGTATTCCAC
Mtr683       -CCGAAATGT TGAAGAGATA ACAAACGAAT TT----ATTT CTAGTATTAA ATGTTCATGC A-----GTAA GAATAAGAGG GGATTGGCCG AGTATTCCAC
Mma671       -CCGAAATGA TGAAGAGATA ACAACCGAAT TT----ATTT CTAGTATTAA ATGTTCATGC A-----GTAA GAATAAGAGG GGATTGGCCG AGTATTCCAC
Mtf502       -CCGAAATGA TGAAGAGATA ACAACCGAAT TT----ATTT CTAGTATTAA ATGTTCATGC A-----GTAA GAATAAGAGG GGATTGGCCG AGTATTCCAC
LphM81       -CCGAAATGA TGAAGAGATA ACAAACGAAT TT----ATTT CTAGTATTAA AAGTTCATGC A-----GTAA GAATAAGAGG GGATTGGCCG AGTATTCCAC
AniM31       -CCGAAATGA TGAAGAGATA ACAAACGAAT TT----TTTT CTAGTATTAA ATGTTCATGC A-----GTAA GAATAAGAGG GGATTGGCCG AGTATTCCAC
MKvi11       -CCGAAATGA TGAAGAGATA ACAAACGAAT TT----AGTT CTAGTATTAA ATGTTCAGGC A-----GTAA GAATAAGAGG GGATTGGCCG AGTATTCCAC
MAros1       -CCGAAATGA TGAAGAGATA ACAAACGAAT TT----AGTT CTAGTATTAA ATGTTCATGC A-----GTAA GAATAAGAGG GGATTGGCCG AGTATTCCAC
MshM21       -CCGAAATGA TGAAGAGATA ACAAACAAAT TTATTCATTT CTAGTATTAA ATGTTCATGC A-----GTAA GAATAAGAGG GGATTGGCCG AGTATTCCAC


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                                                  1910       1920       1930       1940
                               MAar11       TTTTTTT--C GAGTCCTGTT TAGGGAATAA ACAGGGTTTt AGA
                               Aca594       TTTTTTT--C GAGTCCTGTT TAGGGAATAA ACAGGGTTTt AGA
                               MAof11       TTTTTTT--C GAGTCCTGTT TAGGGAATAA ACAGGGTTTt AGA
                               Lol451       TTTTTTT--C GAGTCCTGTT TAGGGAATAA ACAGGGTTTT AGA
                               Lob144       TTTTTTT--C GAGTCCTGAT TAGGGAATAA ACAGGGTTTT AGA
                               Lbr141       TTTTTTT--C GAGTCCTGTT TAGGGAATAA ACAGGGTTTT AGA
                               Lag308       TTTTTTT--C GAGTCCTGTT TAGGGAATAA ACAGGGTTTt AGA
                               MLtp11       TTTTTTT--C GAGTCCTGTT TAGGGAATAA ACAGGGTTTt AGA
                               Ltr680       TTTTTTT--C GAGTCCTGTT TAGGGAATAA ACAGGGTTTT AGA
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MLfl11     TTTTTT---C gaGTCCTGTT TAGGGaAtAA ACAGGGTTTT AGA
LplM57     TTTTTTT--C GAGTCCTGTT TAGGGAATAA ACAGGGTTTt AGA
Lti472     TTTTTTT--C GAGTCCTGTT TAGGGAATAA ACAGGGTTTT AGA
LthVie     TTTTTTT--C GAG-CCTGTT TAGGGAATAA ACAGGGTTTT AGA
MLpu11     TTTTTTT--C GAGTCCTGTT TAGGGAATAA ACAGGGTTTt AGA
Lmo316     TTTTTTT--C GAGTCTTGTT TAGGGAATAA ACAGGGTTTT AGA
LacB11     TTTTTTT--C GAGTCCTGTT TAGGGAATAA ACAGGGTTTT AGA
Lar253     TTTTTTT--C GAGTCCTGTT TAGGGAATAA ACAGGGTTTT AGA
MLas11     TTTTTTT--C GAGTCCTGTT TAGGGAATAA ACAGGGTTTt AGA
MLma11     TTTTTTT--C GAGTCCTGTT TAGGGAATAA ACAGGGTTTt AGA
Lmu283     TTTTTTT--C GAGTCCTGTT TAGGGAATAA ACAGGGTTTt AGA
MLcr11     TTTTTTT--C GAGTCCTGTT TAGGGAATAA ACAGGGTTTt AGA
LpebM2     ---------- ---------- ---------- ---------- ---
Mni674     TTTTTTT--C GAGTCCTGTT TAGGGAATAA ACAGGGTTTT AGA
Mpa603     TTTTTTT--C GAGTCCTGTT TAGGGAATAA ACAGGGTTTT AGA
Msy597     TTTTTTT--C GAGTCCTGTT TAGGGAATAA ACAGGGTTTT AGA
Mne795     TTTTTTT--C GAGTCCTGTT TAGGGAATAA ACAGGGTTTt AGG
Mve442     TTTTTTT--C GAGTCCTGTT TAGGGAATAA ACAGGGTTTt AGA
Mal338     TTTTTTT--C GAGTCCTGTT TAGGGAATAA ACAGGGTTTT AGA
Mto185     TTTTTTT--C GAGTCCTGTT TAGGGAATAA ACAGGGTTTT AGA
Mmo593     TTTTTTT--C GAGTCCTGTT TAGGGAATAA ACAGGGTTTT AGA
Mhi672     TTTTTTT--C GAGTCCTGTT TAGGGAATAA ACAGGGTTTT AGA
Ahi270     TTTTTTTT-C GAGTCCTGTT TAGGGAATAA ACAGGGTTTT AGA
Alo596     TTTTTTT--C GAGTCCTGTT TAGGGAATAA ACAGGGTTTT AGA
AluM53     ---------- ---------- ---------- ---------- ---
Mca572     TTTTTTT--C GAGTCCTGTT TAGGGAATAA ACAGGGTTTT AGA
MMae11     TTTTTTTTTC GAGTCCTGTT TAGGGAATAA aCAGGgTTTt AGA
Mtr683     TTTTTTTTTC GAGTCCTGTT TAGGGAATAA ACAGGGTTTT AGA
Mma671     TTTTTTT--C GAGTCCTGTT TAGGGAATAA ACAGGGTTTt AGA
Mtf502     TTTTTTTT-C GAGTCCTGTT TAGGGAATAA ACAGGGTTTT AGA
LphM81     TTTTTTT--C GAGTCCTGTT TAGGGAATAA ACAGGGTTTt AGA
AniM31     TTTTTTT--C GAGTCCTGTT TAGGGAATAA ACAGGGTTTt AGA
MKvi11     TTTTTTT--C GAGTCCTGTT TAGGGAATAA ACAGGGTTTt AGA
MAros1     TTTTTTT--C GAGTCCTGTT TAGGGAATAA ACAGGGTTTt AGA
MshM21     TTTTTTTT-C GAGTCCTGTT TAGGGAATAA ACAGGGTTTT AGA
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                     10         20         30         40         50         60         70         80         90        100
NAar         AGTATAGTTA TGATTTTTTC GG-CGATCTG TCTATTCAGC AAATAAATGG AAGTTCTATC TATCAATATG TATGGTCTTG GACCATCAAT AATGATTTTT
NAhi         AGTATAGTTA TGATTTTTTC GGTCGATCTG TCTATTCAGC AAATAAATGG AAGTTCTATC TATCAATATG TATGGTCTTG GACCATCAAT AATGATTTTT
NAlo         AGTATAGTTA TGATTTTTTC GGTCGATCTG TCTATTCAGC AAATAAATGG AAGTTCTATC TATCAATATG TATGGTCTTG GACCATCAAT AATGATTTTT
NAca         AGTATAGTTA TGATTTTTTC GGTCGATCTG TCTATTCAGC AAATAAATGG AAGTTCTATC TATCAATATG TATGGTCTTG GACCATCAAT AATGATTTTT
NAof         AGTATAGTTA TGATTTTTTC GGTCGATCTG TCTATTCAGC AAATAAATGG AAGTTCTATC TATCAATATG TATGGTCTTG GACCATCAAT AATGATTTTT
NAlu         AGTATA---- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
NLcr         AGTATAGTTA TGATTTTTTC GGTCGATCTG TCTATTCAGC AAATAAATGG AAGTTCTATC TATCAATATG TATGGTCTTG GACCATCAAT AATGATTTTT
NLag         AGTATAGTTA TGATTTTTTC GGTCGATCTG TCTATTCAGC AAATAAATGG AAGTTCTATC TATCAATATG TATGGTCTTG GACCATCAAT AATGATTTTT
NLbr         AGTATAGTTA TGATTTTTTC GGTCGATCTG TCTATTCAGC AAATAAATGG AAGTTCTATC TATCAATATG TATGGTCTTG GACCATCAAT AATGATTTTT
NLtr         AGTATAGTTA TGATTTTTTC GGTCGATCTG TCTATTCAGC AAATAAATGG AAGTTCTATC TATCAATATG TATGGTCTTG GACCATCAAT AATGATTTTT
NLtp         AGTATAGTTA TGATTTTTTC GGTCGATCTG TCTATTCAGC AAATAAATGG AAGTTCTATC TATCAATATG TATGGTCTTG GACCATCAAT AATGATTTTT
NLfl         AGTATAGTTA TGATTTTTTC GGTCGATCTG TCTATTCAGC AAATAAATGG AAGTTCTATC TATCAATATG TATGGTCTTG GACCATCAAT AATGATTTTT
NLas         AGTATAGTTA TGATTTTTTC GGTCGATCTG TCTATTCAGC AAATAAATGG AAGTTCTATC TATCAATATG TATGGTCTTG GACCATCAAT AATGATTTTT
NLac         AGTATAGTTA TGATTTTTTC GGTCGATCTG TCTATTCAGC AAATAAATGG AAGTTCTATC TATCAATATG TATGGTCTTG GACCATCAAT AATGATTTTT
NLar         AGTATAGTTA TGATTTTTTC GGTCGATCTG TCTATTCAGC AAATAAATGG AAGTTCTATC TATCAATATG TATGGTCTTG GACCATCAAT AATGATTTTT
NLma         AGTATAGTTA TGATTTTTTC GGTCGATCTG TCTATTCAGC AAATAAATGG AAGTTCTATC TATCAATATG TATGGTCTTG GACCATCAAT AATGATTTTT
NLmo         AGTATAGTTA TGATTTTTTC GGTCGATCTG TCTATTCAGC AAATAAATGG AAGTTCTATC TATCAATATG TATGGTCTTG GACCATCAAT AATGATTTTT
NLmu         AGTATAGTTA TGATTTTTTC GGTCGATCTG TCTATTCAGC AAATAAATGG AAGTTCTATC TATCAATATG TATGGTCTTG GACCATCAAT AATGATTTTT
NLob         AGTATAGTTA TGATTTTTTC GGTCGATCTG TCTATTCAGC AAATAAATGG AAGTTCTATC TATCAATATG TATGGTCTTG GACCATCAAT AATGATTTTT
NLol         AGTATAGTTA TGATTTTTTC GGTCGATCTG TCTATTCAGC AAATAAATGG AAGTTCTATC TATCAATATG TATGGTCTTG GACCATCAAT AATGATTTTT
NLpe         AGTATAGTTA TGATTTTTTC GGTCGATCTG TCTATTCAGC AAATAAATGG AAGTTCTATC TATCAATATG TATGGTCTTG GACCATCAAT AATGATTTTT
NLph         AGTATAGTTA TGATTTTTTC GGTCGATCTG TCTATTCAGC AAATAAATGG AAGTTCTATC TATCAATATG TATGGTCTTG GACCATCAAT AATGATTTTT
NLpl         AGTATAGTTA TGATTTTTTC GGTCGATCTG TCTATTCAGC AAATAAATGG AAGTTCTATC TATCAATATG TATGGTCTTG GACCATCAAT AATGATTTTT
NLpu         AGTATAGTTA TGATTTTTTC GGTCGATCTG TCTATTCAGC AAATAAATGG AAGTTCTATC TATCAATATG TATGGTCTTG GACCATCAAT AATGATTTTT
NLth         AGTATAGTTA TGATTTTTTC GGTCGATCTG TCTATTCAGC AAATAAATGG AAGTTCTATC TATCAATATG TATGGTCTTG GACCATCAAT AATGATTTTT
NLti         AGTATAGTTA TGATTTTTTC GGTCGATCTG TCTATTCAGC AAATAAATGG AAGTTCTATC TATCAATATG TATGGTCTTG GACCATCAAT AATGATTTTT
NMma         AGTATAGTTA TGATTTTTTC GGTCGATCTG TCTATTCAGC AAATAAATGG AAGTTCTATC TATCAATATG TATGGTCTTG GACCATCAAT AATGATTTTT
NMtf         AGTATAGTTA TGATTTTTTC GGTCGATCTG TCTATTCAGC AAATAAATGG AAGTTCTATC TATCAATATG TATGGTCTTG GACCATCAAT AATGATTTTT
NMae         AGTATAGTTA TGATTTTTTC GGTCGATCTG TCTATTCAGC AAATAAATGG AAGTTCTATC TATCAATATG TATGGTCTTG GACCATCAAT AATGATTTTT
NMtr         AGTATAGTTA TGATTTTTTC GGTCGATCTG TCTATTCAGC AAATAAATGG AAGTTCTATC TATCAATATG TATGGTCTTG GACCATCAAT AATGATTTTT
NMca         AGTATAGTTA TGATTTTTTC GGTCGATCTG TCTATTCAGC AAATAAATGG AAGTTCTATC TATCAATATG TATGGTCTTG GACCATCAAT AATGATTTTT
NMhi         AGTATAGTTA TGATTTTTTC GGTCGATCTG TCTATTCAGC AAATAAATGG AAGTTCTATC TATCAATATG TATGGTCTTG GACCATCAAT AATGATTTTT
NMto         AGTAtAGTTA TGATTTTTTC GGTCGATCTG TCTATTCAgC AAATAAATGG AAGTTCTATC TATCAATATG TATGGTCTTG GACCATTAAT AATGATTTTT
NMal         AGTAtAGTTA TGATTTTTTC GGTCGATCTG TCTATTCAgC AAATAAATGG AAGTTCTATC TATCAATATG TATGGTCTTG GACCATTAAT AATGATTTTT
NMmo         AGTAtAGTTA TGATTTTTTC GGTCGATCTG TCTATTCAgC AAATAAATGG AAGTTCTATC TATCAATATG TATGGTCTTG GACCATTAAT AATGATTTTT
NMne         AGTATAGTTA TGATTTTTTC GGTCGATCTG TCTATTCAGC AAATAAATGG AAGTTCTATC TATCAATATG TATGGTCTTG GACCATCAAT AATGATTTTT
NMni         AGTATAGTTA TGATTTTTTC GGTCGATCTG TCTATTCAGC AAATAAATGG AAGTTCTATC TATCAATATG TATGGTCTTG GACCATCAAT AATGATTTTT
NMpa         AGTATAGTTA TGATTTTTTC GGTCGATCTG TCTATTCAGC AAATAAATGG AAGTTCTATC TATCAATATG TATGGTCTTG GACCATCAAT AATGATTTTT
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NMsy         AGTATAGTTA TGATTTTTTC GGTCGATCTG TCTATTCAGC AAATAAATGG AAGTTCTATC TATCAATATG TATGGTCTTG GACCATCAAT AATGATTTTT
NMve         AGTATAGTTA TGATTTTTTC GGTCGATCTG TCTATTCAGC AAATAAATGG AAGTTCTATC TATCAATATG TATGGTCTTG GACCATCAAT AATGATTTTT
NAros        AGTATAGTTA TGATTTTTTC GGTCGATCTG TCTATTCAGC AAATAAATGG AAGTTCTATC TATCAATATG TATGGTCTTG GACCATCAAT AATGATTTTT
NAni         AGTATAGTTA TGATTTTTTC GGTCGATCTG TCTATTCAGC AAATAAATGG AAGTTCTATC TATCAATATG TATGGTCTTG GACCATCAAT AATGATTTTT
NKvi         AGTATAGTTA TGATTTTTTC GGTCGATCTG TCTATTCAGC AAATAAATGG AAGTTCTATC TATCAATATG TATGGTCTTG GACCATCAAT AATGATTTTT


             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    110        120        130        140        150        160        170        180        190        200
NAar         CTTTCGAGTT TGGCTACTTT ATTGATTCAC TTACCTCTAT TATGTCAATA TTAATCACTA CTGTTGGAAT TTTTGTTCTT ATTTATAGTG ACAATTATAT
NAhi         CTTTCGAGTT TGGCTACTTT ATTGATTCAC TTACCTCTAT TATGTCAATA TTAATCACTA CTGTTGGAAT TTTTGTTCTT ATTTATAGTG ACAATTATAT
NAlo         CTTTCGAGTT TGGCTACTTT ATTGATTCAC TTACCTCTAT TATGTCAATA TTAATCACTA CTGTTGGAAT TTTTGTTCTT ATTTATAGTG ACAATTATAT
NAca         CTTTCGAGTT TGGCTACTTT ATTGATTCAC TTACCTCTAT TATGTCAATA TTAATCACTA CTGTTGGAAT TTTTGTTCTT ATTTATAGTG ACAATTATAT
NAof         CTTTCGAGTT TGGCTACTTT ATTGATTCAC TTACCTCTAT TATGTCAATA TTAATCACTA CTGTTGGAAT TTTTGTTCTT ATTTATAGTG ACAATTATAT
NAlu         ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
NLcr         CTTTCGAGTT TGGCTACTTT ATTGATTCAC TTACCTCTAT TATGTCAATA TTAATCACTA CTGTTGGAAT TTTTGTTCTT ATTTATAGTG ACAATTATAT
NLag         CTTTCGAGTT TGGCTACTTT ATTGATTCAC TTACCTCTAT TATGTCAATA TTAATCACTA CTGTTGGAAT TTTTGTTCTT ATTTATAGTG ACAATTATAT
NLbr         CTTTCGAGTT TGGCTACTTT ATTGATTCAC TTACCTCTAT TATGTCAATA TTAATCACTA CTGTTGGAAT TTTTGTTCTT ATTTATAGTG ACAATTATAT
NLtr         CTTTCGAGTT TGGCTACTTT ATTGATTCAC TTACCTCTAT TATGTCAATA TTAATCACTA CTGTTGGAAT TTTTGTTCTT ATTTATAGTG ACAATTATAT
NLtp         CTTTCGAGTT TGGCTACTTT ATTGATTCAC TTACCTCTAT TATGTCAATA TTAATCACTA CTGTTGGAAT TTTTGTTCTT ATTTATAGTG ACAATTATAT
NLfl         CTTTCGAGTT TGGCTACTTT ATTGATTCAC TTACCTCTAT TATGTCAATA TTAATCACTA CTGTTGGAAT TTTTGTTCTT ATTTATAGTG ACAATTATAT
NLas         CTTTCGAGTT TGGCTACTTT ATTGATTCAC TTACCTCTAT TATGTCAATA TTAATCACTA CTGTTGGAAT TTTTGTTCTT ATTTATAGTG ACAATTATAT
NLac         CTTTCGAGTT TGGCTACTTT ATTGATTCAC TTACCTCTAT TATGTCAATA TTAATCACTA CTGTTGGAAT TTTTGTTCTT ATTTATAGTG ACAATTATAT
NLar         CTTTCGAGTT TGGCTACTTT ATTGATTCAC TTACCTCTAT TATGTCAATA TTAATCACTA CTGTTGGAAT TTTTGTTCTT ATTTATAGTG ACAATTATAT
NLma         CTTTCGAGTT TGGCTACTTT ATTGATTCAC TTACCTCTAT TATGTCAATA TTAATCACTA CTGTTGGAAT TTTTGTTCTT ATTTATAGTG ACAATTATAT
NLmo         CTTTCGAGTT TGGCTACTTT ATTGATTCAC TTACCTCTAT TATGTCAATA TTAATCACTA CTGTTGGAAT TTTTGTTCTT ATTTATAGTG ACAATTATAT
NLmu         CTTTCGAGTT TGGCTACTTT ATTGATTCAC TTACCTCTAT TATGTCAATA TTAATCACTA CTGTTGGAAT TTTTGTTCTT ATTTATAGTG ACAATTATAT
NLob         CTTTCGAGTT TGGCTACTTT ATTGATTCAC TTACCTCTAT TATGTCAATA TTAATCACTA CTGTTGGAAT TTTTGTTCTT ATTTATAGTG ACAATTATAT
NLol         CTTTCGAGTT TGGCTACTTT ATTGATTCAC TTACCTCTAT TATGTCAATA TTAATCACTA CTGTTGGAAT TTTTGTTCTT ATTTATAGTG ACAATTATAT
NLpe         CTTTCGAGTT TGGCTACTTT ATTGATTCAC TTACCTCTAT TATGTCAATA TTAATCACTA CTGTTGGAAT TTTTGTTCTT ATTTATAGTG ACAATTATAT
NLph         CTTTCGAGTT TGGCTACTTT ATTGATTCAC TTACCTCTAT TATGTCAATA TTAATCACTA CTGTTGGAAT TTTTGTTCTT ATTTATAGTG ACAATTATAT
NLpl         CTTTCGAGTT TGGCTACTTT ATTGATTCAC TTACCTCTAT TATGTCAATA TTAATCACTA CTGTTGGAAT TTTTGTTCTT ATTTATAGTG ACAATTATAT
NLpu         CTTTCGAGTT TGGCTACTTT ATTGATTCAC TTACCTCTAT TATGTCAATA TTAATCACTA CTGTTGGAAT TTTTGTTCTT ATTTATAGTG ACAATTATAT
NLth         CTTTCGAGTT TGGCTACTTT ATTGATTCAC TTACCTCTAT TATGTCAATA TTAATCACTA CTGTTGGAAT TTTTGTTCTT ATTTATAGTG ACAATTATAT
NLti         CTTTCGAGTT TGGCTACTTT ATTGATTCAC TTACCTCTAT TATGTCAATA TTAATCACTA CTGTTGGAAT TTTTGTTCTT ATTTATAGTG ACAATTATAT
NMma         CTTTCGAGTT TGGCTACTTT ATTGATTCAC TTACCTCTAT TATGTCAATA TTAATCACTA CTGTTGGAAT TTTTGTTCTT ATTTATAGTG ACAATTATAT
NMtf         CTTTCGAGTT TGGCTACTTT ATTGATTCAC TTACCTCTAT TATGTCAATA TTAATCACTA CTGTTGGAAT TTTTGTTCTT ATTTATAGTG ACAATTATAT
NMae         CTTTCGAGTT TGGCTACTTT ATTGATTCAC TTACCTCTAT TATGTCAATA TTAATCACTA CTGTTGGAAT TTTTGTTCTT ATTTATAGTG ACAATTATAT
NMtr         CTTTCGAGTT TGGCTACTTT ATTGATTCAC TTACCTCTAT TATGTCAATA TTAATCACTA CTGTTGGAAT TTTTGTTCTT ATTTATAGTG ACAATTATAT
NMca         CTTTCGAGTT TGGCTACTTT ATTGATTCAC TTACCTCTAT TATGTCAATA TTAATCACTA CTGTTGGAAT TTTTGTTCTT ATTTATAGTG ACAATTATAT
NMhi         CTTTCGAGTT TGGCTACTTT ATTGATTCAC TTACCTCTAT TATGTCAATA TTAATCACTA CTGTTGGAAT TTTTGTTCTT ATTTATAGTG ACAATTATAT
NMto         CTTTCGAGTT TGGCTACTTT ATTGATTCAC TTACCTCTAT TATGTCAATA TTAATCACTA CTGTTGGAAT TTTTGTTCTT ATTTATAGTG ACAATTATAT
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NMal        CTTTCGAGTT TGGCTACTTT ATTGATTCAC TTACCTCTAT TATGTCAATA TTAATCACTA CTGTTGGAAT TTTTGTTCTT ATTTATAGTG ACAATTATAT
NMmo        CTTTCGAGTT TGGCTACTTT ATTGATTCAC TTACCTCTAT TATGTCAATA TTAATCACTA CTGTTGGAAT TTTTGTTCTT ATTTATAGTG ACAATTATAT
NMne        CTTTCGAGTT TGGCTACTTT ATTGATTCAC TTACCTCTAT TATGTCAATA TTAATCACTA CTGTTGGAAT TTTTGTTCTT ATTTATAGTG ACAATTATAT
NMni        CTTTCGAGTT TGGCTACTTT ATTGATTCAC TTACCTCTAT TATGTCAATA TTAATCACTA CTGTTGGAAT TTTTGTTCTT ATTTATAGTG ACAATTATAT
NMpa        CTTTCGAGTT TGGCTACTTT ATTGATTCAC TTACCTCTAT TATGTCAATA TTAATCACTA CTGTTGGAAT TTTTGTTCTT ATTTATAGTG ACAATTATAT
NMsy        CTTTCGAGTT TGGCTACTTT ATTGATTCAC TTACCTCTAT TATGTCAATA TTAATCACTA CTGTTGGAAT TTTTGTTCTT ATTTATAGTG ACAATTATAT
NMve        CTTTCGAGTT TGGCTACTTT ATTGATTCAC TTACCTCTAT TATGTCAATA TTAATCACTA CTGTTGGAAT TTTTGTTCTT ATTTATAGTG ACAATTATAT
NAros       CTTTCGAGTT TGGCTACTTT ATTGATTCAC TTACCTCTAT TATGTCAATA TTAATCACTA CTGTTGGAAT TTTTGTTCTT ATTTATAGTG ACAATTATAT
NAni        CTTTCGAGTT TGGCTACTTT ATTGATTCAC TTACCTCTAT TATGTCAATA TTAATCACTA CTGTTGGAAT TTTTGTTCTT ATTTATAGTG ACAATTATAT
NKvi        CTTTCGAGTT TGGCTACTTT ATTGATTCAC TTACCTCTAT TATGTCAATA TTAATCACTA CTGTTGGAAT TTTTGTTCTT ATTTATAGTG ACAATTATAT


            ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   210        220        230        240        250        260        270        280        290        300
NAar        GTCTCATGAT CAAGGATATT TGAGATTTTT TGCTTATATG AGTTTGTTCA ATACTTCAAT GTTGGGATTA GTTACTAGTT CGAATTTGAT ACAAATTTAT
NAhi        GTCTCATGAT CAAGGATATT TGAGATTTTT TGCTTATATG AGTTTGTTCA ATACTTCAAT GTTGGGATTA GTTACTAGTT CGAATTTGAT ACAAATTTAT
NAlo        GTCTCATGAT CAAGGATATT TGAGATTTTT TGCTTATATG AGTTTGTTCA ATACTTCAAT GTTGGGATTA GTTACTAGTT CGAATTTGAT ACAAATTTAT
NAca        GTCTCATGAT CAAGGATATT TGAGATTTTT TGCTTATATG AGTTTGTTCA ATACTTCAAT GTTGGGATTA GTTACTAGTT CGAATTTGAT ACAAATTTAT
NAof        GTCTCATGAT CAAGGATATT TGAGATTTTT TGCTTATATG AGTTTGTTCA ATACTTCAAT GTTGGGATTA GTTACTAGTT CGAATTTGAT ACAAATTTAT
NAlu        ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
NLcr        GTCTCATGAT CAAGGATATT TGAGATTTTT TGCTTATATG AGTTTGTTCA ATACTTCAAT GTTGGGATTA GTTACTAGTT CGAATTTGAT ACAAATTTAT
NLag        GTCTCATGAT CAAGGATATT TGAGATTTTT TGTTTATATG AGTTTGTTCA ATACTTCAAT GTTGGGATTA GTTACTAGTT CGAATTTGAT ACAAATTTAT
NLbr        GTCTCATGAT CAAGGATATT TGAGATTTTT TGCTTATATG AGTTTGTTCA ATACTTCAAT GTTGGGATTA GTTACTAGTT CGAATTTGAT ACAAATTTAT
NLtr        GTCTCATGAT CAAGGATATT TGAGATTTTT TGCTTATATG AGTTTGTTCA ATACTTCAAT GTTGGGATTA GTTACTAGTT CGAATTTGAT ACAAATTTAT
NLtp        GTCTCATGAT CAAGGATATT TGAGATTTTT TGTTTATATG AGTTTGTTCA ATACTTCAAT GTTGGGATTA GTTACTAGTT CGAATTTGAT ACAAATTTAT
NLfl        GTCTCATGAT CAAGGATATT TGAGATTTTT TGTTTATATG AGTTTGTTCA ATACTTCAAT GTTGGGATTA GTTACTAGTT CGAATTTGAT ACAAATTTAT
NLas        GTCTCATGAT CAAGGATATT TGAGATTTTT TGCTTATATG AGTTTGTTCA ATACTTCAAT GTTGGGATTA GTTACTAGTT CGAATTTGAT ACAAATTTAT
NLac        GTCTCATGAT CAAGGATATT TGAGATTTTT TGCTTATATG AGTTTGTTCA ATACTTCAAT GTTGGGATTA GTTACTAGTT CGAATTTGAT ACAAATTTAT
NLar        GTCTCATGAT CAAGGATATT TGAGATTTTT TGCTTATATG AGTTTGTTCA ATACTTCAAT GTTGGGATTA GTTACTAGTT CGAATTTGAT ACAAATTTAT
NLma        GTCTCATGAT CAAGGATATT TGAGATTTTT TGCTTATATG AGTTTGTTCA ATACTTCAAT GTTGGGATTA GTTACTAGTT CGAATTTGAT ACAAATTTAT
NLmo        GTCTCATGAT CAAGGATATT TGAGATTTTT TGCTTATATG AGTTTGTTCA ATACTTCAAT GTTGGGATTA GTTACTAGTT CGAATTTGAT ACAAATTTAT
NLmu        GTCTCATGAT CAAGGATATT TAAGATTTTT TGCTTATATG AGTTTGTTCA ATACTTCAAT GTTGGGATTA GTTACTAGTT CGAATTTGAT ACAAATTTAT
NLob        GTCTCATGAT CAAGGATATT TgAGATTTTT TGCTTATATG AGTTTGTTCA ATACTTCAAT GTTGGGATTA GTTACTAGTT CGAATTTGAT ACAAATTTAT
NLol        GTCTCATGAT CAAGGATATT TGAGATTTTT TGCTTATATG AGTTTGTTCA ATACTTCAAT GTTGGGATTA GTTACTAGTT CGAATTTGAT ACAAATTTAT
NLpe        GTCTCATGAT CAAGGATATT TGAGATTTTT TGCTTATATG AGTTTGTTCA ATACTTCAAT GTTGGGATTA GTTACTAGTT CGAATTTGAT ACAAATTTAT
NLph        GTCTCATGAT CAAGGATATT TGAGATTTTT TGCTTATATG AGTTTGTTCA ATACTTCAAT GTTGGGATTA GTTACTAGTT CGAATTTGAT ACAAATTTAT
NLpl        GTCTCATGAT CAAGGATATT TGAGATTTTT TGCTTATATG AGTTTGTTCA ATACTTCAAT GTTGGGATTA GTTACTAGTT CGAATTTGAT ACAAATTTAT
NLpu        GTCTCATGAT CAAGGATATT TGAGATTTTT TGCTTATATG AGTTTGTTCA ATACTTCAAT GTTGGGATTA GTTACTAGTT CGAATTTGAT ACAAATTTAT
NLth        GTCTCATGAT CAAGGATATT TGAGATTTTT TGCTTATATG AGTTTGTTCA ATACTTCAAT GTTGGGATTA GTTACTAGTT CGAATTTGAT ACAAATTTAT
NLti        GTCTCATGAT CAAGGATATT TGAGATTTTT TGCTTATATG AGTTTGTTCA ATACTTCAAT GCTCGGATTA GTTACTAGTT CGAATTTGAT ACAAATTTAT
NMma        GTCTCATGAT CAAGGATATT TGAGATTTTT TGCTTATATG AGTTTGTTCA ATACTTCAAT GTTGGGATTA GTTACTAGTT CGAATTTGAT ACAAATTTAT
NMtf        GTCTCATGAT CAAGGATATT TGAGATTTTT TGCTTATATG AGTTTGTTCA ATACTTCAAT GTTGGGATTA GTTACTAGTT CGAATTTGAT ACAAATTTAT
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NMae           GTCTCATGAT CAAGGATATT TGAGATTTTT TGCTTATATG AGTTTGTTCA ATACTTCAAT GTTGGGATTA GTTACTAGTT CGAATTTGAT ACAAATTTAT
NMtr           GTCTCATGAT CAAGGATATT TGAGATTTTT TGCTTATATG AGTTTGTTCA ATACTTCAAT GTTGGGATTA GTTACTAGTT CGAATTTGAT ACAAATTTAT
NMca           GTCTCATGAT CAAGGATATT TGAGATTTTT TGCTTATATG AGTTTGTTCA ATACTTCAAT GTTGGGATTA GTTACTAGTT CGAATTTGAT ACAAATTTAT
NMhi           GTCTCATGAT CAAGGATATT TGAGATTTTT TGCTTATATG AGTTTGTTCA ATACTTCAAT GTTGGGATTA GTTACTAGTT CGAATTTGAT ACAAATTTAT
NMto           GTCTCATGAT CAAGGATATT TGAGATTTTT TGCTTATATG AGTTTGTTCA ATACTTCAAT GTTGGGATTA GTTACTAGTT CGAATTTGAT ACAAATTTAT
NMal           GTCTCATGAT CAAGGATATT TGAGATTTTT TGCTTATATG AGTTTGTTCA ATACTTCAAT GTTGGGATTA GTTACTAGTT CGAATTTGAT ACAAATTTAT
NMmo           GTCTCATGAT CAAGGATATT TGAGATTTTT TGCTTATATG AGTTTGTTCA ATACTTCAAT GTTGGGATTA GTTACTAGTT CGAATTTGAT ACAAATTTAT
NMne           GTCTCATGAT CAAGGATATT TGAGATTTTT TGCTTATATG AGTTTGTTCA ATACTTCAAT GTTGGGATTA GTTACTAGTT CGAATTTGAT ACAAATTTAT
NMni           GTCTCATGAT CAAGGATATT TGAGATTTTT TGCTTATATG AGTTTGTTCA ATACTTCAAT GTTGGGATTA GTTACTAGTT CGAATTTGAT ACAAATTTAT
NMpa           GTCTCATGAT CAAGGATATT TGAGATTTTT TGCTTATATG AGTTTGTTCA ATACTTCAAT GTTGGGATTA GTTACTAGTT CGAATTTGAT ACAAATTTAT
NMsy           GTCTCATGAT CAAGGATATT TGAGATTTTT TGCTTATATG AGTTTGTTCA ATACTTCAAT GTTGGGATTA GTTACTAGTT CGAATTTGAT ACAAATTTAT
NMve           GTCTCATGAT CAAGGATATT TAAGATTTTT TGCTTATATG AGTTTGTTCA ATACTTCAAT GTTGGGATTA GTTACTAGTT CGAATTTGAT ACAAATTTAT
NAros          GTCTCATGAT CAAGGATATT TGAGATTTTT TGCTTATATG AGTTTGTTCA ATACTTCAAT GTTGGGATTA GTTACTAGTT CGAATTTGAT ACAAATTTAT
NAni           GTCTCATGAT CAAGGATATT TGAGATTTTT TGCTTATATG AGTTTGTTCA ATACTTCAAT GTTGGGATTA GTTACTAGTT CGAATTTGAT ACAAATTTAT
NKvi           GTCTCATGAT CAAGGATATT TGAGATTTTT TGCTTATATG AGTTTGTTCA ATACTTCAAT GTTGGGATTA GTTACTAGTT CGAATTTGAT ACAAATTTAT


               ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                      310        320        330        340        350        360        370        380        390        400
NAar           ATTTTTTGGG AATTAGTTGG AATGTGTTCT TATCTATTAA TAGGGTTTTG GTTCACACGA CCCGCTGCGG CAAACGCTTG TCAAAAAGCG TTTGTAACTA
NAhi           ATTTTTTGGG AATTAGTTGG AATGTGTTCT TATCTATTAA TAGGGTTTTG GTTCACACGA CCCGCTGCGG CAAACGCTTG TCAAAAAGCG TTTGTAACTA
NAlo           ATTTTTTGGG AATTAGTTGG AATGTGTTCT TATCTATTAA TAGGGTTTTG GTTCACACGA CCCGCTGCGG CAAACGCTTG TCAAAAAGCG TTTGTAACTA
NAca           ATTTTTTGGG AATTAGTTGG AATGTGTTCT TATCTATTAA TAGGGTTTTG GTTCACACGA CCCGCTGCGG CAAACGCTTG TCAAAAAGCG TTTGTAACTA
NAof           ATTTTTTGGG AATTAGTTGG AATGTGTTCT TATCTATTAA TAGGGTTTTG GTTCACACGA CCCGCTGCGG CAAACGCTTG TCAAAAAGCG TTTGTAATTA
NAlu           ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
NLcr           ATTTTTTGGG AATTAGTTGG AATGTGTTCT TATCTATTAA TAGGGTTTTG GTTCACACGA CCCGCTGCGG CAAACGCTTG TCAAAAAGCG TTTGTAACTA
NLag           ATTTTTTGGG AATTAGTTGG AATGTGTTCT TATCTATTAA TAGGGTTTTG GTTCACACGA CCCGCTGCGG CAAACGCTTG TCAAAAAGCG TTTGTAACTA
NLbr           ATTTTTTGGG AATTAGTTGG AATGTGTTCT TATCTATTAA TAGGGTTTTG GTTCACACGA CCCGCTGCGG CAAACGCTTG TCAAAAAGCG TTTGTAACTA
NLtr           ATTTTTTGGG AATTAGTTGG AATGTGTTCT TATCTATTAA TAGGGTTTTG GTTCACACGA CCCGCTGCGG CAAACGCTTG TCAAAAAGCG TTTGTAACTA
NLtp           ATTTTTTGGG AATTAGTTGG AATGTGTTCT TATCTATTAA TAGGGTTTTG GTTCACACGA CCCGCTGCGG CAAACGCTTG TCAAAAAGCG TTTGtAACTA
NLfl           ATTTTTTGGG AATTAGTTGG AATGTGTTCT TATCTATTAA TAGGGTTTTG GTTCACACGA CCCGCTGCGG CAAACGCTTG TCAAAAAGCG TTTGTAACTA
NLas           ATTTTTTGGG AATTAGTTGG AATGTGTTCT TATCTATTAA TAGGGTTTTG GTTCACACGA CCCGCTGCGG CAAACGCTTG TCAAAAAGCG TTTGTAACTA
NLac           ATTTTTTGGG AATTAGTTGG AATGTGTTCT TATCTATTAA TAGGGTTTTG GTTCACACGA CCCGCTGCGG CAAACGCTTG TCAAAAAGCG TTTGTAACTA
NLar           ATTTTTTGGG AATTAGTTGG AATGTGTTCT TATCTATTAA TAGGGTTTTG GTTCACACGA CCCGCTGCGG CAAACGCTTG TCAAAAAGCG TTTGTAACTA
NLma           ATTTTTTGGG AATTAGTTGG AATGTGTTCT TATCTATTAA TAGGGTTTTG GTTCACACGA CCCGCTGCGG CAAACGCTTG TCAAAAAGCG TTTGTAACTA
NLmo           ATTTTTTGGG AATTAGTTGG AATGTGTTCT TATCTATTAA TAGGGTTTTG GTTCACACGA CCCGCTGCGG CAAACGCTTG TCAAAAAGCG TTTGTAACTA
NLmu           ATTTTTTGGG AATTAGTTGG AATGTGTTCT TATCTATTAA TAGGGTTTTG GTTCACACGA CCCGCTGCGG CAAACGCTTG TCAAAAAGCG TTTGTAACTA
NLob           ATTTTTTGGG AATTAGTTGG AATGTGTTCT TATCTATTAA TAGGGTTTTG GTTCACACGA CCCGCTGCGG CAAACGCTTG TCAAAAAGCG TTTGTAACTA
NLol           ATTTTTTGGG AATTAGTTGG AATGTGTTCT TATCTATTAA TAGGGTTTTG GTTCACACGA CCCGCTGCGG CAAACGCTTG TCAAAAAGCG TTTGTAACTA
NLpe           ATTTTTTGGG AATTAGTTGG AATGTGTTCT TATCTATTAA TAGGGTTTTG GTTCACACGA CCCGCTGCGG CAAACGCTTG TCAAAAAGCG TTTGTAACTA
NLph           ATTTTTTGGG AATTAGTTGG AATGTGTTCT TATCTATTAA TAGGGTTTTG GTTCACACGA CCCGCTGCGG CAAACGCTTG TCAAAAAGCG TTTGTAACTA
NLpl           ATTTTTTGGG AATTAGTTGG AATGTGTTCT TATCTATTAA TAGGGTTTTG GTTCACACGA CCCGCTGCGG CAAACGCTTG TCAAAAAGCG TTTGTAACTA
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NLpu            ATTTTTTGGG AATTAGTTGG AATGTGTTCT TATCTATTAA TAGGGTTTTG GTTCACACGA CCCGCTGCGG CAAACGCTTG TCAAAAAGCG TTTGTAACTA
NLth            ATTTTTTGGG AATTAGTTGG AATGTGTTCT TATCTATTAA TAGGGTTTTG GTTCACACGA CCCGCTGCGG CAAACGCTTG TCAAAAAGCG TTTGTAACTA
NLti            ATTTTTTGGG AATTAGTTGG AATGTGTTCT TATCTATTAA TAGGGTTTTG GTTCACACGA CCCGCTGCGG CAAACGCTTG TCAAAAAGCG TTTGTAACTA
NMma            ATTTTTTGGG AATTAGTTGG AATGTGTTCT TATCTATTAA TAGGGTTTTG GTTCACACGA CCCGCTGCGG CAAACGCTTG TCAAAAAGCG TTTGTAACTA
NMtf            ATTTTTTGGG AATTAGTTGG AATGTGTTCT TATCTATTAA TAGGGTTTTG GTTCACACGA CCCGCTGCGG CAAACGCTTG TCAAAAAGCG TTTGTAACTA
NMae            ATTTTTTGGG AATTAGTTGG AATGTGTTCT TATCTATTAA TAGGGTTTTG GTTCACACGA CCCGCTGCGG CAAACGCTTG TCAAAAAGCG TTTGTAACTA
NMtr            ATTTTTTGGG AATTAGTTGG AATGTGTTCT TATCTATTAA TAGGGTTTTG GTTCACACGA CCCGCTGCGG CAAACGCTTG TCAAAAAGCG TTTGTAACTA
NMca            ATTTTTTGGG AATTAGTTGG AATGTGTTCT TATCTATTAA TAGGGTTTTG GTTCACACGA CCCGCTGCGG CAAACGCTTG TCAAAAAGCG TTTGTAACTA
NMhi            ATTTTTTGGG AATTAGTTGG AATGTGTTCT TATCTATTAA TAGGGTTTTG GTTCACACGA CCCGCTGCGG CAAACGCTTG TCAAAAAGCG TTTGTAACTA
NMto            ATTTTTTGGG AATTAGTTGG AATGTGTTCT TATCTATTAA TAGGGTTTTG GTTCACACGA CCCGCTGCGG CAAACGCTTG TCAAAAAGCG TTTGTAACTA
NMal            ATTTTTTGGG AATTAGTTGG AATGGGTTCT TATCTATTAA TAGGGTTTTG GTTCACACGA CCCGCTGCGG CAAACGCTTG TCAAAAAGCG TTTGTAACTA
NMmo            ATTTTTTGGG AATTAGTTGG AATGTGTTCT TATCTATTAA TAGGGTTTTG GTTCACACGA CCCGCTGCGG CAAACGCTTG TCAAAAAGCG TTTGTAACTA
NMne            ATTTTTTGGG AATTAGTTGG AATGTGTTCT TATCTATTAA TAGGGTTTTG GTTCACACGA CCCGCTGCGG CAAACGCTTG TCAAAAAGCG TTTGTAACTA
NMni            ATTTTTTGGG AATTAGTTGG AATGTGTTCT TATCTATTAA TAGGGTTTTG GTTCACACGA CCCGCTGCGG CAAACGCTTG TCAAAAAGCG TTTGTAACTA
NMpa            ATTTTTTGGG AATTAGTTGG AATGTGTTCT TATCTATTAA TAGGGTTTTG GTTCACACGA CCCGCTGCGG CAAACGCTTG TCAAAAAGCG TTTGTAACTA
NMsy            ATTTTTTGGG AATTAGTTGG AATGTGTTCT TATCTATTAA TAGGGTTTTG GTTCACACGA CCCGCTGCGG CAAACGCTTG TCAAAAAGCG TTTGTAACTA
NMve            ATTTTTTGGG AATTAGTTGG AATGTGTTCT TATCTATTAA TAGGGTTTTG GTTCACACGA CCCGCTGCGG CAAACGCTTG TCAAAAAGCG TTTGTAACTA
NAros           ATTTTTTGGG AATTAGTTGG AATGTGTTCT TATCTATTAA TAGGGTTTTG GTTCACACGA CCCGCTGCGG CAAACGCTTG TCAAAAAGCG TTTGTAACTA
NAni            ATTTTTTGGG AATTAGTTGG AATGTGTTCT TATCTATTAA TAGGGTTTTG GTTCACACGA CCCGCTGCGG CAAACGCTTG TCAAAAAGCG TTTGTAACTA
NKvi            ATTTTTTGGG AATTAGTTGG AATGTGTTCT TATCTATTAA TAGGGTTTTG GTTCACACGA CCCGCTGCGG CAAACGCTTG TCAAAAAGCG TTTGTAACTA


                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                       410        420        430        440        450        460        470        480        490        500
NAar            ATCGGATAGG CGATTTTGGT TTATTATTAG GAATCCTAGG TTTTTATTGG CTAACGGGCA GTTTCGAATT TCAAGATTTG TTCGAAATAT TTAATAACTT
NAhi            ATCGGATAGG CGATTTTGGT TTATTATTAG GAATCCTAGG TTTTTATTGG ATAACGGGCA GTTTCGAATT TCAAGATTTG TTCGAAATAT TTAATAACTT
NAlo            ATCGGATAGG CGATTTTGGT TTATTATTAG GAATCCTAGG TTTTTATTGG ATAACGGGCA GTTTCGAATT TCAAGATTTG TTCGAAATAT TTAATAACTT
NAca            ATCGGATAGG CGATTTTGGT TTATTATTAG GAATCTTAGG TTTTTATTGG ATAACGGGCA GTTTCGAATT TCAAGATTTG TTCGAAATAT TTAATAACTT
NAof            ATCGGATAGG CGATTTTGGT TTATTATTAG GAATCCTAGG TTTTTATTGG CTAACGGGCA GTTTCGAATT TCAAGATTTG TTCGAAATAT TTAATAACTT
NAlu            ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
NLcr            ATCGGATAGG CGATTTTGGT TTATTATTAG GAATCCTAGG TTTTTATTGG ATAACGGGCA GTTTCGAATT TCAAGATTTG TTCGAAATAT TTAATAACTT
NLag            ATCGGATAGG CGATTTTGGT TTATTATTAG GAATCCTAGG TTTTTATTGG CTAACGGGCA GTTTCGAATT TCAAGATTTG TTCGAAATAT TTAATAACTT
NLbr            ATCGGATAGG CGATTTTGGT TTATTATTAG GAATCCTAGG TTTTTATTGG CTAACGGGCA GTTTCGAATT TCAAGATTTG TTCGAAATAT TTAATAACTT
NLtr            ATCGGATAGG CGATTTTGGT TTATTATTAG GAATCCTAGG TTTTTATTGG CTAACGGGCA GTTTCGAATT TCAAGATTTG TTCGAAATAT TTAATAACTT
NLtp            AtcGGATAGG CGATTTtGGT TTATTATTaG GAATCCTAGG TTTTTATTGG ATAACGGGCA GTTTCGAATt TCAAGATTTG TTCGAAATAT TTAATAACTT
NLfl            ATCGGATAGG CGATTTTGGT TTATTATTAG GAATCCTAGG TTTTTATTGG CTAACGGGCA GTTTCGAATT TCAAGATTTG TTCGAAATAT TTAATAACTT
NLas            ATCGGATAGG CGATTTTGGT TTATTATTAG GAATCCTAGG TTTTTATTGG ATAACGGGCA GTTTCGAATT TCAAGATTTG TTCGAAATAT TTAATAACTT
NLac            ATCGGATAGG CGATTTTGGT TTATTATTAG GAATCCTAGG TTTTTATTGG ATAACGGGCA GTTTCGAATT TCAAGATTTG TTCGAAATAT TTAATAACTT
NLar            ATCGGATAGG CGATTTTGGT TTATTATTAG GAATCCTAGG TTTTTATTGG ATAACGGGCA GTTTCGAATT TCAAGATTTG TTCGAAATAT TTAATAACTT
NLma            ATCGGATAGG CGATTTTGGT TTATTATTAG GAATCCTAGG TTTTTATTGG ATAACGGGCA GTTTCGAATT TCAAGATTTG TTCGAAATAT TTAATAACTT
NLmo            ATCGGATAGG CGATTTTGGT TTATTATTAG GAATCCTAGG TTTTTATTGG ATAACGGGCA GTTTCGAATT TCAAGATTTG TTCGAAATAT TTAATAACTT
NLmu            ATCGGATAGG CGATTTTGGT TTATTATTAG GAATCCTAGG TTTTTATTGG ATAACGGGgA GTTTCGAATT TCAAGATTTG TTCGAAATAT TTAATAACTT
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NLob         ATCGGATAGG CGATTTTGGT TTATTATTAG GAATCCTAGG TTTTTATTGG CTAACGGGCA GTTTCGAATT TCAAGATTTG TTCGAAATAT TTAATAACTT
NLol         ATCGGATAGG CGATTTTGGT TTATTATTAG GAATCCTAGG TTTTTATTGG CTAACGGGCA GTTTCGAATT TCAAGATTTG TTCGAAATAT TTAATAACTT
NLpe         ATCGGATAGG CGATTTTGGT TTATTATTAG GAATCCTAGG TTTTTATTGG ATAACGGGCA GTTTCGAATT TCAAGATTTG TTCGAAATAT TTAATAACTT
NLph         ATCGGATAGG CGATTTTGGT TTATTATTAG GAATCCTAGG TTTTTATTGG ATAACGGGCA GTTTCGAATT TCAAGATTTG TTCGAAATAT TTAATAACTT
NLpl         ATCGGATAGG CGATTTTGGT TTATTATTAG GAATCCTAGG TTTTTATTGG ATAACGGGCA GTTTCGAATT TCAAGATTTG TTCGAAATAT TTAATAACTT
NLpu         ATCGGATAGG CGATTTTGGT TTATTATTAG GAATCCTAGG TTTTTATTGG ATAACGGGCA GTTTCGAATT TCAAGATTTG TTCGAAATAT TTAATAACTT
NLth         ATCGGATAGG CGATTTTGGT TTATTATTAG GAATCCTAGG TTTTTATTGG CTAACGGGCA GTTTCGAATT TCAAGATTTG TTCGAAATAT TTAATAACTT
NLti         ATCGGATAGG CGATTTTGGT TTATTATTAG GAATCCTAGG TTTTTATTGG ATAACGGGCA GTTTCGAATT TCAAGATTTG TTCGAAATAT TTAATAACTT
NMma         ATCGGATAGG CGATTTTGGT TTATTATTAG GAATCTTAGG TTTTTATTGG ATAACGGGCA GTTTCGAATT TCAAGATTTG TTCGAAATAT TTAATAACTT
NMtf         ATCGGATAGG CGATTTTGGT TTATTATTAG GAATCTTAGG TTTTTATTGG ATAACGGGCA GTTTCGAATT TCAAGATTTG TTCGAAATAT TTAATAACTT
NMae         ATCGGATAGG CGATTTTGGT TTATTATTAG GAATCCTAGG TTTTTATTGG ATAACGGGCA GTTTCGAATT TCAAGATTTG TTCGAAATAT TTAATAACTT
NMtr         ATCGGATAGG CGATTTTGGT TTATTATTAG GAATCCTAGG TTTTTATTGG ATAACGGGCA GTTTCGAATT TCAAGATTTG TTCGAAATAT TTAATAACTT
NMca         ATCGGATAGG CGATTTTGGT TTATTATTAG GAATCCTAGG TTTTTATTGG ATAACGGGCA GTTTCGAATT TCAAGATTTG TTCGAAATAT TTAATAACTT
NMhi         ATCGGATAGG CGATTTTGGT TTATTATTAG GAATCCTAGG TTTTTATTGG ATAACGGGCA GTTTCGAATT TCAAGATTTG TTCGAAATAT TTAATAACTT
NMto         ATCGGGTAGG CGATTTTGGT TTATTATTAG GAATCCTAGG TTTTTATTGG ATAACGGGCA GTTTCGAATT TCAAGATTTG TTCGAAATAT TTAATAACTT
NMal         ATCGGATAGG CGATTTTGGT TTATTATTAG GAATCTTAGG TTTTTATTGG ATAACGGGCA GTTTCGAATT TCAAGATTTG TTCGAAATAT TTAATAACTT
NMmo         ATCGGGTAGG CGATTTTGGT TTATTATTAG GAATCCTAGG TTTTTATTGG ATAACGGGCA GTTTCGAATT TCAAGATTTG TTCGAAATAT TTAATAACTT
NMne         ATCGGATAGG CGATTTTGGT TTATTATTAG GAATCCTAGG TTTTTATTGG ATAACGGGCA GTTTCGAATT TCAAGATTTG TTCGAAATAT TTAATAACTT
NMni         ATCGGATAGG CGATTTTGGT TTATTATTAG GAATCCTAGG TTTTTATTGG ATAACGGGCA GTTTCGAATT TCAAGATTTG TTCGAAATAT TTAATAACTT
NMpa         ATCGGATAGG CGATTTTGGT TTATTATTAG GAATCCTAGG TTTTTATTGG ATAACGGGCA GTTTCGAATT TCAAGATTTG TTCGAAATAT TTAATAACTT
NMsy         ATCGGATAGG CGATTTTGGT TTATTATTAG GAATCCTAGG TTTTTATTGG ATAACGGGCA GTTTCGAATT TCAAGATTTG TTCGAAATAT TTAATAACTT
NMve         ATCGGATAGG CGATTTTGGT TTATTATTAG GAATCCTAGG TTTTTATTGG ATAACGGGCA GTTTCGAATT TCAAGATTTG TTCGAAATAT TTAATAACTT
NAros        ATCGGATAGG CGATTTTGGT TTATTATTAG GAATCTTAGG TTTTTATTGG ATAACGGGCA GTTTCGAATT TCAAGATTTG TTCGAAATAT TTAATAACTT
NAni         ATCGGATAGG CGATTTTGGT TTATTATTAG GAATCCTAGG TTTTTATTGG CTAACGGGCA GTTTCGAATT TCAAGATTTG TTCGAAATAT TTAATAACTT
NKvi         ATCGGATAGG CGATTTTGGT TTATTATTAG GAATCTTAGG TTTTTATTGG ATAACGGGCA GTTTCGAATT TCAAGATTTG TTCGAAATAT TTAATAACTT


             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    510        520        530        540        550        560        570        580        590        600
NAar         GATTTATAAT AATGAGGTTC CTTTTTTATT TGTTACTTTA TGTGCCTCTT TATTATTTGC CGGTGCAGTT GCTAAATCTG CGCAATTTCC TCTTCATGTA
NAhi         GATTTATAAT AATGAGGTTC CTTTTTTATT TGTTACTTTA TGTGCCTCTT TATTATTTGC CGGTGCAGTT GCTAAATCTG CGCAATTTCC TCTTCATGTA
NAlo         GATTTATAAT AATGAGGTTC CTTTTTTATT TGTTACTTTA TGTGCCTCTT TATTATTTGC CGGTGCAGTT GCTAAATCTG CGCAATTTCC TCTTCATGTA
NAca         GATTTATAAT AATGAGGTTC CTTTTTTATT TGTTACTTTA TGTGCCTCTT TATTATTTGC CGGTGCAGTT GCTAAATCTG CGCAATTTCC TCTTCATGTA
NAof         GATTTATAAT AATGAGGTTC CTTTTTTATT TGTTACTTTA TGTGCCTGTT TATTATTTGC CGGTGCAGTT GCTAAATCTG CGCAATTTCC TCTTCATGTA
NAlu         ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
NLcr         GATTTATAAT AATGAGGTTC CTTTTTTATT TGTTACTTTA TGTGCCTGTT TATTATTTGC CGGGGCAGTT GCTAAATCTG CGCAATTTCC TCTTCATGTA
NLag         GATTTATAAT AATGAGGTTC CTTTTTTATT TGTTACTTTA TGTGCCTGTT TATTATTTGC CGGTGCAGTT GCTAAATCTG CGCAATTTCC TCTTCATGTA
NLbr         GATTTATAAT AATGAGGTTC CTTTTTTATT TGTTACTTTA TGTGCCTGTT TATTATTTGC CGGTGCAGTT GCTAAATCTG CGCAATTTCC TCTTCATGTA
NLtr         GATTTATAAT AATGAGGTTC CTTTTTTATT TGTTACTTTA TGTGCCTGTT TATTATTTGC CGGTGCAGTT GCTAAATCTG CGCAATTTCC TCTTCATGTA
NLtp         GATTTATAAT AATGAGGTTC CTTTTTTATT TGTTACTTTA TGTGCCTGTT TATTATTTGC CGGtGCAGtT GCTAAATCTG CGCAATTTCC TCTTCATGTA
NLfl         GATTTATAAT AATGAGGTTC CTTTTTTATT TGTTACTTTA TGTGCCTGTT TATTATTTGC CGGTGCAGTT GCTAAATCTG CGCAATTTCC TCTTCATGTA
NLas         GATTTATAAT AATGAGGTTC CTTTTTTATT TGTTACTTTA TGTGCCTGTT TATTATTTGC CGGGGCAGTT GCTAAATCTG CGCAATTTCC TCTTCATGTA
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NLac          GATTTATAAT AATGAGGTTC CTTTTTTATT TGTTACTTTA TGTGCCTCTT TATTATTTGC CGGTGCAGTT GCTAAATCTG CGCAATTTCC TCTTCATGTA
NLar          GATTTATAAT AATGAGGTTC CTTTTTTATT TGTTACTTTA TGTGCCTGTT TATTATTTGC CGGGGCAGTT GCTAAATCTG CGCAATTTCC TCTTCATGTA
NLma          GATTTATAAT AATGAGGTTC CTTTTTTATT TGTTACTTTA TGTGCCTCTT TATTATTTGC CGGTGCAGTT GCTAAATCTG CGCAATTTCC TCTTCATGTA
NLmo          GATTTATAAT AATGAGGTTC CTTTTTTATT TGTTACTTTA TGTGCCTGTT TATTATTTGC CGGTGCAGTT GCTAAATCTG CGCAATTTCC TCTTCATGTA
NLmu          GATTTATAAT AATGAGGTTC CTTTTTTATT TGTTACTTTA TGTGCCTGTT TATTATTTGC CGGGGCAGTT GCTAAATCTG CGCAATTTCC TCTTCATGTA
NLob          GATTTATAAT AATGAGGTTC CTTTTTTATT TGTTACTTTA TGTGCCTGTT TATTATTTGC CGGTGCAGTT GCTAAATCTG CGCAATTTCC TCTTCATGTA
NLol          GATTTATAAT AATGAGGTTC CTTTTTTATT TGTTACTTTA TGTGCCTGTT TATTATTTGC CGGTGCAGTT GCTAAATCTG CGCAATTTCC TCTTCATGTA
NLpe          GATTTATAAT AATGAGGTTC CTTTTTTATT TGTTACTTTA TGTGCCTGTT TATTATTTGC CGGGGCAGTT GCTAAATCTG CGCAATTTCC TCTTCATGTA
NLph          GATTTATAAT AATGAGGTTC CTTTTTTATT TGTTACTTTA TGTGCCTCTT TATTATTTGC CGGTGCAGTT GCTAAATCTG CGCAATTTCC TCTTCATGTA
NLpl          GATTTATAAT AATGAGGTTC CTTTTTTATT TGTTACTTTA TGTGCCTGTT TATTATTTGC CGGTGCAGTT GCTAAATCTG CGCAATTTCC TCTTCATGTA
NLpu          GATTTATAAT AATGAGGTTC CTTTTTTATT TGGTACTTTA TGTGCCTGTT TATTATTTGC CGGTGCAGTT GCTAAATCTG CGCAATTTCC TCTTCATGTA
NLth          GATTTATAAT AATGAGGTTC CTTTTTTATT TGTTACTTTA TGTGCCTGTT TATTATTTGC CGGTGCAGTT GCTAAATCTG CGCAATTTCC TCTTCATGTA
NLti          GATTTATAAT AATGAGGTTC CTTTTTTATT TGTTACTTTA TGTGCCTGTT TATTATTTGC TGGTGCAGTT GCTAAATCTG CGCAATTTCC TCTTCATGTA
NMma          GATTTATAAT AATGAGGTTC CTTTTTTATT TGTTACTTTA TGTGCCTCTT TATTATTTGC CGGTGCAGTT GCTAAATCTG CGCAATTTCC TCTTCATGTA
NMtf          GATTTATAAT AATGAGGTTC CTTTTTTATT TGTTACTTTA TGTGCCTCTT TATTATTTGC CGGTGCAGTT GCTAAATCTG CGCAATTTCC TCTTCATGTA
NMae          GATTTATAAT AATGAGGTTC CTTTTTTATT TGTTACTTTA TGTGCCTCTT TATTATTTGC CGGTGCAGTT GCTAAATCTG CGCAATTTCC TCTTCATGTA
NMtr          GATTTATAAT AATGAGGTTC CTTTTTTATT TGTTACTTTA TGTGCCTCTT TATTATTTGC CGGTGCAGTT GCTAAATCTG CGCAATTTCC TCTTCATGTA
NMca          GATTTATAAT AATGAGGTTC CTTTTTTATT TGTTACTTTA TGTGCCTCTT TATTATTTGC CGGTGCAGTT GCTAAATCTG CGCAATTTCC TCTTCATGTA
NMhi          GATTTATAAT AATGAGGTTC CTTTTTTATT TGTTACTTTA TGTGCCTGTT TATTATTTGC CGGTGCAGTT GCTAAATCTG CGCAATTTCC TCTTCATGTA
NMto          GATTTATAAT AATGAGGTTC CTTTTTTATT TGTTACTTTA TGTGCCTGTT TATTATTTGC CGGTGCAGTT GCTAAATCTG CGCAATTTCC TCTTCATGTA
NMal          GATTTATAAT AATGAGGTTC CTTTTTTATT TGTTACTTTA TGTGCCTCTT TATTATTTGC CGGTGCAGTT GCTAAATCTG CGCAATTTCC TCTTCATGTA
NMmo          GATTTATAAT AATGAGGTTC CTTTTTTATT TGTTACTTTA TGTGCCTGTT TATTATTTGC CGGTGCAGTT GCTAAATCTG CGCAATTTCC TCTTCATGTA
NMne          GATTTATAAT AATGAGGTTC CTTTTTTATT TGTTACTTTA TGTGCCTGTT TATTATTTGC CGGGGCAGTT GCTAAATCTG CGCAATTTCC TCTTCATGTA
NMni          GATTTATAAT AATGAGGTTC CTTTTTTATT TGTTACTTTA TGTGCCTGTT TATTATTTGC CGGGGCAGTT GCTAAATCTG CGCAATTTCC TCTTCATGTA
NMpa          GATTTATAAT AATGAGGTTC CTTTTTTATT TGTTACTTTA TGTGCCTGTT TATTATTTGC CGGGGCAGTT GCTAAATCTG CGCAATTTCC TCTTCATGTA
NMsy          GATTTATAAT AATGAGGTTC CTTTTTTATT TGTTACTTTA TGTGCCTGTT TATTATTTGC CGGGGCAGTT GCTAAATCTG CGCAATTTCC TCTTCATGTA
NMve          GATTTATAAT AATGAGGTTC CTTTTTTATT TGTTACTTTA TGTGCCTGTT TATTATTTGC CGGGGCAGTT GCTAAATCTG CGCAATTTCC TCTTCATGTA
NAros         GATTTATAAT AATGAGGTTC CTTTTTTATT TGTTACTTTA TGTGCCTCTT TATTATTTGC CGGTGCAGTT GCTAAATCTG CGCAATTTCC TCTTCATGTA
NAni          GATTTATAAT AATGAGGTTC CTTTTTTATT TGTTACTTTA TGTGCCTGTT TATTATTTGC CGGTGCAGTT GCTAAATCTG CGCAATTTCC TCTTCATGTA
NKvi          GATTTATAAT AATGAGGTTC CTTTTTTATT TGTTACTTTA TGTGCCTCTT TATTATTTGC CGGTGCAGTT GCTAAATCTG CGCAATTTCC TCTTCATGTA


              ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     610        620        630        640        650        660        670        680        690        700
NAar          TGGTTACCTG ATGCCATGGA GGGGCCTACT CCTATTTCGG CTCTTATACA TGCTGCCACT ATGGTAGCAG CGGGAATTTT TCTTGTCGCC CGCCTTCTTC
NAhi          TGGTTACCTG ATGCCATGGA GGGGCCTACT CCTATTTCGG CTCTTATACA TGCTGCCACT ATGGTAGCAG CGGGAATTTT TCTTGTCGCC CGCCTTCTTC
NAlo          TGGTTACCTG ATGCCATGGA GGGGCCTACT CCTATTTCGG CTCTTATACA TGCTGCCACT ATGGTAGCAG CGGGAATTTT TCTTGTCGCC CGCCTTCTTC
NAca          TGGTTACCTG ATGCCATGGA GGGGCCTACT CCTATTTCGG CTCTTATACA TGCTGCCACT ATGGTAGCAG CGGGAATTTT TCTTGTCGCC CGCCTTCTTC
NAof          TGGTTACCTG ATGCCATGGA GGGGCCTACT CCTATTTCGG CTCTTATACA TGCTGCCACT ATGGTAGCAG CGGGAATTTT TCTTGTCGCC CGCCTTCTTC
NAlu          ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
NLcr          TGGTTACCTG ATGCCATGGA GGGGCCTACT CCTATTTCGG CTCTTATACA TGCTGCCACT ATGGTAGCAG CGGGAATTTT TCTTGTCGCC CGCCTTCTTC
NLag          TGGTTACCTG ATGCCATGGA GGGGCCTACT CCTATTTCGG CTCTTATACA TGCTGCCACT ATGGTAGCAG CGGGAATTTT TCTTGTCGCC CGCCTTCTTC
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NLbr          TGGTTACCTG ATGCCATGGA GGGGCCTACT CCTATTTCGG CTCTTATACA TGCTGCCACT ATGGTAGCAG CGGGAATTTT TCTTGTCGCC CGCCTTCTTC
NLtr          TGGTTACCTG ATGCCATGGA GGGGCCTACT CCTATTTCGG CTCTTATACA TGCTGCCACT ATGGTAGCAG CGGGAATTTT TCTTGTCGCC CGCCTTCTTC
NLtp          TGGTTACCTG AtGCCATGGA GGGGCCTACT CCTATTTCGG CTCTTATACA TGCTGCCACT ATGGTAGCAG CGGGAATTTT TCTTGTCGCC CGCCTTCTTC
NLfl          TGGTTACCTG ATGCCATGGA GGGGCCTACT CCTATTTCGG CTCTTATACA TGCTGCCACT ATGGTAGCAG CGGGAATTTT TCTTGTCGCC CGCCTTCTTC
NLas          TGGTTACCTG ATGCCATGGA GGGGCCTACT CCTATTTCGG CTCTTATACA TGCTGCCACT ATGGTAGCAG CGGGAATTTT TCTTGTCGCC CGCCTTCTTC
NLac          TGGTTACCTG ATGCCATGGA GGGGCCTACT CCTATTTCGG CTCTTATACA TGCTGCCACT ATGGTAGCAG CGGGAATTTT TCTTGTCGCC CGCCTTCTTC
NLar          TGGTTACCTG ATGCCATGGA GGGGCCTACT CCTATTTCGG CTCTTATACA TGCTGCCACT ATGGTAGCAG CGGGAATTTT TCTTGTCGCC CGCCTTCTTC
NLma          TGGTTACCTG ATGCCATGGA GGGGCCTACT CCTATTTCGG CTCTTATACA TGCTGCCACT ATGGTAGCAG CGGGAATTTT TCTTGTCGCC CGCCTTCTTC
NLmo          TGGTTACCTG ATGCCATGGA GGGGCCTACT CCTATTTCGG CTCTTATACA TGCTGCCACT ATGGTAGCAG CGGGAATTTT TCTTGTCGCC CGCCTTCTTC
NLmu          TGGTTACCTG ATGCCATGGA GGGGCCTACT CCTATTTCGG CTCTTATACA TGCTGCCACT ATGGTAGCAG CGGGAATTTT TCTTGTCGCC CGCCTTCTTC
NLob          TGGTTACCTG ATGCCATGGA GGGGCCTACT CCTATTTCGG CTCTTATACA TGCTGCCACT ATGGTAGCAG CGGGAATTTT TCTTGTCGCC CGCCTTCTTC
NLol          TGGTTACCTG ATGCCATGGA GGGGCCTACT CCTATTTCGG CTCTTATACA TGCTGCCACT ATGGTAGCAG CGGGAATTTT TCTTGTCGCC CGCCTTCTTC
NLpe          TGGTTACCTG ATGCCATGGA GGGGCCTACT CCTATTTCGG CTCTTATACA TGCTGCCACT ATGGTAGCAG CGGGAATTTT TCTTGTCGCC CGCCTTCTTC
NLph          TGGTTACCTG ATGCCATGGA GGGGCCTACT CCTATTTCGG CTCTTATACA TGCTGCCACT ATGGTAGCAG CGGGAATTTT TCTTGTCGCC CGCCTTCTTC
NLpl          TGGTTACCTG ATGCCATGGA GGGGCCTACT CCTATTTCGG CTCTTATACA TGCTGCCACT ATGGTAGCAG CGGGAATTTT TCTTGTCGCC CGCCTTCTTC
NLpu          TGGTTACCTG ATGCCATGGA GGGGCCTACT CCTATTTCGG CTCTTATACA TGCTGCCACT ATGGTAGCAG CGGGAATTTT TCTTGTCGCC CGCCTTCTTC
NLth          TGGTTACCTG ATGCCATGGA GGGGCCTACT CCTATTTCGG CTCTTATACA TGCTGCCACT ATGGTAGCAG CGGGAATTTT TCTTGTCGCC CGCCTTCTTC
NLti          TGGTTACCTG ATGCCATGGA GGGGCCTACT CCTATTTCGG CTCTTATACA TGCTGCCACT ATGGTAGCAG CGGGAATTTT TCTTGTCGCC CGCCTTCTTC
NMma          TGGTTACCTG ATGCCATGGA GGGGCCTACT CCTATTTCGG CTCTTATACA TGCTGCCACT ATGGTAGCAG CGGGAATTTT TCTTGTCGCC CGCCTTCTTC
NMtf          TGGTTACCTG ATGCCATGGA GGGGCCTACT CCTATTTCGG CTCTTATACA TGCTGCCACT ATGGTAGCAG CGGGAATTTT TCTTGTCGCC CGCCTTCTTC
NMae          TGGTTACCTG ATGCCATGGA GGGTCCTACT CCTATTTCGG CTCTTATACA TGCTGCCACT ATGGTAGCAG CGGGAATTTT TCTTGTCGCC CGCCTTCTTC
NMtr          TGGTTACCTG ATGCCATGGA GGGTCCTACT CCTATTTCGG CTCTTATACA TGCTGCCACT ATGGTAGCAG CGGGAATTTT TCTTGTCGCC CGCCTTCTTC
NMca          TGGTTACCTG ATGCCATGGA GGGGCCTACT CCTATTTCGG CTCTTATACA TGCTGCCACT ATGGTAGCAG CGGGAATTTT TCTTGTCGCC CGCCTTCTTC
NMhi          TGGTTACCTG ATGCCATGGA GGGGCCTACT CCTATTTCGG CTCTTATACA TGCTGCCACT ATGGTAGCAG CGGGAATTTT TCTTGTCGCC CGCCTTCTTC
NMto          TGGTTACCTG ATGCCATGGA GGGGCCTACT CCTATTTCGG CTCTTATACA TGCTGCCACT ATGGTAGCAG CGGGAATTTT TCTTGTCGCC CGCCTTCTTC
NMal          TGGTTACCTG ATGCCATGGA GGGGCCTACT CCTATTTCGG CTCTTATACA TGCTGCCACT ATGGTAGCAG CGGGAATTTT TCTTGTCGCC CGCCTTCTTC
NMmo          TGGTTACCTG ATGCCATGGA GGGGCCTACT CCTATTTCGG CTCTTATACA TGCTGCCACT ATGGTAGCAG CGGGAATTTT TCTTGTCGCC CGCCTTCTTC
NMne          TGGTTACCTG ATGCCATGGA GGGGCCTACT CCTATTTCGG CTCTTATACA TGCTGCCACT ATGGTAGCAG CGGGAATTTT TCTTGTCGCC CGCCTTCTTC
NMni          TGGTTACCTG ATGCCATGGA GGGGCCTACT CCTATTTCGG CTCTTATACA TGCTGCCACT ATGGTAGCAG CGGGAATTTT TCTTGTCGCC CGCCTTCTTC
NMpa          TGGTTACCTG ATGCCATGGA GGGGCCTACT CCTATTTCGG CTCTTATACA TGCTGCCACT ATGGTAGCAG CGGGAATTTT TCTTGTCGCC CGCCTTCTTC
NMsy          TGGTTACCTG ATGCCATGGA GGGGCCTACT CCTATTTCGG CTCTTATACA TGCTGCCACT ATGGTAGCAG CGGGAATTTT TCTTGTCGCC CGCCTTCTTC
NMve          TGGTTACCTG ATGCCATGGA GGGGCCTACT CCTATTTCGG CTCTTATACA TGCTGCCACT ATGGTAGCAG CGGGAATTTT TCTTGTCGCC CGCCTTCTTC
NAros         TGGTTACCTG ATGCCATGGA GGGGCCTACT CCTATTTCGG CTCTTATACA TGCTGCCACT ATGGTAGCAG CGGGAATTTT TCTTGTCGCC CGCCTTCTTC
NAni          TGGTTACCTG ATGCCATGGA GGGGCCTACT CCTATTTCGG CTCTTATACA TGCTGCCACT ATGGTAGCAG CGGGAATTTT TCTTGTCGCC CGCCTTCTTC
NKvi          TGGTTACCTG ATGCCATGGA GGGGCCTACT CCTATTTCGG CTCTTATACA TGCTGCCACT ATGGTAGCAG CGGGAATTTT TCTTGTCGCC CGCCTTCTTC


              ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     710        720        730        740        750        760        770        780        790        800
NAar          CTCTTTTCAT AGTTATACCT TACATAATGA ATCTAATATC TTTGATAGGT ATAATAACGG TATTATTAGG GGCTACTTTA GCCCTTGCTC AAAAAGATAT
NAhi          CTCTTTTCAT AGTTATACCT TACATAATGA ATCTAATATC TTTGATAGGT ATAATAACGG TATTATTAGG GGCTACTTTA GCCCTTGCTC AAAAAGATAT
NAlo          CTCTTTTCAT AGTTATACCT TACATAATGA ATCTAATATC TTTGATAGGT ATAATAACGG TATTATTAGG GGCTACTTTA GCCCTTGCTC AAAAAGATAT
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NAca          CTCTTTTCAT AGTTATACCT TACATAATGA ATCTAATATC TTTGATAGGT ATAATAACGG TATTATTAGG GGCTACTTTA GCCCTTGCTC AAAAAGATAT
NAof          CTCTTTTCAT AGTTATACCT TACATAATGA ATCTAATATC TTTGATAGGT ATAATAACGG TATTATTAGG GGCTACTTTA GCCCTTGCTC AAAAAGATAT
NAlu          ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
NLcr          CTCTTTTCAT AGTTATACCT TACATAATGA ATCTAATATC TTTGATAGGT ATAATAACGG TATTATTAGG GGCTACTTTA GCCCTTGCTC AAAAAGATAT
NLag          CTCTTTTCAT AGTTATACCT TACATAATGA ATCTAATATC TTTGATAGGT ATAATAACGG TATTATTAGG GGCTACTTTA GCCCTTGCTC AAAAAGATAT
NLbr          CTCTTTTCAT AGTTATACCT TACATAATGA ATCTAATATC TTTGATAGGT ATAATAACGG TATTATTAGG GGCTACTTTA GCCCTTGCTC AAAAAGATAT
NLtr          CTCTTTTCAT AGTTATACCT TACATAATGA ATCTAATATC TTTGATAGGT ATAATAACGG TATTATTAGG GGCTACTTTA GCCCTTGCTC AAAAAGATAT
NLtp          CTCTTTTCAT AGTTATACCT TACATAATGA ATCTAATATC TTTGATAGGT ATAATAACGG TATTATTAGG GGCTACTTTA GCCCTTGCTC AAAAAGATAT
NLfl          CTCTTTTCAT AGTTATACCT TACATAATGA ATCTAATATC TTTGATAGGT ATAATAACGG TATTATTAGG GGCTACTTTA GCCCTTGCTC AAAAAGATAT
NLas          CTCTTTTCAT AGTTATACCT TACATAATGA ATCTAATATC TTTGATAGGT ATAATAACGG TATTATTAGG GGCTACTTTA GCCCTTGCTC AAAAAGATAT
NLac          CTCTTTTCAT AGTTATACCT TACATAATGA ATCTAATATC TTTGATAGGT ATAATAACGG TATTATTAGG GGCTACTTTA GCCCTTGCTC AAAAAGATAT
NLar          CTCTTTTCAT AGTTATACCT TACATAATGA ATCTAATATC TTTGATAGGT ATAATAACGG TATTATTAGG GGCTACTTTA GCCCTTGCTC AAAAAGATAT
NLma          CTCTTTTCAT AGTTATACCT TACATAATGA ATCTAATATC TTTGATAGGT ATAATAACGG TATTATTAGG GGCTACTTTA GCCCTTGCTC AAAAAGATAT
NLmo          CTCTTTTCAT AGTTATACCT TACATAATGA ATCTAATATC TTTGATAGGT ATAATAACGG TATTATTAGG GGCTACTTTA GCCCTTGCTC AAAAAGATAT
NLmu          CTCTTTTCAT AGTTATACCT TACATAATGA ATCTAATATC TTTGATAGGT ATAATAACGG TATTATTAGG GGCTACTTTA GCCCTTGCTC AAAAAGATAT
NLob          CTCTTTTCAT AGTTATACCT TACATAATGA ATCTAATATC TTTGATAGGT ATAATAACGG TATTATTAGG GGCTACTTTA GCCCTTGCTC AAAAAGATAT
NLol          CTCTTTTCAT AGTTATACCT TACATAATGA ATCTAATATC TTTGATAGGT ATAATAACGG TATTATTAGG GGCTACTTTA GCCCTTGCTC AAAAAGATAT
NLpe          CTCTTTTCAT AGTTATACCT TACATAATGA ATCTAATATC TTTGATAGGT ATAATAACGG TATTATTAGG GGCTACTTTA GCCCTTGCTC AAAAAGATAT
NLph          CTCTTTTCAT AGTTATACCT TACATAATGA ATCTAATATC TTTGATAGGT ATAATAACGG TATTATTAGG GGCTACTTTA GCCCTTGCTC AAAAAGATAT
NLpl          CTCTTTTCAT AGTTATACCT TACATAATGA ATCTAATATC TTTGATAGGT ATAATAACGG TATTATTAGG GGCTACTTTA GCCCTTGCTC AAAAAGATAT
NLpu          CTCTTTTCAT AGTTATACCT TACATAATGA ATCTAATATC TTTGATAGGT ATAATAACGG TATTATTAGG GGCTACTTTA GCCCTTGCTC AAAAAGATAT
NLth          CTCTTTTCAT AGTTATACCT TACATAATGA ATCTAATATC TTTGATAGGT ATAATAACGG TATTATTAGG GGCTACTTTA GCCCTTGCTC AAAAAGATAT
NLti          CTCTTTTCAT AGTTATACCT TACATAATGA ATCTAATATC TTTGATAGGT ATAATAACGG TATTATTAGG GGCTACTTTA GCCCTTGCTC AAAAAGATAT
NMma          CTCTTTTCAT AGTTATACCT TACATAATGA ATCTAATATC TTTGATAGGT ATAATAACGG TATTATTAGG GGCTACTTTA GCCCTTGCTC AAAAAGATAT
NMtf          CTCTTTTCAT AGTTATACCT TACATAATGA ATCTAATATC TTTGATAGGT ATAATAACGG TATTATTAGG GGCTACTTTA GCCCTTGCTC AAAAAGATAT
NMae          CTCTTTTCAT AGTTATACCT TACATAATGA ATCTAATATC TTTGATAGGT ATAATAACGG TATTATTAGG GGCTACTTTA GCCCTTGCTC AAAAAGATAT
NMtr          CTCTTTTCAT AGTTATACCT TACATAATGA ATCTAATATC TTTGATAGGT ATAATAACGG TATTATTAGG GGCTACTTTA GCCCTTGCTC AAAAAGATAT
NMca          CTCTTTTCAT AGTTATACCT TACATAATGA ATCTAATATC TTTGATAGGT ATAATAACGG TATTATTAGG GGCTACTTTA GCCCTTGCTC AAAAAGATAT
NMhi          CTCTTTTCAT AGTTATACCT TACATAATGA ATCTAATATC TTTGATAGGT ATAATAACGG TATTATTAGG GGCTACTTTA GCCCTTGCTC AAAAAGATAT
NMto          CTCTTTTCAT AGTTATACCT TACATAATGA ATCTAATATC TTTGATAGGT ATAATAACGG TATTATTAGG GGCTACTTTA GCCCTTGCTC AAAAAGATAT
NMal          CTCTTTTCAT AGTTATACCT TACATAATGA ATCTAATATC TTTGATAGGT ATAATAACGG TATTATTAGG GGCTACTTTA GCCCTTGCTC AAAAAGATAT
NMmo          CTCTTTTCAT AGTTATACCT TACATAATGA ATCTAATATC TTTGATAGGT ATAATAACGG TATTATTAGG GGCTACTTTA GCCCTTGCTC AAAAAGATAT
NMne          CTCTTTTCAT AGTTATACCT TACATAATGA ATCTAATATC TTTGATAGGT ATAATAACGG TATTATTAGG GGCTACTTTA GCCCTTGCTC AAAAAGATAT
NMni          CTCTTTTCAT AGTTATACCT TACATAATGA ATCTAATATC TTTGATAGGT ATAATAACGG TATTATTAGG GGCTACTTTA GCCCTTGCTC AAAAAGATAT
NMpa          CTCTTTTCAT AGTTATACCT TACATAATGA ATCTAATATC TTTGATAGGT ATAATAACGG TATTATTAGG GGCTACTTTA GCCCTTGCTC AAAAAGATAT
NMsy          CTCTTTTCAT AGTTATACCT TACATAATGA ATCTAATATC TTTGATAGGT ATAATAACGG TATTATTAGG GGCTACTTTA GCCCTTGCTC AAAAAGATAT
NMve          CTCTTTTCAT AGTTATACCT TACATAATGA ATCTAATATC TTTGATAGGT ATAATAACGG TATTATTAGG GGCTACTTTA GCCCTTGCTC AAAAAGATAT
NAros         CTCTTTTCAT AGTTATACCT TACATAATGA ATCTAATATC TTTGATAGGT ATAATAACGG TATTATTAGG GGCTACTTTA GCCCTTGCTC AAAAAGATAT
NAni          CTCTTTTCAT AGTTATACCT TACATAATGA ATCTAATATC TTTGATAGGT ATAATAACGG TATTATTAGG GGCTACTTTA GCCCTTGCTC AAAAAGATAT
NKvi          CTCTTTTCAT AGTTATACCT TACATAATGA ATCTAATATC TTTGATAGGT ATAATAACGG TATTATTAGG GGCTACTTTA GCCCTTGCTC AAAAAGATAT
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               ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                      810        820        830        840        850        860        870        880        890        900
NAar           TAAGAGGGGT TTAGCCTATT CTACAATGTC CCAACTGGGC TATATGATGT TAGCTCTAGG TATGGGGTCT TATCGAGCCG CTTTATTTCA TTTGATTACT
NAhi           TAAGAGGGGT TTAGCCTATT CTACAATGTC CCAACTGGGC TATATGATGT TAGCTCTAGG TATGGGGTCT TATCGAGCCG CTTTATTTCA TTTGATTACT
NAlo           TAAGAGGGGT TTAGCCTATT CTACAATGTC CCAACTGGGC TATATGATGT TAGCTCTAGG TATGGGGTCT TATCGAGCCG CTTTATTTCA TTTGATTACT
NAca           TAAGAGGGGT TTAGCCTATT CTACAATGTC CCAACTGGGc TATATGATGT TAGCTCTAGG TATGGGGTCT TATCGAGCCG CTTTATTTCA TTTGATTACT
NAof           TAAGAGGGGT TTAGCCTATT CTACAATGTC CCAACTGGGc TATATGATGT TAGCTCTAGG TATGGGGTCT TATCGAGCCG CTTTATTTCA TTTGATTACT
NAlu           ---------- ---------- -------GTC CCAActGGGc TATATGATGT TAGCTCTAGG TATgGGGTCT tATCGAGCCG CTTTATTTCA TTTGATTACT
NLcr           TAAGAGGGGT TTAGCCTATT CTACAATGTC CCAACTGGGC TATATGATGT TAGCTCTAGG TATGGGGTCT TATCGAGCCG CTTTATTTCA TTTGATTACT
NLag           TAAGAGGGGT TTAGCCTATT CTACAATGTC CCAACTGGGC TATATGATGT TAGCTCTAGG TATGGGGTCT TATCGAGCCG CTTTATTTCA TTTGATTACT
NLbr           TAAGAGGGGT TTAGCCTATT CTACAATGTC CCAACTGGGC TATATGATGT TAGCTCTAGG TATGGGGTCT TATCGAGCCG CTTTATTTCA TTTGATTACT
NLtr           TAAGAGGGGT TTAGCCTATT CTACAATGTC CCAACTGGGC TATATGATGT TAGCTCTAGG TATGGGGTCT TATCGAGCCG CTTTATTTCA TTTGATTACT
NLtp           TAAGAGGGGT TTAGCCTATT CTACAATGTC CCAACTGGGC TATATGATGT TAGCTCTAGG TATGGGGTCT TATCGAGCCG CTTTATTTCA TTTGATTACT
NLfl           TAAGAGGGGT TTAGCCTATT CTACAATGTC CCAACTGGGC TATATGATGT TAGCTCTAGG TATGGGGTCT TATCGAGCCG CTTTATTTCA TTTGATTACT
NLas           TAAGAGGGGT TTAGCCTATT CTACAATGTC CCAACTGGGC TATATGATGT TAGCTCTAGG TATGGGGTCT TATCGAGCCG CTTTATTTCA TTTGATTACT
NLac           TAAGAGGGGT TTAGCCTATT CTACAATGTC CCAACTGGGC TATATGATGT TAGCTCTAGG TATGGGGTCT TATCGAGCCG CTTTATTTCA TTTGATTACT
NLar           TAAGAGGGGT TTAGCCTATT CTACAATGTC CCAACTGGGC TATATGATGT TAGCTCTAGG TATGGGGTCT TATCGAGCCG CTTTATTTCA TTTGATTACT
NLma           TAAGAGGGGT TTAGCCTATT CTACAATGTC CCAACTGGGC TATATGATGT TAGCTCTAGG TATGGGGTCT TATCGAGCCG CTTTATTTCA TTTGATTACT
NLmo           TAAGAGGGGT TTAGCCTATT CTACAATGTC CCAACTGGGC TATATGATGT TAGCTCTAGG TATGGGGTCT TATCGAGCCG CTTTATTTCA TTTGATTACT
NLmu           TAAGAgGGGT TTAGCCTATT CTACAATGTC CCAACTGGGC TATATGATGT TAGCTCTAGG TATGGGGTCT TATCGAGCCG CTTTATTTCA TTTGATTACT
NLob           TAAGAGGGGT TTAGCCTATT CTACAATGTC CCAACTGGGC TATATGATGT TAGCTCTAGG TATGGGGTCT TATCGAGCCG CTTTATTTCA TTTGATTACT
NLol           TAAGAGGGGT TTAGCCTATT CTACAATGTC CCAACTGGGC TATATGATGT TAGCTCTAGG TATGGGGTCT TATCGAGCCG CTTTATTTCA TTTGATTACT
NLpe           TAAGAGGGGT TTAGCCTATT CTACAATGTC CCAACTGGGC TATATGATGT TAGCTCTAGG TATGGGGTCT TATCGAGCCG CTTTATTTCA TTTGATTACT
NLph           TAAGAGGGGT TTAGCCTATT CTACAATGTC CCAACTGGGC TATATGATGT TAGCTCTAGG TATGGGGTCG TATCGAGCCG CTTTATTTCA TTTGATTACT
NLpl           TAAGAGGGGT TTAGCCTATT CTACAATGTC CCAACTGGGC TATATGATGT TAGCTCTAGG TATGGGGTCT TATCGAGCCG CTTTATTTCA TTTGATTACT
NLpu           TAAGAGGGGT TTAGCCTATT CTACAATGTC CCAACTGGGC TATATGATGT TAGCTCTAGG TATGGGGTCT TATCGAGCCG CTTTATTTCA TTTGATTACT
NLth           TAAGAGGGGT TTAGCCTATT CTACAATGTC CCAACTGGGC TATATGATGT TAGCTCTAGG TATGGGGTCT TATCGAGCCG CTTTATTTCA TTTGATTACT
NLti           TAAGAGGGGT TTAGCCTATT CTACAATGTC CCAACTGGGC TATATGATGT TAGCTCTAGG TATGGGGTCT TATCGAGCCG CTTTATTTCA TTTGATTACT
NMma           TAAGAGGGGT TTAGCCTATT CTACAATGTC CCAACTGGGC TATATGATGT TAGCTCTAGG TATGGGGTCT TATCGAGCCG CTTTATTTCA TTTGATTACT
NMtf           TAAGAGGGGT TTAGCCTATT CTACAATGTC CCAACTGGGC TATATGATGT TAGCTCTAGG TATGGGGTCT TATCGAGCCG CTTTATTTCA TTTGATTACT
NMae           TAAGAGGGGT TTAGCCTATT CTACAATGTC CCAACTGGGC TATATGATGT TAGCTCTAGG TATGGGGTCT TATCGAGCCG CTTTATTTCA TTTGATTACT
NMtr           TAAGAGGGGT TTAGCCTATT CTACAATGTC CCAACTGGGC TATATGATGT TAGCTCTAGG TATGGGGTCT TATCGAGCCG CTTTATTTCA TTTGATTACT
NMca           TAAGAGGGGT TTAGCCTATT CTACAATGTC CCAACTGGGC TATATGATGT TAGCTCTAGG TATGGGGTCT TATCGAGCCG CTTTATTTCA TTTGATTACT
NMhi           TAAGAGGGGT TTAGCCTATT CTACAATGTC CCAACTGGGC TATATGAtGT TAGCTCTAGG TATGGGGTCT TATCGAGCCG CTTTATTTCA TTTGATTACT
NMto           TAAGAGGGGT TTAGCCTATT CTACAATGTC CCAACtGGGc TATATGATGT TAGCTCTAGG TATGGGGTCT TATCGAGCCG CTTTATTtCA TTTGATTACT
NMal           TAAGAGGGGT TTAGCCTATT CTACAATGTC CCAACTGGGc TATATGATGT TAGCTCTAGG TATGGGGTCT TATCGAGCCG CTTTATTTCA TTTGATTACT
NMmo           TAAGAGGGGT TTAGCCTATT CTACAATGTC CCAACTGGGC TATATGATGT TAGCTCTAGG TATGGGGTCT TATCGAGCCG CTTTATTtCA TTTGATTACT
NMne           TAAGAGGGGT TTAGCCTATT CTACAATGTC CCAACTGGGC TATATGATGT TAGCTCTAGG TATGGGGTCT TATCGAGCCG CTTTATTTCA TTTGATTACT
NMni           TAAGAGGGGT TTAGCCTATT CTACAATGTC CCAACTGGGC TATATGATGT TAGCTCTAGG TATGGGGTCT TATCGAGCCG CTTTATTTCA TTTGATTACT
NMpa           TAAGAGGGGT TTAGCCTATT CTACAATGTC CCAACTGGGC TATATGATGT TAGCTCTAGG TATGGGGTCT TATCGAGCCG CTTTATTTCA TTTGATTACT
NMsy           TAAGAGGGGT TTAGCCTATT CTACAATGTC CCAACTGGGc TATATGATGT TAGCTCTAGG TATGGGGTCT TATCGAGCCg cTTTATTtCa TTtGATTaCt
NMve           TAAGAGGGGT TTAGCCTATT CTACAATGTC CCAACTGGGC TATATGATGT TAGCTCTAGG TATGGGGTCT TATCGAGCCG CTTTATTTCA TTTGATTACT
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NAros          TAAGAGGGGT TTAGCCTATT CTACAATGTC CCAACTGGGc TATATGATGT TAGCTCTAGG TATGGGGTCT TATCGAGCCG CTTTATTTCA TTTGATTACT
NAni           TAAGAGGGGT TTAGCCTATT CTACAATGTC CCAACTGGGc TATATGATGT TAGCTCTAGG TATGGGGTCT TATCGAGCCG CTTTATTTCA TTTGATTACT
NKvi           TAAGAGGGGT TTAGCCTATT CTACAATGTC CCAACTGGGC TATATGATGT TAGCTCTAGG TATGGGGTCT TATCGAGCCG CTTTATTTCA TTTGATTACT


               ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     910        920        930        940        950        960        970        980        990       1000
NAar           CATGCTTATT CGAAAGCATT GTTGTTTTTA GGATCTGGAT CAATTATTCA TTCCATGGAA GCTATTGTTG GATATTCTCC AGAGAAAAGC CAGAATATGG
NAhi           CATGCTTATT CGAAAGCATT GTTGTTTTTA GGATCtGGAT CAATTATTCA TTCCATGGAA GCTATTGTTG GATATTCTCC AGAGAAAAGC CAGAATATGG
NAlo           CATGCTTATT CGAAAGCATT GTTGTTTTTA GGATCTGGAT CAATTATTCA TTCCATGGAA GCTATTGTTG GATATTCTCC AGAGAAAAGC CAGAATATGG
NAca           CATGCTTATT CGAAAGCATT GTTGTTTTTA GGATCYGGAT CAATTATTCA TTCCATGGAA GCTATTGTTG GATATTCTCC AGAGAAAAGC CAGAATATGG
NAof           CATGCTTATT CGAAAGCATT GTTGTTTTTA GGATCYGGAT CAATTATTCA TTCCATGGAA GCTATTGTTG GATATTCTCC AGAGAAAAGC CAGAATATGG
NAlu           CATGCTTATT CGAAAGCATT GTtgtTTTTA GGATCTGGAT CAATTATTCA TTCCATGGAA GCTATTGTTG GATATTCTCC AGAGAAAAGC CAGAATATGG
NLcr           CAtGCTTATT CGAAAGCATT GTTGTTTTTA GGATCTGGAT CAATTATTCA TTCCATGGAA GCTATTGTTG GATATTCTCC AGAGAAAAGC CAGAATATGG
NLag           CATGCTTATT CGAAAGCATT GTTGTTTTTA GGATCTGGAT CAATTATTCA TTCCATGGAA GCTATTGTTG GATATTCTCC AGAGAAAAGC CAGAATATGG
NLbr           CATGCTTATT CGAAAGCATT GTTGTTTTTA GGATCTGGAT CAATTATTCA TTCCATGGAA GCTATTGTTG GATATTCTCC AGAGAAAAGC CAGAATATGG
NLtr           CATGCTTATT CGAAAGCATT GTTGTTTTTA GGATCTGGAT CAATTATTCA TTCCATGGAA GCTATTGTTG GATATTCTCC AGAGAAAAGC CAGAATATGG
NLtp           CATGCTTATT CGAAAGCATT GTTGTTTTTA GGATCTGGAT CAATTATTCA TTCCATGGAA GCTATTGTTG GATATTCTCC AGAGAAAAGC CAGAATATGG
NLfl           CATGCTTATT CGAAAGCATT GTTGTTTTTA GGATCTGGAT CAATTATTCA TTCCATGGAA GCTATTGTTG GATATTCTCC AGAGAAAAGC CAGAATATGG
NLas           CATGCTTATT CGAAAGCATT GTTGTTTTTA GGATCTGGAT CAATTATTCA TTCCATGGAA GCTATTGTTG GATATTCTCC AGAGAAAAGC CAGAATATGG
NLac           CATGCTTATT CGAAAGCATT GTTGTTTTTA GGATCTGGAT CAATTATTCA TTCCATGGAA GCTATTGTTG GATATTCTCC AGAGAAAAGC CAGAATATGG
NLar           CATGCTTATT CGAAAGCATT GTTGTTTTTA GGATCTGGAT CAATTATTCA TTCCATGGAA GCTATTGTTG GATATTCTCC AGAGAAAAGC CAGAATATGG
NLma           CATGCTTATT CGAAAGCATT GTTGTTTTTA GGATCTGGAT CAATTATTCA TTCCATGGAA GCTATTGTTG GATATTCTCC AGAGAAAAGC CAGAATATGG
NLmo           CATGCTTATT CGAAAGCATT GTTGTTTTTA GGATCTGGAT CAATTATTCA TTCCATGGAA GCTATTGTTG GATATTCTCC AGAGAAAAGC CAGAATATGG
NLmu           CATGCTTATT CGAAAGCATT GTTGTTTTTA GGATCTGGAT CAATTATTCA TTCCATGGAA GCTATTGTTG GATATTCTCC AGAGAAAAGC CAGAATATGG
NLob           CATGCTTATT CGAAAGCATT GTTGTTTTTA GGATCTGGAT CAATTATTCA TTCCATGGAA GCTATTGTTG GATATTCTCC AGAGAAAAGC CAGAATATGG
NLol           CATGCTTATT CGAAAGCATT GTTGTTTTTA GGATCTGGAT CAATTATTCA TTCCATGGAA GCTATTGTTG GATATTCTCC AGAGAAAAGC CAGAATATGG
NLpe           CATGCTTATT CGAAAGCATT GTTGTTTTTA GGATCTGGAT CAATTATTCA TTCCATGGAA GCTATTGTTG GATATTCTCC AGAGAAAAGC CAGAATATGG
NLph           CATGCTTATT CGAAAGCATT GTTGTTTTTA GGATCTGGAT CAATTATTCA TTCCATGGAA GCTATTGTTG GATATTCTCC AGAGAAAAGC CAGAATATGG
NLpl           CATGCTTATT CGAAAGCATT GTTGTTTTTA GGATCTGGAT CAATTATTCA TTCCATGGAA GCTATTGTTG GATATTCTCC AGAGAAAAGC CAGAATATGG
NLpu           CATGCTTATT CGAAAGCATT GTTGTTTTTA GGATCTGGAT CAATTATTCA TTCCATGGAA GCTATTGTTG GATATTCTCC AGAGAAAAGC CAGAATATGG
NLth           CATGCTTATT CGAAAGCATT GTTGTTTTTA GGATCTGGAT CAATTATTCA TTCCATGGAA GCTATTGTTG GATATTCTCC AGAGAAAAGC CAGAATATGG
NLti           CATGCTTATT CGAAAGCATT GTTGTTTTTA GGATCTGGAT CAATTATTCA TTCCATGGAA GCTATTGTTG GATATTCTCC AGAGAAAAGC CAGAATATGG
NMma           CATGCTTATT CGAAAGCATT GTTGTTTTTA GGATCTGGAT CAATTATTCA TTCCATGGAA GCTATTGTTG GATATTCTCC AGAGAAAAGC CAGAATATGG
NMtf           CATGCTTATT CGAAAGCATT GTTGTTTTTA GGATCTGGAT CAATTATTCA TTCCATGGAA GCTATTGTTG GATATTCTCC AGAGAAAAGC CAGAATATGG
NMae           CATGCTTATT CGAAAGCATT GTTGTTTTTA GGATCTGGAT CAATTATTCA TTCCATGGAA GCTATTGTTG GATATTCTCC AGAGAAAAGC CAGAATATGG
NMtr           CATGCTTATT CGAAAGCATT GTTGTTTTTA GGATCTGGAT CAATTATTCA TTCCATGGAA GCTATTGTTG GATATTCTCC AGAGAAAAGC CAGAATATGG
NMca           CATGCTTATT CGAAAGCATT GTTGTTTTTA GGATCTGGAT CAATTATTCA TTCCATGGAA GCTATTGTTG GATATTCTCC AGAGAAAAGC CAGAATATGG
NMhi           CATGCTTATT CGAAAGCATT GTTGTTTTTA GGATCTGGAT CAATTATTCA TTCCATGGAA GCTATTGTTG GATATTCTCC AGAGAAAAGC CAGAATATGG
NMto           CAtGCTTATt CGAAAGCATt GTTGtTTTTA GGATCTGGAT CAATTATtCA TtCCAtGGAA GCTATtGTtG GATATTCTCC AGAGAAAAGC CAGAATATGG
NMal           CATGCTTATT CGAAAGCATT GTTGTTTTTA GGATCtGGAT CAATTATTCA TTCCATGGAA GCTATTGTTG GATATTCTCC AGAGAAAAGC CAGAATATGG
NMmo           CAtGCTTATt CGAAAGCATt GTTGtTTTTA GGATCTGGAT CAATTATtCA TtCCAtGGAA GCTATtGTtG GATATTCTCC AGAGAAAAGC CAGAATATGG
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NMne            CATGCTTATT CGAAAGCATT GTTGTTTTTA GGATCTGGAT CAATTATTCA TTCCATGGAA GCTATTGTTG GATATTCTCC AGAGAAAAGC CAGAATATGG
NMni            CATGCTTATT CGAAAGCATT GTTGTTTTTA GGATCTGGAT CAATTATTCA TTCCATGGAA GCTATTGTTG GATATTCTCC AGAGAAAAGC CAGAATATGG
NMpa            CATGCTTATT CGAAAGCATG GTTGTTTTTA GGATCTGGAT CAATTATTCA TTCCATGGAA GCTATTGTTG GATATTCTCC AGAGAAAAGC CAGAATATGG
NMsy            CAtGCTtAtT CGAAaGCATT GTTGTTTTtA GGATCTGGAT CAATtatTCa ttCCAtGGAA GCTATTGTTG GATATtCTCC AGAGAAAAGC CAGAATATGG
NMve            CATGCTTATT CGAAAGCATG GTTGTTTTTA GGATCTGGAT CAATTATTCA TTCCATGGAA GCTATTGTTG GATATTCTCC AGAGAAAAGC CAGAATATGG
NAros           CATGCTTATT CGAAAGCATT GTTGTTTTTA GGATCCGGAT CAATTATTCA TTCCATGGAA GCTATTGTTG GATATTCTCC AGAGAAAAGC CAGAATATGG
NAni            CATGCTTATT CGAAAGCATT GTTGTTTTTA GGATCYGGAT CAATTATTCA TTCCATGGAA GCTATTGTTG GATATTCTCC AGAGAAAAGC CAGAATATGG
NKvi            CATGCTTATT CGAAAGCATT GTTGTTTTTA GGATCCGGAT CAATTATTCA TTCCATGGAA GCTATTGTTG GATATTCTCC AGAGAAAAGC CAGAATATGG


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                      1010       1020       1030       1040       1050       1060       1070       1080       1090       1100
NAar            TTTTTATGGG CGGTTTAAGA AAGCATGTGC CCGTTACACA AATTGCTTTT TTAGTAGGTA CGCTTTCTCT TTGTGGTATT CCACCCCTTG CTTGTTTTTG
NAhi            TTTTTATGGG CGGTTTAAGA AAGCATGTGC CCGTTACACA AATTGCTTTT TTAGTAGGTA CGCTTTCTCT TTGTGGTATT CCACCCCTTG CTTGTTTTTG
NAlo            TTTTTATGGG CGGTTTAAGA AAGCATGTGC CCGTTACACA AATTGCTTTT TTAGTAGGTA CGCTTTCTCT TTGTGGTATT CCACCCCTTG CTTGTTTTTG
NAca            TTTTTATGGG CGGTTTAAGA AAGCATGTGC CCGTTACACA AATTGCTTTT TTAGTAGGTA CGCTTTCTCT TTGTGGTATT CCACCCcTTG CTTGTTTTTG
NAof            TTTTTATGGG CGGTTTAAGA AAGCATGTGC CCGTTACACA AATTGCTTTT TTAGTAGGTA CGCTTTCTCT TTGTGGTATT CCACCCCTTG CTTGTTTTTG
NAlu            TTTTTATGGG CGGTTTAAGA AAGCATGTGC CCGTTACACA AATTGCTTTT TTAGTAGGTA CGCTTTCTCT TTGTGGTATT CCACCCCTTG CTTGTTTTTG
NLcr            TTTTTATGGG CGGTTTAAGA AAGCATGTGC CCGTTACACA AATTGCTTTT TTAGTAGGTA CGCTTTCTCT TTGTGGTATT CCACCCCTTG CTTGTTTTTG
NLag            TTTTTATGGG CGGTTTAAGA AAGCATGTGC CCGTTACACA AATTGCTTTT TTAGTAGGTA CGCTTTCTCT TTGTGGTATT CCACCCCTTG CTTGTTTTTG
NLbr            TTTTTATGGG CGGTTTAAGA AAGCATGTGC CCGTTACACA AATTGCTTTT TTAGTAGGTA CGCTTTCTCT TTGTGGTATT CCACCCCTTG CTTGTTTTTG
NLtr            TTTTTATGGG CGGTTTAAGA AAGCATGTGC CCGTTACACA AATTGCTTTT TTAGTAGGTA CGCTTTCTCT TTGTGGTATT CCACCCCTTG CTTGTTTTTG
NLtp            TTTTTATGGG CGGTTTAAGA AAGCATGTGC CCGTTACACA AATTGCTTTT TTAGTAGGTA CGCTTTCTCT TTGTGGTATT CCACCCCTTG CTTGTTTTTG
NLfl            TTTTTATGGG CGGTTTAAGA AAGCATGTGC CCGTTACACA AATTGCTTTT TTAGTAGGTA CGCTTTCTCT TTGTGGTATT CCACCCCTTG CTTGTTTTTG
NLas            TTTTTATGGG CGGTTTAAGA AAGCATGTGC CCGTTACACA AATTGCTTTT TTAGTAGGTA CGCTTTCTCT TTGTGGTATT CCACCCCTTG CTTGTTTTTG
NLac            TTTTTATGGG CGGTTTAAGA AAGCATGTGC CCGTTACACA AATTGCTTTT TTAGTAGGTA CGCTTTCTCT TTGTGGTATT CCACCCCTTG CTTGTTTTTG
NLar            TTTTTATGGG CGGTTTAAGA AAGCATGTGC CCGTTACACA AATTGCTTTT TTAGTAGGTA CGCTTTCTCT TTGTGGTATT CCACCCCTTG CTTGTTTTTG
NLma            TTTTTATGGG CGGTTTAAGA AAGCATGTGC CCGTTACACA AATTGCTTTT TTAGTAGGTA CGCTTTCTCT TTGTGGTATT CCACCCCTTG CTTGTTTTTG
NLmo            TTTTTATGGG CGGTTTAAGA AAGCATGTGC CCGTTACACA AATTGCTTTT TTAGTAGGTA CGCTTTCTCT TTGTGGTATT CCACCCCTTG CTTGTTTTTG
NLmu            TTTTTATGGG CGGTTTAAGA AAGCATGTGC CCGTTACACA AATTGCTTTT TTAGTAGGTA CGCTTTCTCT TTGTGGTATT CCACCCCTTG CTTGTTTTTG
NLob            TTTTTATGGG CGGTTTAAGA AAGCATGTGC CCGTTACACA AATTGCTTTT TTAGTAGGTA CGCTTTCTCT TTGTGGTATT CCACCCCTTG CTTGTTTTTG
NLol            TTTTTATGGG CGGTTTAAGA AAGCATGTGC CCGTTACACA AATTGCTTTT TTAGTAGGTA CGCTTTCTCT TTGTGGTATT CCACCCCTTG CTTGTTTTTG
NLpe            TTTTTATGGG CGGTTTAAGA AAGCATGTGC CCGTTACACA AATTGCTTTT TTAGTAGGTA CGCTTTCTCT TTGTGGTATT CCACCCCTTG CTTGTTTTTG
NLph            TTTTTATGGG CGGTTTAAGA AAGCATGTGC CCGTTACACA AATTGCTTTT TTAGTAGGTA CGCTTTCTCT TTGTGGTATT CCACCCCTTG CTTGTTTTTG
NLpl            TTTTTATGGG CGGTTTAAGA AAGCATGTGC CCGTTACACA AATTGCTTTT TTAGTAGGTA CGCTTTCTCT TTGTGGTATT CCACCCCTTG CTTGTTTTTG
NLpu            TTTTTATGGG CGGTTTAAGA AAGCATGTGC CCGTTACACA AATTGCTTTT TTAGTAGGTA CGCTTTCTCT TTGTGGTATT CCACCCCTTG CTTGTTTTTG
NLth            TTTTTATGGG CGGTTTAAGA AAGCATGTGC CCGTTACACA AATTGCTTTT TTAGTAGGTA CGCTTTCTCT TTGTGGTATT CCACCCCTTG CTTGTTTTTG
NLti            TTTTTATGGG CGGTTTAAGA AAGCATGTGC CCGTTACACA AATTGCTTTT TTAGTAGGTA CGCTTTCTCT TTGTGGTATT CCACCCCTTG CTTGTTTTTG
NMma            TTTTTATGGG CGGTTTAAGA AAGCATGTGC CCGTTACACA AATTGCTTTT TTAGTAGGTA CGCTTTCTCT TTGTGGTATT CCACCCCTTG CTTGTTTTTG
NMtf            TTTTTATGGG CGGTTTAAGA AAGCATGTGC CCGTTACACA AATTGCTTTT TTAGTAGGTA CGCTTTCTCT TTGTGGTATT CCACCCCTTG CTTGTTTTTG
NMae            TTTTTATGGG CGGTTTAAGA AAGCATGTGC CCGTTACACA AATTGCTTTT TTAGTAGGTA CGCTTTCTCT TTGTGGTATT CCACCCCTTG CTTGTTTTTG
NMtr            TTTTTATGGG CGGTTTAAGA AAGCATGTGC CCGTTACACA AATTGCTTTT TTAGTAGGTA CGCTTTCTCT TTGTGGTATT CCACCCCTTG CTTGTTTTTG
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NMca         TTTTTATGGG CGGTTTAAGA AAGCATGTGC CCGTTACACA AATTGCTTTT TTAGTAGGTA CGCTTTCTCT TTGTGGTATT CCACCCCTTG CTTGTTTTTG
NMhi         TTTTTATGGG CGGTTTAAGA AAGCATGTGC CCGTTACACA AATTGCTTTT TTAGTAGGTA CGCTTTCTCT TTGTGGTATT CCACCCCTTG CTTGTTTTTG
NMto         TTTTTATGGG CGGTTTAAGA AAGCATGTGC CCGTTACACA AATTGCTTTT TTAGTAGGtA CgCTTTCtCt ttGtGGTatt CCaCCCCTtG CtTGTTTTttG
NMal         TTTTTATGGG CGGTTTAAGA AAGCATGTGC CCGTTACACA AATTGCTTTT TTAGTAGGTA CGCTTTCTCT TTGTGGTATT CCACCCCTTG CTTGTTTTTG
NMmo         TTTTTATGGG CGGTTTAAGA AAGCATGTGC CCGTTACACA AATTGCTTTT TTAGTAGGtA CgCTTTCtCt ttGtGGTatt CCaCCCCTtG CtTGTTTTttG
NMne         TTTTTATGGG CGGTTTAAGA AAGCATGTGC CCGTTACACA AATTGCTTTT TTAGTAGGTA CGCTTTCTCT TTGTGGTATT CCACCCCTTG CTTGTTTTTG
NMni         TTTTTATGGG CGGTTTAAGA AAGCATGTGC CCGTTACACA AATTGCTTTT TTAGTAGGTA CGCTTTCTCT TTGTGGTATT CCACCCCTTG CTTGTTTTTG
NMpa         TTTTTATGGG CGGTTTAAGA AAGCATGTGC CCGTTACACA AATTGCTTTT TTAGTAGGTA CGCTTTCTCT TTGTGGTATT CCACCCCTTG CTTGTTTTTG
NMsy         TTTTTatGGG CGGTTTAAGA AAGCATGTgC CCGTTACACA AATTGCTTTT TTAGtAGGta CGCTTTCTCT tTGTGGTAtt CCACCCCTTG CTTGTTTtTG
NMve         TTTTTATGGG CGGTTTAAGA AAGCATGTGC CCGTTACACA AATTGCTTTT TTAGTAGGTA CGCTTTCTCT TTGTGGTATT CCACCCCTTG CTTGTTTTTG
NAros        TTTTTATGGG CGGTTTAAGA AAGCATGTGC CCGTTACACA AATTGCTTTT TTAGTAGGTA CGCTTTCTCT TTGTGGTATT CCACCCCTTG CTTGTTTTTG
NAni         TTTTTATGGG CGGTTTAAGA AAGCATGTGC CCGTTACACA AATTGCTTTT TTAGTAGGTA CGCTTTCTCT TTGTGGTATT CCACCCCTTG CTTGTTTTTG
NKvi         TTTTTATGGG CGGTTTAAGA AAGCATGTGC CCGTTACACA AATTGCTTTT TTAGTAGGTA CGCTTTCTCT TTGTGGTATT CCACCCCTTG CTTGTTTTTG


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                   1110       1120       1130       1140       1150       1160       1170       1180       1190       1200
NAar         GTCCAAAGAT GAAATTCTTA GTGACAGTTG GTTGTATTCA CCTATTTT-G CAATAATCGC TTGGTCCACC GCCGGATTAA CAGCATTTTA TATGTTTCGA
NAhi         GTCCAAAGAT GAAATTCTTA GTGACAGTTG GTTGTATTCA CCTATTTTTG CAATAATCGC TTGGTCCACC GCCGGATTAA CAGCATTTTA TATGTTTCGA
NAlo         GTCCAAAGAT GAAATTCTTA GTGACAGTTG GTTGTATTCA CCTATTTT-G CAATAATCGC TTGGTCCACC GCCGGATTAA CAGCATTTTA TATGTTTCGA
NAca         GTCCAAAGAT GAAATTCTTA GTGACAGTTG GTTGTATTCA CCTatTTTTG CAATAATCGC TTGGTCCACC GCCGGATTAA CAGCATTTTA TATGTTTCGA
NAof         GTCCAAAGAT GAAATTCTTA GTGACAGTTG GTTGTATTCA CCTATTTTTG CAATAATCGC TTGGTCCACC GCCGGATTAA CAGCATTTTA TATGTTTCGA
NAlu         GTCCAAAGAT GAAATTCTTA GTGACAGTTG GTTGTATTCA CCTATTTTTG CAATAATCGC TTGGTCCACC GCCGGATTAA CAGCATTTTA TATGTTTCGA
NLcr         GTCCAAAGAT GAAATTCTTA GTGACAGTTG GTTGTATTCA CCTATTTT-G CAATAATCGC TTGGTCCACC GCCGGATTAA CAGCATTTTA TATGTTTCGA
NLag         GTCCAAAGAT GAAATTCTTA GTGACAGTTG GTTGTATTCA CCTATTTTTG CAATAATCGC TTGGTCCACC GCCGGATTAA CAGCATTTTA TATGTTTCGA
NLbr         GTCCAAAGAT GAAATTCTTA GTGACAGTTG GTTGTATTCA CCTATTTTTG CAATAATCGC TTGGTCCACC GCCGGATTAA CAGCATTTTA TATGTTTCGA
NLtr         GTCCAAAGAT GAAATTCTTA GTGACAGTTG GTTGTATTCA CCTATTTT-G CAATAATCGC TTGGTCCACC GCCGGATTAA CAGCATTTTA TATGTTTCGA
NLtp         GTCCAAAGAT GAAATTCTTA GTGACAGTTG GTTGTATTCA CCTATTTT-G CAATAATCGC TTGGTCCACC GCCGGATTAA CAGCATTTTA TATGTTTCGA
NLfl         GTCCAAAGAT GAAATTCTTA GTGACAGTTG GTTGTATTCA CCTATTTT-G CAATAATCGC TTGGTCCACC GCCGGATTAA CAGCATTTTA TATGTTTCGA
NLas         GTCCAAAGAT GAAATTCTTA GTGACAGTTG GTTGTATTCA CCTATTTT-G CAATAATMGC TTGGTCCACC GCCGGATTAA CAGCATTTTA TATGTTTCGA
NLac         GTCCAAAGAT GAAATTCTTA GTGACAGTTG GTTGTATTCA CCTATTTTTG CAATAATCGC TTGGTCCACC GCCGGATTAA CAGCATTTTA TATGTTTCGA
NLar         GTCCAAAGAT GAAATTCTTA GTGACAGTTG GTTGTATTCA CCTATTTTTG CAATAATCGC TTGGTCCACC GCCGGATTAA CAGCATTTTA TATGTTTCGA
NLma         GTCCAAAGAT GAAATTCTTA GTGACAGTTG GTTGTATTCA CCTatTTTTG CAATAATCGC TTGGTCCACC GCCGGATTAA CAGCATTTTA TATGTTTCGA
NLmo         GTCCAAAGAT GAAATTCTTA GTGACAGTTG GTTGTATTCA CCTATTTT-G CAATAATCGC TTGGTCCACC GCCGGATTAA CAGCATTTTA TATGTTTCGA
NLmu         GTCCAAAGAT GAAATTCTTA GTGACAGTTG GTTGTATTCA CCTATTTT-G CAATAATCGC TTGGTCCACC GCCGGATTAA CAGCATTTTA TATGTTTCGA
NLob         GTCCAAAGAT GAAATTCTTA GTGACAGTTG GTTGTATTCA CCTATTTT-G CAATAATCGC TTGGTCCACC GCCGGATTAA CAGCATTTTA TATGTTTCGA
NLol         GTCCAAAGAT GAAATTCTTA GTGACAGTTG GTTGTATTCA CCTATTTT-G CAATAATCGC TTGGTCCACC GCCGGATTAA CAGCATTTTA TATGTTTCGA
NLpe         GTCCAAAGAT GAAATTCTTA GTGACAGTTG GTTGTATTCA CCTATTTT-G CAATAATCGC TTGGTCCACC GCCGGATTAA CAGCATTTTA TATGTTTCGA
NLph         GTCCAAAGAT GAAATTCTTA GTGACAGTTG GTTGTATTCA CCTATTTTTG CAATAATCGC TTGGTCCACC GCCGGATTAA CAGCATTTTA TATGTTTCGA
NLpl         GTCCAAAGAT GAAATTCTTA GTGACAGTTG GTTGTATTCA CCTATTTT-G CAATAATCGC TTGGTCCACC GCCGGATTAA CAGCATTTTA TATGTTTCGA
NLpu         GTCCAAAGAT GAAATTCTTA GTGACAGTTG GTTGTATTCA CCTATTTT-G CAATAATCGC TTGGTCCACC GCCGGATTAA CAGCATTTTA TATGTTTCGA
NLth         GTCCAAAGAT GAAATTCTTA GTGACAGTTG GTTGTATTCA CCTATTTT-G CAATAATCGC TTGGTCCACC GCCGGATTAA CAGCATTTTA TATGTTTCGA
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NLti        GTCCAAAGAT GAAATTCTTA GTGACAGTTG GTTGTATTCA CCTATTTT-G CAATAATCGC TTGGTCCACC GCCGGATTAA CAGCATTTTA TATGTTTCGA
NMma        GTCCAAAGAT GAAATTCTTA GTGACAGTTG GTTGTATTCA CCTATTTT-G CAATAATCGC TTGGTCCACC GCTGGATTAA CAGCATTTTA TATGTTTCGA
NMtf        GTCCAAAGAT GAAATTCTTA GTGACAGTTG GTTGTATTCA CCTATTTTTG CAATAATCGC TTGGTCCACC GCTGGATTAA CAGCATTTTA TATGTTTCGA
NMae        GTCCAAAGAT GAAATTCTTA GTGACAGTTG GTTGTATTCA CCTATTTTTG CAATAATCGC TTGGTCCACC GCCGGATTAA CAGCATTTTA TATGTTTCGA
NMtr        GTCCAAAGAT GAAATTCTTA GTGACAGTTG GTTGTATTCA CCTATTTTTG CAATAATCGC TTGGTCCACC GCCGGATTAA CAGCATTTTA TATGTTTCGA
NMca        GTCCAAAGAT GAAATTCTTA GTGACAGTTG GTTGTATTCA CCTATTTT-G CAATAATCGC TTGGTCCACC GCCGGATTAA CAGCATTTTA TATGTTTCGA
NMhi        GTCCAAAGAT GAAATTCTTA GTGACAGTTG GTTGTATTCA CCTATTTTTG CAATAATCGC TTGGTCCACC GCCGGATTAA CAGCATTTTA TATGTTTCGA
NMto        GTCCAAAGAt GAAATTcttA GTGaCaGttG GTTGtATtCa CCTaTTtttG CAATAATCGC TtGgTCCACC GCCGGATtAa CAGCATTTTA TATGTTTCGA
NMal        GTCCAAAGAT GAAATTCTTA GTGACAGTTG GTTGTATTCA CCTATTTTTG CAATAATCGC TTGGTCCACC GCCGGATTAA CAGCATTTTA TATGTTTCGA
NMmo        GTCCAAAGAt GAAATTcttA GTGaCaGttG GTTGTATtCa CCTaTTtttG CAATAATCGC TtGgTCCACC GCCGGATtAa CAGCATTTTA TATGTTTCGA
NMne        GTCCAAAGAT GAAATTCTTA GTGACAGTTG GTTGTATTCA CCTATTTTTG CAATAATCGC TTGGTCCACC GCCGGATTAA CAGCATTTTA TATGTTTCGA
NMni        GTCCAAAGAT GAAATTCTTA GTGACAGTTG GTTGTATTCA CCTATTTTTG CAATAATCGC TTGGTCCACC GCCGGATTAA CAGCATTTTA TATGTTTCGA
NMpa        GTCCAAAGAT GAAATTCTTA GTGACAGTTG GTTGTATTCA CCTATTTTTG CAATAATCGC TTGGTCCACC GCCGGATTAA CAGCATTTTA TATGTTTCGA
NMsy        GTCCAAAGAT GAAATTCTTA GTGACAGTTG GTTGTATTCA CCTATTTTtG CAATAATCGC ttGGTCCACC GCCGGATTAA CAGCATTTTA TATGTTTCGA
NMve        GTCCAAAGAT GAAATTCTTA GTGACAGTTG GTTGTATTCA CCTATTTTTG CAATAATCGC TTGGTCCACC GCCGGATTAA CAGCATTTTA TATGTTTCGA
NAros       GTCCAAAGAT GAAATTCTTA GTGACAGTTG GTTGTATTCA CCTATTTTTG CAATAATCGC TTGGTCCACC GCCGGATTAA CAGCATTTTA TATGTTTCGA
NAni        GTCCAAAGAT GAAATTCTTA GTGACAGTTG GTTGTATTCA CCTATTTTTG CAATAATCGC TTGGTCCACC GCCGGATTAA CAGCATTTTA TATGTTTCGA
NKvi        GTCCAAAGAT GAAATTCTTA GTGACAGTTG GTTGTATTCA CCTATTTTTG CAATAATCGC TTGGTCCACC GCCGGATTAA CAGCATTTTA TATGTTTCGA


            ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  1210       1220       1230       1240       1250       1260       1270       1280       1290       1300
NAar        ATCTATTTAC TTACTTTTGA AGGACATTTA AACATTTCTT TTCAAAAATA TAGTGGCAAA AAAAGTAGCT CTTTCTATTC AATAAAACTA TGGGGTAAAG
NAhi        ATCTATTTAC TTACTTTTGA AGGACATTTA AACATTTATT TTCAAAAATA TAGTGGCAAA AAAAGTAGCT CTTTCTATTC AATAAAACTA TGGGGTAAAG
NAlo        ATCTATTTAC TTACTTTTGA AGGACATTTA AACATTTATT TTCAAAAATA TAGTGGAAAA AAAAGTTGCT CTTTCTATTC AATAAAACTA TGGGGTAAAG
NAca        ATCTATTTAC TTACTTTTGA AGGACATTTA AACATTTCTT TTCAAAAATA TAGTGGCAAA AAAAGTAGCT CTTTCTATTC AATAAAACTA TGGGGTAAAG
NAof        ATCTATTTAC TTACTTTTGA AGGACATTTA AACATTTCTT TTCAAAAATA TAGTGGCAAA AAAAGTAGCT CTTTCTATTC AATAAAACTA TGGGGTAAAG
NAlu        ATCTATTTAC TTACTTTtGA AGGACATTTA AACATTTATT TTCAAAAATA TAGTGGCAAA AAAAGTAGCT CTTTCTATTC AATAAAACTA TGGGGTAAAG
NLcr        ATCTATTTAC TTACTTTTGA AGGACATTTA AACATTTATT TTCAAAAATA TAGTGGCAAA AAAAGTAGCT CTTTCTATTC AATAAAACTA TGGGGTAAAG
NLag        ATCTATTTAC TTACTTTTGA AGGACATTTA AACATTTATT TTCAAAAATA TAGTGGCAAA AAAAGTAGCT CTTTCTATTC AATAAAACTA TGGGGTAAAG
NLbr        ATCTATTTAC TTACTTTTGA AGGACATTTA AACATTTATT TTCAAAAATA TAGTGGCAAA AAAAGTAGCT CTTTCTATTC AATAAAACTA TGGGGTAAAG
NLtr        ATCTATTTAC TTACTTTTGA AGGACATTTA AACATTTATT TTCAAAAATA TAGTGGCAAA AAAAGTAGCT CTTTCTATTC AATAAAACTA TGGGGTAAAG
NLtp        ATCTATTTAC TTACTTTTGA AGGACATTTA AACATTTATT TTCAAAAATA TAGTGGCAAA AAAAGTAGCT CTTTCTATTC AATAAAACTA TGGGGTAAAG
NLfl        ATCTATTTAC TTACTTTTGA AGGACATTTA AACATTTATT TTCAAAAATA TAGTGGCAAA AAAAGTAGCT CTTTCTATTC AATAAAACTA TGGGGTAAAG
NLas        ATCTATTTAC TTACTTTTGA AGGACATTTA AACATTTATT TTCAAAAATA TAGTGGCAAA AAAAGTAGCT CTTTCTATTC AATAAAACTA TGGGGTAAAG
NLac        ATCTATTTAC TTACTTTTGA AGGACATTTA AACATTTATT TTCAAAAATA TAGTGGCAAA AAAAGTAGCT CTTTCTATTC AATAAAACTA TGGGGTAAAG
NLar        ATCTATTTAC TTACTTTTGA AGGACATTTA AACATTTATT TTCAAAAATA TAGTGGCAAA AAAAGTAGCT CTTTCTATTC AATAAAACTA TGGGGTAAAG
NLma        ATCTATTTAC TTACTTTTGA AGGACATTTA AACATTTATT TTCAAAAATA TAGTGGCAAA AAAAGTAGCT CTTTCTATTC AATAAAACTA TGGGGTAAAG
NLmo        ATCTATTTAC TTACTTTTGA AGGACATTTA AACATTTATT TTCAAAAATA TAGTGGCAAA AAAAGTAGCT CTTTCTATTC AATAAAACTA TGGGGTAAAG
NLmu        ATCTATTTAC TTACTTTTGA AGGACATTTA AACATTTATT TTCAAAAATA TAGTGGCAAA AAAAGTAGCT CTTTCTATTC AATAAAACTA TGGGGGAAAG
NLob        ATCTATTTAC TTACTTTTGA AGGACATTTA AACATTTATT TTCAAAAATA TAGTGGCAAA AAAAGTAGCT CTTTCTATTC AATAAAACTA TGGGGTAAAG
NLol        ATCTATTTAC TTACTTTTGA AGGACATTTA AACATTTATT TTCAAAAATA TAGTGGCAAA AAAAGTAGCT CTTTCTATTC AATAAAACTA TGGGGTAAAG
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NLpe         ATCTATTTAC TTACTTTTGA AGGACATTTA AACATTTATT TTCAAAAATA TAGTGGCAAA AAAAGTAGCT CTTTCTATTC AATAAAACTA TGGGGTAAAG
NLph         ATCTATTTAC TTACTTTTGA AGGACATTTA AACATTTATT TTCAAAAATA TAGTGGCAAA AAAAGTAGCT CTTTCTATTC AATAAAACTA TGGGGTAAAG
NLpl         ATCTATTTAC TTACTTTTGA AGGACATTTA AACATTTATT TTCAAAAATA TAGTGGCAAA AAAAGTAGCT CTTTCTATTC AATAAAACTA TGGGGTAAAG
NLpu         ATCTATTTAC TTACTTTTGA AGGACATTTA AATATTTATT TTCAAAAATA TAGTGGCAAA AAAAGTAGCT CTTTCTATTC AATAAAACTA TGGGGTAAAG
NLth         ATCTATTTAC TTACTTTTGA AGGACATTTA AACATTTATT TTCAAAAATA TAGTGGCAAA AAAAGTAGCT CTTTCTATTC AATAAAACTA TGGGGTAAAG
NLti         ATCTATTTAC TTACTTTTGA AGGACATTTA AACATTTATT TTCAAAAATA TAGTGGCAAA AAAAGTAGCT CTTTCTATTC AATAAAACTA TGGGGTAAAG
NMma         ATCTATTTAC TTACTTTTGA AGGACATTTA AACATTTATT TTCAAAAATA TAGTGGCAAA AAAAGTAGCT CTTTCTATTC AATAAAACTA TGGGGTAAAG
NMtf         ATCTATTTAC TTACTTTTGA AGGACATTTA AACATTTATT TTCAAAAATA TAGTGGCAAA AAAAGTAGCT CTTTCTATTC AATAAAACTA TGGGGTAAAG
NMae         ATCTATTTAC TTACTTTTGA AGGACATTTA AACATTTATT TTCAAAAATA TAGTGGCAAA AAAAGTAGCT CTTTCTATTC AATAAAACTA TGGGGTAAAG
NMtr         ATCTATTTAC TTACTTTTGA AGGACATTTA AACATTTATT TTCAAAAATA TAGTGGCAAA AAAAGTAGCT CTTTCTATTC AATAAAACTA TGGGGTAAAG
NMca         ATCTATTTAC TTACTTTTGA AGGACATTTA AACATTTATT TTCAAAAATA TAGTGGCAAA AAAAGTAGCT CTTTCTATTC AATAAAACTA TGGGGTAAAG
NMhi         ATCTATTTAC TTACTTTTGA AGGACATTTA AACATTTATT TTCAAAAATA TAGTGGCAAA AAAAGTAGCT CTTTCTATTC AATAAAACTA TGGGGTAAAG
NMto         ATCTATttaC ttACTTTtTGA AGGaCATttA aaCATTTATT TTCAAAAATA taGTGGCAAA AAAAGtaGCT CTTTCTATTC AATAAAaCTA TGGGGTAAAG
NMal         ATCTATTTAC TTACTTTTGA AGGACATTTA AACATTTATT TTCAAAAATA TAGTGGCAAA AAAAGTAGCT CTTTCTATTC AATAAAACTA TGGGGTAAAG
NMmo         ATCTATttaC ttACTTtTGA AGGaCATttA aaCATTTATT TTCAAAAATA taGTGGCAAA AAAAGtaGCT CTTTCTATTC AATAAAaCTA TGGGGTAAAG
NMne         ATCTATTTAC TTACTTTTGA AGGACATTTA AACATTTATT TTCAAAAATA TAGTGGCAAA AAAAGTAGCT CTTTCTATTC AATAAAACTA TGGGGTAAAG
NMni         ATCTATTTAC TTACTTTTGA AGGACATTTA AACATTTATT TTCAAAAATA TAGTGGCAAA AAAAGTAGCT CTTTCTATTC AATAAAACTA TGGGGTAAAG
NMpa         ATCTATTTAC TTACTTTTGA AGGACATTTA AACATTTATT TTCAAAAATA TAGTGGCAAA AAAAGTAGCT CTTTCTATTC AATAAAACTA TGGGGTAAAG
NMsy         ATCTATTtAC TTACTTttGA AGGACATTTA AACATTTATT TTCAAAAATA TAGTGGCAAA AAAAGTAGCT CTTTCTATTC AATAAAACTA tGGGGTAAAG
NMve         ATCTATTTAC TTACTTTTGA AGGACATTTA AACATTTATT TTCAAAAATA TAGTGGCAAA AAAAGTAGCT CTTTCTATTC AATAAAACTA TGGGGGAAAG
NAros        ATCTATTTAC TTACTTTTGA AGGACATTTA AACATTTATT TTCAAAAATA TAGTGGCAAA AAAAGTAGCT CTTTCTATTC AATAAAACTA TGGGGTAAAG
NAni         ATCTATTTAC TTACTTTTGA AGGACATTTA AACATTTATT TTCAAAAATA CAGTGGCAAA AAAAGGAGCT CTTTCTATTC AATAAAACTA TGGGGTAAAG
NKvi         ATCTATTTAC TTACTTTTGA AGGACATTTA AACATTTATT TTCAAAAATA TAGTGGCAAA AAAAGTAGCT CTTTCTATTC AATAAAACTA TGGGGTAAAG


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                   1310       1320       1330       1340       1350       1360       1370       1380       1390       1400
NAar         AAGAGCAAAA AATGATTAAC AGAAATTTTG GTTTATTTCC TTTATT---- --AACAATGA AGAAAAACGA GAAGCCATAT ATAATCGGTG GTAATGTAAA
NAhi         AAGAGCAAAA AATAATTAAC CTAAATTTTC GTTTATTTCC TTTATT---- --AACAATGA AGAAAAACGA GAAGCCATAT ATAATCGGTG GTAATGTAAA
NAlo         AAGAGCAAAA AATAATTAAC CTAAATTTTC GTTTATTTCC TTTATT---- --AACAATGA AGAAAAACGA GAAGCCATAT ATAATTGGTG GTAATGTAAA
NAca         AAGAGCAAAA AATGATTAAC AGAAATTTTG GTTTATTTCC TTTATT---- --AACAATGA AGAAAAACGA GAAGCCATAT ATAATCGGTG GTAATGTAAA
NAof         AAGAGCAAAA AATGATTAAC AGAAATTTTG GTTTATTTCC TTTATT---- --AACAATGA AGAAAAACGA GAAGCCATAT ATAATCGGTG GTAATGTAAA
NAlu         AAGAGCAAAA AATAATTAAC CTAAATTTTC GTTTACTTCC TTTATT---- --AACAATGA AGAAAAATGA GAAGCCATAT ATAATCGGtG GTAATGTAAA
NLcr         AAGAGCAAAA AATAATTAAC CTAAATTTGC GTTTATTTCC TTTATT---- --AACAATGA AGAAAAACGA GAAGCCATAT ATAATCGGTG GTAATGTAAA
NLag         AAGAGCAAAA AATAATTAAC CTAAATTTGC GTTTATTTCC TTTATT---- --AACAATGA AGAAAAACGA GAAGCCATAT ATAATCGGTG GTAATGTAAA
NLbr         AAGAGCAAAA AATAATTAAC CTAAATTTGC GTTTATTTCC TTTATT---- --AACAATGA AGAAAAACGA GAAGCCATAT ATAATCGGTG GTAATGTAAA
NLtr         AAGAGCAAAA AATAATTAAC CTAAATTTGC GTTTATTTCC TTTATT---- --AACAATGA AGAAAAACGA GAAGCCATAT ATAATCGGTG GTAATGTAAA
NLtp         AAGAGCAAAA AATAATTAAC CTAAATTTGC GTTTATTTCC TTTATT---- --AACAATGA AGAAAAACGA GAAGCCATAT ATA------G GTAATGTAAA
NLfl         AAGAGCAAAA AATAATTAAC CTAAATTTGC GTTTATTTCC TTTATT---- --AACAATGA AGAAAAACGA GAAGCCATAT ATAATCGGTG GTAATGTAAA
NLas         AAGAGCAAAA AATAATTAAC CTAAATTTGC GTTTATTTCC TTTATT---- --AACAATGA AGAAAAACGA GAAGCCATAT ATAATCGGTG GTAATGTAAA
NLac         AAGAGCAAAA AATAATTAAC CTAAATTTGC GTTTATTTCC TTTATT---- --AACAATGA AGAAAAATGA GAAGCCATAT ATAATCGGTG GTAATGTAAA
NLar         AAGAGCAAAA AATAATTAAC CTAAATTTGC GTTTATTTCC TTTATT---- --AACAATGA AGAAAAACGA GAAGCCATAT ATAATCGGTG GTAATGTAAA
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NLma          AAGAGCAAAA AATAATTAAC CTAAATTTGC GTTTATTTCC TTTATT---- --AACAATGA AGAAAAATGA GAAGCCATAT ATAATCGGTG GTAATGTAAA
NLmo          AAGAGCAAAA AATAATTAAC CTAAATTTGC GTTTATTTCC TTTATT---- --AACAATGA AGAAAAACGG GAAGCCATAT ATAATCGGTG GTAATGTAAA
NLmu          AAGAGCAAAA AATAATTAAC CTAAATTTGC GTTTATTTCC TTTATT---- --AACAATGA AGAAAAACGA GAAGCCATAT ATAATCGGTG GTAATGTAAA
NLob          AAGAGCAAAA AATAATTAAC CTAAATTTGC GTTTATTTCC TTTATT---- --AACAATGA AGAAAAACGA GAAGCCATAT ATAATCGGTG GTAATGTAAA
NLol          AAGAGCAAAA AATAATTAAC CTAAATTTGC GTTTATTTCC TTTATT---- --AACAATGA AGAAAAACGA GAAGCCATAT ATAATCGGTG GTAATGTAAA
NLpe          AAGAGCAAAA AATAATTAAC CTAAATTTGC GTTTATTTCC TTTATT---- --AACAATGA AGAAAAACGA GAAGCCATAT ATAATCGGTG GTAATGTAAA
NLph          AAGAGCAAAA AATAATTAAC CTAAATTTGC GTTTATTTCC TTTATT---- --AACAATGA AGAAAAACGA GAAGCCATAT ATAATCGGTG GTAATGTAAA
NLpl          AAGAGCAAAA AATAATTAAC CTAAATTTGC GTTTATTTCC TTTATT---- --AACAATGA AGAAAAACGA GAAGCCATAT ATAATCGGTG GTAATGTAAA
NLpu          AAGAGCAAAA AATAATTAAC CTAAATTTGC GTTTATTTCC TTTATT---- --AACAATGA AGAAAAACGA GAAGCCATAT ATAATCGGTG GTAATGTAAA
NLth          AAGAGCAAAA AATAATTAAC CTAAATTTGC GTTTATTTCC TTTATT---- --AACAATGA AGAAAAACGA GAAGCCATAT ATAATCGGTG GTAATGTAAA
NLti          AAGAGCAAAA AATAATTAAC CTAAATTTGC GTTTATTTCC TTTATT---- --AACAATGA AGAAAAACGA GAAGCCATAT ATAATCGGTG GTAATGTAAA
NMma          AAGAGCAAAA AATGATTAAC ATAAATTTTC GTTTATTTCC TTTATT---- --AACAATGA AGAAAAACGA GAAGCCATAT ATAATCGGTG GTAATGTAAA
NMtf          AAGAGCAAAA AATGATTAAC ATAAATTTTC GTTTATTTCC TTTATT---- --AACAATGA AGAAAAACGA GAAGCCATAT ATAATCGATG GTAATGTAAA
NMae          AAGAGCAAAA AATAATTAAC CTAAATTTTC GTTTATTTCC TTTATT---- --AACAATGA AGAAAAACGA GAAGCCATAT ATAATTGGTG GTAATGTAAA
NMtr          AAGAGCAAAA AATAATTAAC CTAAATTTTC GTTTATTTCC TTTATT---- --AACAATGA AGAAAAACGA GAAGCCATAT ATAATTGGTG GTAATGTAAA
NMca          AAGAGCAAAA AATAATTAAC CTAAATTTTC GTTTATTTCC TTTATT---- --AACAATGA AGAAAAACGA GAAGCCATAT ATAATCGGTG GTAATGTAAA
NMhi          AAGAGCAAAA AATAATTAAC CTAAATTTTC GTTTATTTCC TTTATT---- --AACAATGA AGAAAAACGA GAAGCCATAT ATAATCGGTG GTAATGTAAA
NMto          AAGAGCAAAA AATAAtTAAC CTAAATtTtC GTTTATTTCC TTTATT---- --AACAATGA AGAAAAACGA GAAGCCATAT ATAATCGGTG GTAAtGtAAA
NMal          AAGAGCAAAA AATAATTAAC CTAAATTTGC GTTTATTTCC TTTATT---- --AACAATGA AGAAAAACGA GAAGCCATAT ATAATCGGTG GTAATGTAAA
NMmo          AAGAGCAAAA AATAAtTAAC CTAAATtTtC GTTTATTTCC TTTATT---- --AACAATGA AGAAAAACGA GAAGCCATAT ATAATCGGTG GTAAtGtAAA
NMne          AAGAGCAAAA AATAATTAAC CTAAATTTGC GTTTATTTCC TTTATT---- --AACAATGA AGAAAAACGA GAAGCCATAT ATAATCGGTG GTAATGTAAA
NMni          AAGAGCAAAA AATAATTAAC CTAAATTTGC GTTTATTTCC TTTATT---- --AACAATGA AGAAAAACGA GAAGCCATAT ATAATCGGTG GTAATGTAAA
NMpa          AAGAGCAAAA AATAATTAAC CTAAATTTGC GTTTATTTCC TTTATT---- --AACAATGA AGAAAAACGA GAAGCCATAT ATAATCGGTG GTAATGTAAA
NMsy          AAGAGCAAAA AATAATTaAC CTAAATtTGC GTTTATTTCC TTTATT---- --AACAATGA AGAAAAACGA GAAGCCATAT ATAATCGGTG GTAATGTAAA
NMve          AAGAGCAAAA AATAATTAAC CTAAATTTGC GTTTATTTCC TTTATT---- --AACAATGA AGAAAAACGA GAAGCCATAT ATAATCGGTG GTAATGTAAA
NAros         AAGAGCAAAA AATGATTAAC AGAAATTTTC GTTTATTTCC TTTATTAAGA TTAAGAATGA AGAAAAACGA GAAGCCATAT ATAATCGGTG GTAATGTAAA
NAni          AAGAGCAAAA AATGATTAAC AGAAATTTTC GTTTATTTCC TTTATT---- --AACAATGA AGAAAAACGA GAAGCCATAT ATAATCGGTG GTAATGTAAA
NKvi          AAGAGCAAAA AATGATTAAC AGAAATTTTC GTTTATTTCC TTTATT---- --AACAATGA AGAAAAATGA GAAGCCATAT AGAATCGGTG GTAATGTAAA


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                    1410       1420       1430       1440       1450       1460       1470       1480       1490       1500
NAar          AAAAGGAGCT CTTATTACTA TTACGAATTT TGGCTACAAG GAGGCTTTTT CTTATCCTCA TGAATCAGAT AATACTATGC TATTTCCGAT GCTTATATTG
NAhi          AAAAGGAGCT ATTATTACTA TTACGAATTT TGGCTACAAG GAGGCTTTTT CTTATCCTCA TGAATCAGAT AATACTATGC TATTTCCTAT GCTTATATTG
NAlo          AAAAGGAGCT ATTATTACTA TTACGAATTT TGGCTACAAG GAGGCTTTTT CTTATCCTCA TGAATCAGAT AATACTATGC TATTTCCTAT GCTTATATTG
NAca          AAAAGGAGCT CTTATTACTA TTACGAATTT TGGCTACAAG GAGGCTTTTT CTTATCCTCA TGAATCAGAT AATACTATGC TATTTCCGAT GCTTATATTG
NAof          AAAAGGAGCT CTTATTACTA TTACGAATTT TGGCTACAAG GAGGCTTTTT CTTATCCTCA TGAATCAGAT AATACTATGC TATTTCCGAT GCTTATATTG
NAlu          AAAAGGAGCT ATTATTACTA TTACGAATTT TGGCTACAAG GAGGCTTTTT CTTATCCTCA TGAATCAGAT AATACTATGC TATTTCCTAT GCTTATATTG
NLcr          AAAAGGAGCT ATTATTACTA TTACGAATTT TGGCTACAAG GAGGCTTTTT CTTATCCTCA TGAATCAGAT AATACTATGC TATTTCCTAT GCTTATATTG
NLag          AAAAGGAGCT ATTATTACTA TTACGAATTT TGGCTACAAG GAGGCTTTTT CTTATCCTCA TGAATCAGAT AATACTATGC TATTTCCTAT GCTTATATTG
NLbr          AAAAGGAGCT ATTATTACTA TTACGAATTT TGGCTACAAG GAGGCTTTTT CTTATCCTCA TGAATCAGAT AATACTATGC TATTTCCTAT GCTTATATTG
NLtr          AAAAGGAGCT ATTATTACTA TTACGAATTT TGGCTACAAG GAGGCTTTTT CTTATCCTCA TGAATCAGAT AATACTATGC TATTTCCTAT GCTTATATTG
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NLtp         AAAAGGAGCT ATTATTACTA TTACGAATTT TGGCTACAAG GAGGCTTTTT CTTATCCTCA TGAATCAGAT AATACTATGC TATTTCCTAT GCTTATATTG
NLfl         AAAAGGAGCT ATTATTACTA TTACGAATTT TGGCTACAAG GAGGCTTTTT CTTATCCTCA TGAATCAGAT AATACTATGC TATTTCCTAT GCTTATATTG
NLas         AAAAGGAGCT ATTATTACTA TTAAGAATTT TGGCTACAAG GAGGCTTTTT CTTATCCTCA TGAATCAGAT AATACTATGC TATTTCCTAT GCTTATATTG
NLac         AAAAGGAGCT ATTATTACTA TTACGAATTT TGGCTACAAG GAGGCTTTTT CTTATCCTCA TGAATCAGAT AATACTATGC TATTTCCTAT GCTTATATTG
NLar         AAAAGGAGCT ATTATTACTA TTACGAATTT TGGCTACAAG GAGGCTTTTT CTTATCCTCA TGAATCAGAT AATACTATGC TATTTCCTAT GCTTATATTG
NLma         AAAAGGAGCT ATTATTACTA TTACGAATTT TGGCTACAAG GAGGCTTTTT CTTATCCTCA TGAATCAGAT AATACTATGC TATTTCCTAT GCTTATATTG
NLmo         AAAAGGAGCT ATTATTACTA TTACGAATTT TGGCTACAAG GAGGCTTTTT CTTATCCTCA TGAATCAGAT AATACTATGC TATTTCCTAT GCTTATATTG
NLmu         AAAAGGAGCT ATTATTACTA TTACGAATTT TGGCTACAAG GAGGCTTTTT CTTATCCTCA TGAATCAGAT AATACTATGC TATTTCCTAT GCTTATATTG
NLob         AAAAGGAGCT ATTATTACTA TTACGAATTT TGGCTACAAG GAGGCTTTTT CTTATCCTCA TGAATCAGAT AATACTATGC TATTTCCTAT GCTTATATTG
NLol         AAAAGGAGCT ATTATTACTA TTACGAATTT TGGCTACAAG GAGGCTTTTT CTTATCCTCA TGAATCAGAT AATACTATGC TATTTCCTAT GCTTATATTG
NLpe         AAAAGGAGCT ATTATTACTA TTACGAATTT TGGCTACAAG GAGGCTTTTT CTTATCCTCA TGAATCAGAT AATACTATGC TATTTCCTAT GCTTATATTG
NLph         AAAAGGAGCT ATTATTACTA TTACGAATTT TGGCTACAAG GAGGCTTTTT CTTATCCTCA TGAATCAGAT AATACTATGC TATTTCCTAT GCTTATATTG
NLpl         AAAAGGAGCT ATTATTACTA TTACGAATTT TGGCTACAAG GAGGCTTTTT CTTATCCTCA TGAATCAGAT AATACTATGC TATTTCCTAT GCTTATATTG
NLpu         AAAAGGAGCT ATTATTACTA TTACGAATTT TGGCTACAAG GAGGCTTTTT CTTATCCTCA TGAATCAGAT AATACTATGC TATTTCCTAT GCTTATATTG
NLth         AAAAGGAGCT ATTATTACTA TTACGAATTT TGGCTACAAG GAGGCTTTTT CTTATCCTCA TGAATCAGAT AATACTATGC TATTTCCTAT GCTTATATTG
NLti         AAAAGGAGCT ATTATTACTA TTACGAATTT TGGCTACAAG GAGGCTTTTT CTTATCCTCA TGAATCAGAT AATACTATGC TATTTCCTAT GCTTATATTG
NMma         AAAAGGAGCT CTTATTACTA TTACGAATTT TGGCTACAAG GAGGCTTTTT CTTATCCTCA TGAATCGGAT AATACTATGC TATTTCCTAT GCTTATATTG
NMtf         AAAAGGAGCT CTTATTACTA TTACGAATTT TGGCTACAAG GAGGCTTTTT CTTATCCTCA TGAATCAGAT AATACTATGC TATTTCCTAT GCTTATATTG
NMae         AAAAGGAGCT ATTATTACTA TTACGAATTT TGGCTACAAG GAGGCTTTTT CTTATCCTCA TGAATCAGAT AATACTATGC TATTTCCTAT GCTTATATTG
NMtr         AAAAGGAGCT ATTATTACTA TTACGAATTT TGGCTACAAG GAGGCTTTTT CTTATCCTCA TGAATCAGAT AATACTATGC TATTTCCTAT GCTTATATTG
NMca         AAAAGGAGCT ATTATTACTA TTACGAATTT TGGCTACAAG GAGGCTTTTT CTTATCCTCA TGAATCAGAT AATACTATGC TATTTCCTAT GCTTATATTG
NMhi         AAAAGGAGCT ATTATTACTA TTACGAATTT TGGCTACAAG GAGGCTTTTT CTTATCCTCA TGAATCAGAT AATACTATGC TATTTCCTAT GCTTATATTG
NMto         AAAAGGAGCT ATTATTACTA TTACGAATTT TGGCTACAAG GAGGCTTTTT CTTATCCTCA TGAATCAGAT AATACTATGC TATTTCCTAT GCTTATATTG
NMal         AAAAGGAGCT ATTATTACTA TTACGAATTT TGGCTACAAG GAGGCTTTTT CTTATCCTCA TGAATCAGAT AATACTATGC TATTTCCTAT GCTTATATTG
NMmo         AAAAGGAGCT ATTATTACTA TTACGAATTT TGGCTACAAG GAGGCTTTTT CTTATCCTCA TGAATCAGAT AATACTATGC TATTTCCTAT GCTTATATTG
NMne         AAAAGGAGCT ATTATTACTA TTACGAATTT TGGCTACAAG GAGGCTTTTT CTTATCCTCA TGAATCAGAT AATACTATGC TATTTCCTAT GCTTATATTG
NMni         AAAAGGAGCT ATTATTACTA TTACGAATTT TGGCTACAAG GAGGCTTTTT CTTATCCTCA TGAATCAGAT AATACTATGC TATTTCCTAT GCTTATATTG
NMpa         AAAAGGAGCT ATTATTACTA TTACGAATTT TGGCTACAAG GAGGCTTTTT CTTATCCTCA TGAATCAGAT AATACTATGC TATTTCCTAT GCTTATATTG
NMsy         AAAAGGAGCT ATTATTACTA TTACGAATTT TGGCTACAAG GAGGCTTTTT CTTATCCTCA TGAATCAGAT AATACTATGC TATTTCCTAT GCTTATATTG
NMve         AAAAGGAGCT ATTATTACTA TTACGAATTT TGGCTACAAG GAGGCTTTTT CTTATCCTCA TGAATCAGAT AATACTATGC TATTTCCTAT GCTTATATTG
NAros        AAAAGGAGCT CTTATTACTA TTACGAATTT TGGCTACAAG GAGGCTTTTT CTTATCCTCA TGAATCAGAT AATACTATGC TATTTCCGAT GCTTATATTG
NAni         AAAAAGAGCT CTTATTACTA TTACGAATTT TGGCTACAAG GAGGCTTTTT CTTATCCTCA TGAATCAGAT AATACTATGC TATTTCCTAT GCTTATATTG
NKvi         AAAAGGAGCT CTTATTACTA TTACGAATTT TGGCTACAAG GAGGCTTTTT CTTATCCTCA TGAATCAGAT AATACTATGC TATTTCCGAT GCTTATATTG


             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   1510       1520       1530       1540       1550       1560       1570       1580       1590       1600
NAar         CTTCTATTTA CTTTATTTGT TGGAGCTATA GCAATTCCTT TTAATCAAGA AAGAGTGGAT ATATTATCAA AATTATTAAC TCCATCTATA AATCTTTTAC
NAhi         CTTCTATTTA CTTTATTTGT TGGAGCTATA GCAATTCCTT TTAATCAAGA AAGAGTGGAT ATATTATCAA AATTATTAAC TCCATCTATA AATCTTTTAC
NAlo         CTTCTATTTA CTTTATTTGT TGGAGCTATA GCAATTCCTT TTAATCAAGA AAGAGTGGAT ATATTATCAA AATTATTAAC TCCATCTATA AATCTTTTAC
NAca         CTTCTATTTA CTTTATTTGT TGGAGCTATA GCAATTCCTT TTAATCAAGA AAGAGTGGAT ATATTATCAA AATTATTAAC TCCATCTATA AATCTTTTAC
NAof         CTTCTATTTA CTTTATTTGT TGGAGCTATA GCAATTCCTT TTAATCAAGA AAGAGTGGAT ATATTATCAA AATTATTAAC TCCATCTATA AATCTTTTAC
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NAlu          CTTCTATTTA CTTTATTTGT TGGAGCTATA GCAATTCCTT TTAATCAAGA AAGAGTGGAT ATATTATCAA AATTATTAAC TCCATCTATA AATCTTTTAC
NLcr          CTTCTATTTA CTTTATTTGT TGGAGCTATA GCAATTCCTT TTAATCAAGA AAGAGTGGAT ATATTATCAA AATTATTAAC TCCATCTATA AATCTTTTAC
NLag          CTTCTATTTA CTTTATTTGT TGGAGCTATA GCAATTCCTT TTAATCAAGA AAGAGTGGAT ATATTATCAA AATTATTAAC TCCATCTATA AATCTTTTAC
NLbr          CTTCTATTTA CTTTATTTGT TGGAGCTATA GCAATTCCTT TTAATCAAGA AAGAGTGGAT ATATTATCAA AATTATTAAC TCCATCTATA AATCTTTTAC
NLtr          CTTCTATTTA CTTTATTTGT TGGAGCTATA GCAATTCCTT TTAATCAAGA AAGAGTGGAT ATATTATCAA AATTATTAAC TCCATCTATA AATCTTTTAC
NLtp          CTTCTATTTA CTTTATTTGT TGGAGCTATA GCAATTCCTT TTAATCAAGA AAGAGTGGAT ATATTATCAA AATTATTAAC TCCATCTATA AATCTTTTAC
NLfl          CTTCTATTTA CTTTATTTGT TGGAGCTATA GCAATTCCTT TTAATCAAGA AAGAGTGGAT ATATTATCAA AATTATTAAC TCCATCTATA AATCTTTTAC
NLas          CTTCTATTTA CTTTATTTGT TGGAGCTATA GCAATTCCTT TTAATCAAGA AAGAGTGGAT ATATTATCAA AATTATTAAC TCCATCTATA AATCTTTTAC
NLac          CTTCTATTTA CTTTATTTGT TGGAGCTATA GCAATTCCTT TTAATCAAGA AAGAGTGGAT ATATTATCAA AATTATTAAC TCCATCTATA AATCTTTTAC
NLar          CTTCTATTTA CTTTATTTGT TGGAGCTATA GCAATTCCTT TTAATCAAGA AAGAGTGGAT ATATTATCAA AATTATTAAC TCCATCTATA AATCTTTTAC
NLma          CTTCTATTTA CTTTATTTGT TGGAGCTATA GCAATTCCTT TTAATCAAGA AAGAGTGGAT ATATTATCAA AATTATTAAC TCCATCTATA AATCTTTTAC
NLmo          CTTCTATTTA CTTTATTTGT TGGAGCTATA GCAATTCCTT TTAATCAAGA AAGAGTGGAT ATATTATCAA AATTATTAAC TCCATCTATA AATCTTTTAC
NLmu          CTTCTATTTA CTTTATTTGT TGGAGCTATA GCAATTCCTT TTAATCAAGA AAGAGTGGAT ATATTATCAA AATTATTAAC TCCATCTATA AATCTTTTAC
NLob          CTTCTATTTA CTTTATTTGT TGGAGCTATA GCAATTCCTT TTAATCAAGA AAGAGTGGAT ATATTATCAA AATTATTAAC TCCATCTATA AATCTTTTAC
NLol          CTTCTATTTA CTTTATTTGT TGGAGCTATA GCAATTCCTT TTAATCAAGA AAGAGTGGAT ATATTATCAA AATTATTAAC TCCATCTATA AATCTTTTAC
NLpe          CTTCTATTTA CTTTATTTGT TGGAGCTATA GCAATTCCTT TTAATCAAGA AAGAGTGGAT ATATTATCAA AATTATTAAC TCCATCTATA AATCTTTTAC
NLph          CTTCTATTTA CTTTATTTGT TGGAGCTATA GCAATTCCTT TTAATCAAGA AAGAGTGGAT ATATTATCAA AATTATTAAC TCCATCTATA AATCTTTTAC
NLpl          CTTCTATTTA CTTTATTTGT TGGAGCTATA GCAATTCCTT TTAATCAAGA AAGAGTGGAT ATATTATCAA AATTATTAAC TCCATCTATA AATCTTTTAC
NLpu          CTTCTATTTA CTTTATTTGT TGGAGCTATA GCAATTCCTT TTAATCAAGA AAGAGTGGAT ATATTATCAA AATTATTAAC TCCATCTATA AATCTTTTAC
NLth          CTTCTATTTA CTTTATTTGT TGGAGCTATA GCAATTCCTT TTAATCAAGA AAGAGTGGAT ATATTATCAA AATTATTAAC TCCATCTATA AATCTTTTAC
NLti          CTTCTATTTA CTTTATTTGT TGGAGCTATA GCAATTCCTT TTAATCAAGA AAGAGTGGAT ATATTATCAA AATTATTAAC TCCATCTATA AATCTTTTAC
NMma          CTTCTATTTA CTTTATTTGT TGGAGCTATA GCAATTCCTT TTAATCAAGA AAGAGTGGAT ATATTATCAA AATTATTAAC TCCATCTATA AATCTTTTAC
NMtf          CTTCTATTTA CTTTATTTGT TGGAGCTATA GCAATTCCTT TTAATCAAGA AAGAGTGGAT ATATTATCAA AATTATTAAC TCCATCTATA AATCTTTTAC
NMae          CTTCTATTTA CTTTATTTGT TGGAGCTATA GCAATTCCTT TTAATCAAGA AAGAGTGGAT ATATTATCAA AATTATTAAC TCCCTCTATA AATCTTTTAC
NMtr          CTTCTATTTA CTTTATTTGT TGGAGCTATA GCAATTCCTT TTAATCAAGA AAGAGTGGAT ATATTATCAA AATTATTAAC TCCATCTATA AATCTTTTAC
NMca          CTTCTATTTA CTTTATTTGT TGGAGCTATA GCAATTCCTT TTAATCAAGA AAGAGTGGAT ATATTATCAA AATTATTAAC TCCATCTATA AATCTTTTAC
NMhi          CTTCTATTTA CTTTATTTGT TGGAGCTATA GCAATTCCTT TTAATCAAGA AAGAGTGGAT ATATTATCAA AATTATTAAC TCCCTCTATA AATCTTTTAC
NMto          CTTCTATTTA CTTTATTTGT TGGAGCTATA GCAATTCCTT TTAATCAAGA AAGAGTGGAT ATATTATCAA AATTATTAAC TCCATCTATA AATCTTTTAC
NMal          CTTCTATTTA CTTTATTTGT TGGAGCTATA GCAATTCCTT TTAATCAAGA AAGAGTGGAT ATATTATCAA AATTATTAAC TCCCTCTATA AATCTTTTAC
NMmo          CTTCTATTTA CTTTATTTGT TGGAGCTATA GCAATTCCTT TTAATCAAGA AAGAGTGGAT ATATTATCAA AATTATTAAC TCCATCTATA AATCTTTTAC
NMne          CTTCTATTTA CTTTATTTGT TGGAGCTATA GCAATTCCTT TTAATCAAGA AAGAGTGGAT ATATTATCAA AATTATTAAC TCCATCTATA AATCTTTTAC
NMni          CTTCTATTTA CTTTATTTGT TGGAGCTATA GCAATTCCTT TTAATCAAGA AAGAGTGGAT ATATTATCAA AATTATTAAC TCCATCTATA AATCTTTTAC
NMpa          CTTCTATTTA CTTTATTTGT TGGAGCTATA GCAATTCCTT TTAATCAAGA AAGAGTGGAT ATATTATCAA AATTATTAAC TCCATCTATA AATCTTTTAC
NMsy          CTTCTATTTA CTTTATTTGT tGGAGCTATA GCAATTCCTT TTAATCAAGA AAGAGTGGAT ATATTATCAA AATTATTAAC TCCATCTATA AATCTTTTAC
NMve          CTTCTATTTA CTTTATTTGT TGGAGCTATA GCAATTCCTT TTAATCAAGA AAGAGTGGAT ATATTATCAA AATTATTAAC TCCATCTATA AATCTTTTAC
NAros         CTTCTATTTA CTTTATTTGT TGGAGCTATA GCAATTCCTT TTAATCAAGA AAGAGTGGAT ATATTATCAA AATTATTAAC TCCATCTATA AATCTTTTAC
NAni          CTTCTATTTA CTTTATTTGT TGGAGCTATA GCAATTCCTT TTAATCAAGA AAGAGTGGAT ATATTATCAA AATTATTAAC TCCATCTATA AATCTTTTAC
NKvi          CTTCTATTTA CTTTATTTGT TGGAGCTATA GCAATTCCTT TTAATCAAGA AAGAGTGGAT ATATTATCAA AATTATTAAC TCCMTCTATA AATCTTTTAC

              ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    1610       1620       1630       1640       1650       1660       1670       1680       1690       1700
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NAar          ATCAAAATTC AAATGATTTT GAGGATTCAT ATCAATTTTT AACAAATGCA ACTTTTTCGG TGAGTATAGC TTGTTTCGGA ATATTTACAG CATTCCTTTT
NAhi          ATCAAAATTC AAATGATTTT GAGGATTCAT ATCAATTTTT AACAAATGCA ACTTTTTCGG TGAGTATAGC TTGTTTCGGA ATATTTACAG CATTCCTTTT
NAlo          ATCAAAATTC AAATGATTTT GAGGATTCAT ATCAATTTTT AACAAATGCA ACTTTTTCGG TGAGTATAGC TTGTTTCGGA ATATTTACAG CATTCCTTTT
NAca          ATCAAAATTC AAATGATTTT GAGGATTCAT ATCAATTTTT AACAAATGCA ACTTTTTCGG TGAGTATAGC TTGTTTCGGA ATATTTACAG CATTCCTTTT
NAof          ATCAAAATTC AAATGATTTT GAGGATTCAT ATCAATTTTT AACAAATGCA ACTTTTTCGG TGAGTATAGC TTGTTTCGGA ATATTTACAG CATTCCTTTT
NAlu          ATCAAAATTC AAATGATTTT GAAGATTCAT ATCAATTTTT AACAAATGCA ACTTTTTCGG TGAGTATAGC TTGTTTCGGA ATATTTACAG CATTCCTTTT
NLcr          ATCAAAATTC AAATGATTTT GAGGATTCAT ATCAATTTTT AACAAATGCA ACTTTTTCGG TGAGTATAGC TTGTTTCGGA ATATTTACAG CATTTCTTTT
NLag          ATCAAAATTC AAATGATTTT GAGGATTCAT ATCAATTTTT AACAAATGCA ACTTTTTCGG TGAGTATAGC TTGTTTCGGA ATATTTACAG CATTCCTTTT
NLbr          ATCAAAATTC AAATGATTTT GAGGATTCAT ATCAATTTTT AACAAATGCA ACTTTTTCGG TGAGTATAGC TTGTTTCGGA ATATTTACAG CATTCCTTTT
NLtr          ATCAAAATTC AAATGATTTT GAGGATTCAT ATCAATTTTT AACAAATGCA ACTTTTTCGG TGAGTATAGC TTGTTTCGGA ATATTTACAG CATTCCTTTT
NLtp          ATCAAAATTC AAATGATTTT GAGGATTCAT ATCAATTTTT AACAAATGCA ACTTTTTCGG TGAGTATAGC TTGTTTCGGA ATATTTACAG CATTCCTTTT
NLfl          ATCAAAATTC AAATGATTTT GAGGATTCAT ATCAATTTTT AACAAATGCA ACTTTTTCGG TGAGTATAGC TTGTTTCGGA ATATTTACAG CATTCCTTTT
NLas          ATCAAAATTC AAATGATTTT GAGGATTCAT ATCAATTTTT AACAAATGCA ACTTTTTCGG TGAGTATAGC TTGTTTCGGA ATATTTACAG CATTTCTTTT
NLac          ATCAAAATTC AAATGATTTT GAGGATTCAT ATCAATTTTT AACAAATGCA ACTTTTTCGG TGAGTATAGC TTGTTTCGGA ATATTTACAG CATTCCTTTT
NLar          ATCAAAATTC AAATGATTTT GAGGATTCAT ATCAATTTTT AACAAATGCA ACTTTTTCGG TGAGTATAGC TTGTTTCGGA ATATTTACAG CATTCCTTTT
NLma          ATCAAAATTC AAATGATTTT GAGGATTCAT ATCAATTTTT AACAAATGCA ACTTTTTCGG TAAGTATAGC TTGTTTCGGA ATATTTACAG CATTCCTTTT
NLmo          ATCAAAATTC AAATGATTTT GAGGATTCAT ATCAATTTTT AACAAATGCA ACTTTTTCGG TGAGTATAGC TTGTTTCGGA ATATTTACAG CATTCCTTTT
NLmu          ATCAAAATTC AAATGATTTT GAGGATTCAT ATCAATTTTT AACAAATGCA ACTTTTTCGG TGAGTATAGC TTGTTTCGGA ATATTTACAG CATTTCTTTT
NLob          ATCAAAATTC AAATGATTTT GAGGATTCAT ATCAATTTTT AACAAATGCA ACTTTTTCGG TGAGTATAGC TTGTTTCGGA ATATTTACAG CATTCCTTTT
NLol          ATCAAAATTC AAATGATTTT GAGGATTCAT ATCAATTTTT AACAAATGCA ACTTTTTCGG TGAGTATAGC TTGTTTCGGA ATATTTACAG CATTCCTTTT
NLpe          ATCAAAATTC AAATGATTTT GAGGATTCAT ATCAATTTTT AACAAATGCA ACGTTTTCGG TGAGTATAGC TTGTTTCGGA ATATTTACAG CATTTCTTTT
NLph          ATCAAAATTC AAATGATTTT GAGGATTCAT ATCAATTTTT AACAAATGCA ACTTTTTCGG TGAGTATAGC TTGTTTCGGA ATATTTACAG CATTCCTTTT
NLpl          ATCAAAATTC AAATGATTTT GAGGATTCAT ATCAATTTTT AACAAATGCA ACTTTTTCGG TGAGTATAGC TTGTTTCGGA ATATTTACAG CATTCCTTTT
NLpu          ATCAAAATTC AAATGATTTT GAGGATTCAT ATCAATTTTT AACAAATGCA ACTTTTTCGG TGAGTATAGC TTGTTTCGGA ATATTTACAG CATTCCTTTT
NLth          ATCAAAATTC AAATGATTTT GAGGATTCAT ATCAATTTTT AACAAATGCA ACTTTTTCGG TGAGTATAGC TTGTTTCGGA ATATTTACAG CATTCCTTTT
NLti          ATCAAAATTC AAATGATTTT GAGGATTCAT ATCAATTTTT AACAAATGCA ACTTTTTCGG TGAGTATAGC TTGTTTCGGA ATATTTACAG CATTTCTTTT
NMma          ATCAAAAATC AAATGATTTT GAGGATTCAT ATCAATTTTT CACAAATGCA ACTTTTTCGG TGAGTATAGC TTGTTTCGGA ATATTTACAG CATTCCTTTT
NMtf          ATCAAAATTC AAATGATTTT GAGGATTCAT ATCAATTTTT CACAAATGCA ACTTTTTCGG TGAGTATAGC TTGTTTCGGA ATATTTACAG CATTCCTTTT
NMae          ATCCAAATTC AAATGATTTT GAGGATTCAT ATCAATTTTT AACAAATGCA ACTTTTTCGG TGAGAATAGC TTGTTTCGGA ATATTTACAG CATTCCTTTT
NMtr          ATCAAAATTC AAATGATTTT GAGGATTCAT ATCAATTTTT AACAAATGCA ACTTTTTCGG TGAGTATAGC TTGTTTCGGA ATATTTACAG CATTCCTTTT
NMca          ATCAAAATTC AAATGATTTT GAGGATTCAT ATCAATTTTT AACAAATGCA ACTTTTTCGG TGAGTATAGC TTGTTTCGGA ATATTTACAG CATTCCTTTT
NMhi          ATCAAAATTC AAATGATTTT GAGGATTCAT ATCAATTTTT AACAAATGCA ACTTTTTCGG TGAGTATAGC TTGTTTCGGA ATATTTACAG CATTCCTTTT
NMto          ATCAAAATTC AAATGATTTT GAGGATTCAT ATCAATTTTT AACAAATGCA ACTTTTTCGG TGAGTATaGC TTGTTTCGGA ATATTTACAG CATTCCTTTT
NMal          ATCAAAATTC AAATGATTTT GAGGATTCAT ATCAATTTTT AACAAATGCA ACTTTTTCGG TGAGTATAGC TTGTTTCGGA ATATTTACAG CATTCCTTTT
NMmo          ATCAAAATTC AAATGATTTT GAGGATTCAT ATCAATTTTT AACAAATGCA ACTTTTTCGG TGAGTATaGC TTGTTTCGGA ATATTTACAG CATTCCTTTT
NMne          ATCAAAATTC AAATGATTTT GAGGATTCAT ATCAATTTTT AACAAATGCA ACTTTTTCGG TGAGTATAGC TTGTTTCGGA ATATTTACAG CATTTCTTTT
NMni          ATCAAAATTC AAATGATTTT GAGGATTCAT ATCAATTTTT AACAAATGCA ACTTTTTCGG TGAGTATAGC TTGTTTCGGA ATATTTACAG CATTTCTTTT
NMpa          ATCAAAATTC AAATGATTTT GAGGATTCAT ATCAATTTTT AACAAATGCA ACTTTTTCGG TGAGTATAGC TTGTTTCGGA ATATTTACAG CATTTCTTTT
NMsy          ATCAAAATTC AAATGATTTT GAGGATTCAT ATCAATTTTT AACAAATGCA ACTTTTTCGG TGAGTATAGC TTGTTTCGGA ATATTTACAG CATTTCTTTT
NMve          ATCAAAATTC AAATGATTTT GAGGATTCAT ATCAATTTTT AACAAATGCA ACTTTTTCGG TGAGTATAGC TTGTTTCGGA ATATTTACAG CATTTCTTTT
NAros         ATCAAAATTC AAATGATTTT GAGGATTCAT ATCAATTTTT AACAAATGCA ACTTTTTCGG TGAGTATAGC TTGTTTCGGA ATATTTACAG CATTCCTTTT
NAni          ATCAAAATTC AAATGATTTT GAGGATTCGT ATCAATTTTT AACAAATGCA ACTTTTTCGG TGAGTATAGC TTGTTTCGGA ATATTTACAG CATTCCTTTT
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NKvi            ATCAAAATTC AAATGATTTT GAGGATTCAT ATCAATTTTT AACAAATGCA ACTTTTTCGG TGAGTATAGC TTGTTTCGGA ATATTTACAG CATTCCTTTT


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                      1710       1720       1730       1740       1750       1760       1770       1780       1790       1800
NAar            ATATAAGCCT TTTTATTCAT CTTTACAAAA TTTGAACTTA CTAAATTCGT TTGCGAAAAG GGGTCCTAAA AGGATTTTAT TGGATAAAAT AATATATTTG
NAhi            ATATAAGCCT TTTTATTCAT CTTTACAAAA TTTGAACTTA CTAAATTCGT TTGCGAAAAG GGGTCCTAAA AGGATTTTAT TGGATAAAAT TATATATTTG
NAlo            ATATAAGCCT TTTTATTCAT CTTTACAAAA TTTGAACTTA CTAAATTCGT TTGCGAAAAG GGGTCCTAAA AGGATTTTAT TGGATAAAAT AATATATTTG
NAca            ATATAAGCCT TTTTATTCAT CTTTACCAAA TTTGAACTTA CTAAATTCGT TTGCGAAAAG GGGTCCTAAA AGGATTTTAT TGGATAAAAT AATATATTTG
NAof            ATATAAGCCT TTTTATTCAT CTTTACTAAA TTTGAACTTA CTAAATTCGT TTGCGAAAAG GGGTCCTAAA AGGATTTTAT TGGATAAAAT AATATATTTG
NAlu            ATATAAGCCT TTTTATTCAT CTTTACAAAA TTTGAACTTA CTAAATTCGT TTGCGAAAaG GGGTCCTAAA AGGATTTTAT tGGAtAAAAT AATATATTTG
NLcr            ATATAAGCCT TTTTATTCAT CTTTACAAAA TTTGAACTTA CTAAATTCGT TTGCGAAAAG GGGTCCTAAA AGGATTTTAT TGGATAAAAT AATATATTTG
NLag            ATATAAGCCT TTTTATTCAT CTTTACAAAA TTTGAACTTA CTAAATTCGT TTGCGAAAAG GGGTCCTAAA AGGATTTTAT TGGATAAAAT AATATATTTG
NLbr            ATATAAGCCT TTTTATTCAT CTTTACAAAA TTTGAACTTA CTAAATTCGT TTGCGAAAAG GGGTCCTAAA AGGATTTTAT TGGATAAAAT AATATATTTG
NLtr            ATATAAGCCT TTTTATTCAT CTTTACAAAA TTTGAACTTA CTAAATTCGT TTGCGAAAAG GGGTCCTAAA AGGATTTTAT TGGATAAAAT AATATATTTG
NLtp            ATATAAGCCT TTTTATTCAT CTTTACAAAA TTTGAACTTA CTAAATTCGT TTGCGAAAAG GGGTCCTAAA AGGATTTTAT TGGATAAAAT AATATATTTG
NLfl            ATATAAGCCT TTTTATTCAT CTTTACAAAA TTTGAACTTA CTAAATTCGT TTGCGAAAAG GGGTCCTAAA AGGATTTTAT TGGATAAAAT AATATATTTG
NLas            ATATAAGCCT TTTTATTCAT CTTTACAAAA TTTGAACTTA CTAAATTCGT TTGCGAAAAG GGGTCCTAAA AGGATTTTAT TGGATAAAAT AATATATTTG
NLac            ATATAAGCCT TTTTATTCAT CTTTACAAAA TTTGAACTTA CTAAATTCGT TTGCGAAAAG GGGTCCTAAA AGGATTTTAT TGGATAAAAT AATATATTTG
NLar            ATATAAGCCT TTTTATTCAT CTTTACAAAA TTTGAACTTA CTAAATTCGT TTGCGAAAAG GGGTCCTAAA AGGATTTTAT TGGATAAAAT AATATATTTG
NLma            ATATAAGCCT TTTTATTCAT CTTTACAAAA TTTGAACTTA CTAAATTCGT TTGCGAAAAG GGGTCCTAAA AGGATTTTAT TGGATAAAAT AATATATTTG
NLmo            ATATAAGCCT TTTTATTCAT CTTTACAAAA TTTGAACTTA CTAAATTCGT TTGCGAAAAG GGGTCCTAAA AGGATTTTAT TGGATAAAAT AATATATTTG
NLmu            ATATAAGCCT TTTTATTCAT CTTTACAAAA TTTGAACTTA CTAAATTCGT TTGCGAAAAG GGGTCCTAAA AGGATTTTAT TGGATAAAAT AATATATTTG
NLob            ATATAAGCCT TTTTATTCAT CTTTACAAAA TTTGAACTTA CTAAATTCGT TTGCGAAAAG GGGTCCTAAA AGGATTTTAT TGGATAAAAT AATATATTTG
NLol            ATATAAGCCT TTTTATTCAT CTTTACAAAA TTTGAACTTA CTAAATTCGT TTGCGAAAAG GGGTCCTAAA AGGATTTTAT TGGATAAAAT AATATATTTG
NLpe            ATATAAGCCT TTTTATTCAT CTTTACAAAA TTTGAACTTA CTAAATTCGT TTGCGAAAAG GGGTCCTAAA AGGATTTTAT TGGATAAAAT AATATATTTG
NLph            ATATAAGCCT TTTTATTCAT CTTTACAAAA TTGGAACTTA CTAAATTCGT TTGCGAAAAG GGGTCCTAAA AGGATTTTAT TGGATAAAAT AATATATTTG
NLpl            ATATAAGCCT TTTTATTCAT CTTTACAAAA TTTGAACTTA CTAAATTCGT TTGCGAAAAG GGGTCCTAAA AGGATTTTAT TGGATAAAAT AATATATTTG
NLpu            ATATAAGCCT TTTTATTCAT CTTTACAAAA TTTAAACTTA CTAAATTCGT TTGCGAAAAG GGGTCCTAAA AGGATTTTAT TGGATAAAAT AATATATTTG
NLth            ATATAAGCCT TTTTATTCAT CTTTACAAAA TTTGAACTTA CTAAATTCGT TTGCGAAAAG GGGTCCTAAA AGGATTTTAT TGGATAAAAT AATATATTTG
NLti            ATATAAGCCT TTTTATTCAT CTTTACAAAA TTTGAACTTA CTAAATTCGT TTTCGAAAAG GGGTCCTAAA AGGATTTTAT TGGATAAAAT AATATATTTG
NMma            ATATAAGCCC TTTTATTCAT CTTTACAAAA TTTGAACTTA CTAAATTCGT TTGCGAAAAG GGGTCCTAAA AGGATTTTAT TGGATAAAAT AATATATTTG
NMtf            ATATAAGCCC TTTTATTCAT CTTTACAAAA TTTGAACTTA CTAAATTCGT TTGCGAAAAG GGGTCCTAAA AGGATTTTTT TGGATAAAAT AATATATTTG
NMae            ATATAAGCCT TTTTATTCAT CTTTACAAAA TTTGAACTTA CTAAATTCGT TTGCGAAAAG GGGTCCTAAA AGGATTTTAT TGGATAAAAT AATATATTTG
NMtr            ATATAAGCCT TTTTATTCAT CTTTACAAAA TTTGAACTTA CTAAATTCGT TTGCGAAAAG GGGTCCTAAA AGGATTTTAT TGGATAAAAT AATATATTTG
NMca            ATATAAGCCT TTTTATTCAT CTTTACAAAA TTTGAACTTA CTAAATTCGT TTGCGAAAAG GGGTCCTAAA AGGATTTTAT TGGATAAAAT TATATATTTG
NMhi            ATATAAGCCT TTTTATTCAT CTTTACAAAA TTTGAACTTA CTAAATTCGT TTGCGAAAAG GGGTCCTAAA AGGATTTTAT TGGATAAAAT AATAtATttG
NMto            ATATAAGCCT TTTTATTCAT CTTTACAAAA TTTGAacTTA CTAAATTCGT TTGCGAAAAG GGGTCCTAaA AGGatTTTAT TGGATaAAAT AATAtATttG
NMal            ATATAAGCCT TTTTATTCAT CTTTACAAAA TTTGAACTTA CTAAATTCGT TTGCGAAAAG GGGTCCTAAA AGGATTTTAT TGGATaAAAT AATAtATttG
NMmo            ATATAAGCCT TTTTATTCAT CTTTACAAAA TTTGAacTTA CTAAATTCGT TTGCGAAAAG GGGTCCTAaA AGGatTTTAT TGGATaAAAT AATAtATttG
NMne            ATATAAGCCT TTTTATTCAT CTTTACAAAA TTTGAACTTA CTAAATTCGT TTGCGAAAAG GGGTCCTAAA AGGATTTTAT TGGATAAAAT AATATATTTG
NMni            ATATAAGCCT TTTTATTCAT CTTTACAAAA TTTGAACTTA CTAAATTCGT TTGCGAAAAG GGGTCCTAAA AGGATTTTAT TGGATAAAAT AATATATTTG
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NMpa         ATATAAGCCT TTTTATTCAT CTTTACAAAA TTTGAACTTA CTAAATTCGT TTGCGAAAAG GGGTCCTAAA AGGATTTTAT TGGATAAAAT AATATATTTG
NMsy         ATATAAGCCT TTTTATTCAT CTTTACAAAA TTTGAACTTA CTAAATTCGT TTGCGAAAAG GGGTCCTAAA AGGATTTTAT TGGATAAAAT AATATATTTG
NMve         ATATAAGCCT TTTTATTCAT CTTTACAAAA TTTGAACTTA CTAAATTCGT TTGCGAAAAG GGGTCCTAAA AGGATTTTAT TGGATAAAAT AATATATTTG
NAros        ATATAAGCCT TTTTATTCAT CTTTACAAAA TTTGAACTTA CTAAATTCGT TTGCGAAAAG GGGTCCTAAA AGGATTTTAT TGGATAAAAT AATATATTTG
NAni         ATATAAGCCT TTTTATTCAT CTTTACAAAA TTTGAACTTA CTAAATTCGT TTGCGAAAAG GGGTCCTAAA AGGATTTTAT TGGATAAAAT AATATATTTG
NKvi         ATATAAGCCT TTTTATTCAT CTTTACAAAA TTTGAACTTA CTAAATTCGT TTGCGAAAAG GGGTCCTAAA AGGATTTTAT TGGATAAAAT AATATATTTG


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                                1810       1820       1830       1840
             NAar          ATATATGATT GGTCATATAA TCGTGGTTAC ATAGATACGT
             NAhi          ATATATGATT GGTCATATAA TCGTGGTTAC ATAGATACGT
             NAlo          ATATATGATT GGTCATATAA TCGTGGTTAC ATAGATACGT
             NAca          ATATATGATT GGTCATATAA TCGTGGTTAC ATAGATACGT
             NAof          ATATATGATT GGTCATATAA TCGTGGTTAC ATAGATACGT
             NAlu          ATAtATGATT GGTCATATAA TCGTGGTTAC ATAGATACGT
             NLcr          ATATATGATT GGTCATATAA TCGTGGTTAC ATAGATACGT
             NLag          ATATATGATT GGTCATATAA TCGTGGTTAC ATAGATACGT
             NLbr          ATATATGATT GGTCATATAA TCGTGGTTAC ATAGATACGT
             NLtr          ATATATGATT GGTCATATAA TCGTGGTTAC ATAGATACGT
             NLtp          ATATATGATT GGTCATATAA TCGTGGTTAC ATAGATACGT
             NLfl          ATATATGATT GGTCATATAA TCGTGGTTAC ATAGATACGT
             NLas          ATATATGATT GGTCATATAA TCGTGGTTAC ATAGATACGT
             NLac          ATATATGATT GGTCATATAA TCGTGGTTAC ATAGATACGT
             NLar          ATATATGATT GGTCATATAA TCGTGGTTAC ATAGATACGT
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             NLmo          ATATATGATT GGTCATATAA TCGTGGTTAC ATAGATACGT
             NLmu          ATATATGATT GGTCATATAA TCGTGGTTAC ATAGATACGT
             NLob          ATATATGATT GGTCATATAA TCGTGGTTAC ATAGATACGT
             NLol          ATATATGATT GGTCATATAA TCGTGGTTAC ATAGATACGT
             NLpe          ATATATGATT GGTCATATAA TCGTGGTTAC ATAGATACGT
             NLph          ATATATGATT GGTCATATAA TCGTGGTTAC ATAGATACGT
             NLpl          ATATATGATT GGTCATATAA TCGTGGTTAC ATAGATACGT
             NLpu          CTATATGATT GGTCATATAA TCGTGGTTAC ATAGATACGT
             NLth          ATATATGATT GGTCATATAA TCGTGGTTAC ATAGATACGT
             NLti          ATATATGATT GGTCATATAA TCGCGGTTAC ATAGATACGT
             NMma          ATATATGATT GGTCATATAA TCGTGGTTAC ATAGATACGT
             NMtf          ATATATGATT GGTCATATAA TCGTGGTTAC ATAGATACGT
             NMae          ATATATGATT GGTCATATAA TCGTGGTTAC ATAGATACGT
             NMtr          ATATATGATT GGTCATATAA TCGTGGTTAC ATAGATACGT
             NMca          ATATATGATT GGTCATATAA TCGTGGTTAC ATAGATACGT
             NMhi          ATATATGATT GGTCATAtAA TCGTGGTtAC atAGATACGT
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NMto        ATATATGATT GGTCATAtAA TCGTGGTtAC atAGATACGT
NMal        ATATATGATT GGTCATAtAA TCGTGGTtAC atAGATACGT
NMmo        ATATATGATT GGTCATAtAA TCGTGGTtAC atAGATACGT
NMne        ATATATGATT GGTCATATAA TCGTGGTTAC ATAGATACGT
NMni        ATATATGATT GGTCATATAA TCGTGGTTAC ATAGATACGT
NMpa        ATATATGATT GGTCATATAA TCGTGGTTAC ATAGATACGT
NMsy        ATATATGATT GGTCATATAA TCGTGGTTAC ATAGATACGT
NMve        ATATATGATT GGTCATATAA TCGTGGTTAC ATAGATACGT
NAros       ATATATGATT GGTCATATAA TCGTGGTTAC ATAGATACGT
NAni        ATATATGATT GGTCATATAA TCGTGGTTAC ATAGATACGT
NKvi        ATATATGATT GGTCATATAA TCGTGGTTAC ATAGATACGT
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*ces*A1b P1

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                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                        10         20         30         40         50         60         70         80         90        100
Lmo01           CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GACGAAAAGC TTGTCTGCGC TGCGCTAGTC
Lmo02           CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ACCAAGGAAG GACGAAAAGC TTGTCTGCGC TGCGCTAGTC
Lmo03           CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GACGAAAAGC TTGTCTGCGC TGCGCTAGTC
Lmo04           CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GACGAAAAGC TTGTCTGCGC TGCGCTAGTC
Lmo05           CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GACGAAAAGC TTGTCTGCGC TGCGCTAGTC
Lmo06           CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GACGAAAAGC TTGTCTGCGC TGCGCTAGTC
Lmo07           CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GACGAAAAGC TTGTCTGCGC TGCGCTAGTC
Lmo08           CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ACCAAGGAAG GACGAAAAGC TTGTCTGCGC TGCGCTAGTC
Lmo09           CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ACCAAGGAAG GACGAAAAGC TTGTCTGCGC TGCGCTAGTC
Lmo10           CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GACGAAAAGC TTGTCTGCGC TGCGCTAGTC
Lmo11           CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GACGAAAAGC TTGTCTGCGC TGCGCTAGTC
Lmo12           CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GACGAAAAGC TTGTCTGCGC TGCGCTAGTC
Lmo13           CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GACGAAAAGC TTGTCTGCGC TGCGCTAGTC
Lti01           CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Lti02           CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Lti03           CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Lti04           CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Lti05           CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Lti06           CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Lti07           CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Lti08           CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Lti09           CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Mhi01           CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Mhi02           CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Mhi03           CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Mhi04           CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
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Mhi06           CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Mhi07           CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Lth01           CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCCCTAGTC
Lth02           CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Lth03           CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTAGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Lth04           CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCCCTAGTC
Lth05           CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCCCTAGTC
Lth06           CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAGGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Lth07           CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Lth08           CCCTTAGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Lth09           CCCTTAGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
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Lth10       CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Lth11       CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTAGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Lth12       CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Lth13       CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGCCTGCGT TGCGCTAGTC
Mal01       CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Mal02       CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Mal03       CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Mal04       CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
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Mal09       CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Ltr01       CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Ltr02       CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCG AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Ltr03       CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Ltr04       CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Ltr05       CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Ltr06       CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Ltr07       CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Lag01       CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCAT TGCGCTAGTC
Lag02       CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCAT TGCGCTAGTC
Lag03       CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCAT TGCGCTAGTC
Lag04       CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCAT TGCGCTAGTC
Lag05       CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCAT TGCGCTAGTC
Lfl01       CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Lfl02       CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Ltp01       CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGTCTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Lbr01       CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Lbr02       CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Lbr03       CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Lob01       CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Lob02       CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Lob03       CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Lob04       CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Lob05       CCCTTTGCGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Lob06       CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCAGCGT TGCGCTAGTC
Lob07       CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Lol01       CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Lol02       CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Lol03       CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Lol04       CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
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Mae01        CCCTTTGTGT CTTGCCATGA ATGTAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGGAAAGC TTGTCTGCGT TGCGCTAGTC
Mae02        CCCTTTGTGT CTTGCCATGA ATGTAATTTT CCAATTTGTA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGGAAAGC TTGTCTGCGT TGCGCTAGTC
Mae03        CCCTTTGTGT CTTGCCATGA ATGTAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGGAAAGC TTGTCTGCGT TGCGCTAGTC
Mae04        CCCTTTGTGT CTTGCCATGA ATGTAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGGAAAGC TTGTCTGCGT TGCGCTAGTC
Mae05        CCCTTTGTGT CTTGCCATGA ATGTAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGGAAAGC TTGTCTGCGT TGCGCTAGTC
Mae06        CCCTTTGTGT CTTGCCATGA ATGTAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGGAAAGC TTGTCTGCGT TGCGCTAGTC
Mae07        CCCTTTGTGT CTTGCCATGA ATGTAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGGAAAGC TTGTCTGCGT TGCGCTAGTC
Mae08        CCCTTTGTGT CTTGCCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT CGAGTATGAC ATTAAGGAAG GTCGAAAAGC TTGTCTTCGT TGCGCTACAC
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Mmo09        CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC GTCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Mmo10        CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTACGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Mto01        CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
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Mto06        CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Mto07        CCCTTTGTGT CTTGCCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTTCGT TGCGCTACTC
Ahi01        CCC------- --TGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Ahi02        CCC------- --TGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Ahi03        CCC------- --TGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
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Ahi06        CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGCCTGCGT TGCGCTAGTC
Ahi07        CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Ahi08        CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Alo01        CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATATGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Alo02        CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATATGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Alo03        CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATATGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Alo04        CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATATGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Alo05        CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATATGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Alo06        CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATATGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Alo07        CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATATGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Alo08        CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATATGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Alo09        CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATATGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
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Alo10       CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATATGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Mca01       CCCTTTGTGT CTTGCCATGA ATGCAACTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Mca02       CCCTTTGTGT CTTGCCATGA ATGCAACTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Mca03       CCCTTTGTGT CTTGCCATGA ATGCAACTTT CCAATTTGCA AGACTTGTTT CGAGTACGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Mca04       CCCTTTGTGT CTTGCCATGA ATGCAACTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Mtf01       CCCTTTGTGT CTTGCCATGA ATGCAATTTC CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Mtf02       CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Mtf03       CCCTTTGTGT CGTGCCATGA ATGCAATTTC CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Mtf04       CCCTTTGTGT CGTGCCATGA ATGCAATTTC CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Mtf05       CCCTTTGTGT CTTGCCATGA ATGCAACTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Mma01       CCCTTTGTGT CTTGCCTTGA ATGCAACTTT CCAATCTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCTCTAGTC
Mma02       CCCTTTGTGT CTTGCCTTGA ATGCAACTTT CCAATCTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCTCTAGTC
Mma03       CCCTTTGTGT CTTGCCTTGA ATGCAACTTT CCAATCTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCTCTAGTC
Mma04       CCCTTTGTGT CTTGCCTTGA ATGCAACTTT CCAATCTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCTCTAGTC
Mma05       CCCTTTGTGT CTTGCCTTGA ATGCAACTTT CCAATCTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCTCTAGTC
Las01       CCCTTTGTGT CTTGCAATGA ATGCAATTTT CCTATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCGAGTC
Las02       CCCTTTGTGT CTTGCAATGA ATGCAATTTT CCTATTTGCA AGACTTGTTT GGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCGAGTC
Las03       CCCTTTGTGT CTTGCAATGA ATGCAATTTT CCTATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCGAGTC
Las04       CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Las05       CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Las06       CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Las07       CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Las08       CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Lpe01       CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Lpe02       CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Lpe03       CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Lpe04       CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCTATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCGAGTC
Lac01       CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Lac02       CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAGAAGC TTGTCTGCGT TGCGCTAGTT
Lac03       CCCTTTGTGT CTTGCCGTGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Lac04       CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Lac05       CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Lac06       CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
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Lac08       CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACCTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Lma01       CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC TTCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
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Lcr01       CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Lcr02       CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Msy01       CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Msy02       CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Msy03       CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
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Msy04         CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Msy05         CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Lmu01         CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Lmu02         CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Lmu03         CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Lmu04         CCCTTTGTGT CTTGCCATGA ATGCAATTCT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Lmu05         CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAGAAGC TTGTCTGCGT TGCGCTAGTC
Lmu06         CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAGAAGC TTGTCTGCGT TGCGCTAGTC
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Lmu08         CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Lmu09         CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Mpa01         CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
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Mpa03         CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Mpa04         CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Mpa05         CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Mpa06         CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Mve01         CCCTTTGTGT CTTGCCATGA ATGCAATCTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Mve02         CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTATTC
Mve03         CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTATTC
Mni01         CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Mni02         CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
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Mni04         CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Mni05         CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Mni06         CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Mne01         CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Aof01         CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGT TTGTCTGCGT TGCGGTAGTC
Aca01         CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGT TTGTCTGCGT TGCGGTAGTC
Aca02         CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGGTAGTC
Ani40         CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGGTAGTC


              ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     110        120        130        140        150        160        170        180        190        200
Lmo01         CATACGATGG TATG--TTTA C-------TT TTAGTTCTTG ATAAATCTTT GTATTTCCCA AATGCTTGTT TGATTTCCCA ---------- ----------
Lmo02         CATACGATGG TATG--TTTA C-------TT TTAGTTCTTG ATAAATCTTT GTGTTTCCCA AATGCTTGTT TGATTTCCCA ---------- ----------
Lmo03         CATACGATGG TATG--TTTA C-------TT TTAGTTCTTG ATAAATCTTT GTGTTTCCCT AATGCTTGTT TGATTTCCCA ---------- ----------
Lmo04         CATACGATGG TATG--TTTA C-------TT TTAGTTCTTG ATAAATCTTT GTGTTTCCCA AATGCTTGTT TGATTTCCCA ---------- ----------
Lmo05         CATACGATGG TATG--TTTA C-------TT TTAGTTCTTG ATAAATCTTT GTGTTTCCCA AATGCTTGTT TGATTTCCCA ---------- ----------
Lmo06         CATACGATGG TATG--TTTA C-------TT TTAGTTCTTG ATAAATCTTT GTATTTCCCA AATGCTTGTT TGATTTCCCA ---------- ----------
Lmo07         CATACGATGG TATG--TTTA C-------TT TTAGTTCTTG ATAAATCTTT GTATTTCCCA AATGCTTGTT TGATTTCCCA ---------- ----------
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Lmo08         CATACGATGG TATG--TTTA C-------TT TTAGTTCTTG ATAAATCTTT GTGTTTCCCA AATGCTTGTT TGATTTCCCA ---------- ----------
Lmo09         CATACGATGG TATG--TTTA C-------TT TTAGTTCTTG ATAAATCTTT GTGTTTCCCA AATGCTTGTT TGATTTCCCA ---------- ----------
Lmo10         CATACGATGG TATG--TTTA C-------TT TTAGTTCTTG ATAAATCTTT GTGTTTCCCT AATGCTTGTT TGATTTCCCA ---------- ----------
Lmo11         CATACGATGG TATG--TTTA C-------TT TTAGTTCTTG ATAAATCTTT GTGTTTCCCT AATGCTTGTT TGATTTCCCA ---------- ----------
Lmo12         CATACGATGG TATG--TTTA C-------TT TTAGTTCTTG ATAAATCTTT GTGTTTCCCA AATGCTTGTT TGATTTCCCA ---------- ----------
Lmo13         CATACGATGG TATG--TTTA C-------TT TTAGTTCTTG ATAAATCTTT GTGTTTCCCA AATGCTTGTT TGATTTCCCA ---------- ----------
Lti01         CATACGATGG TATG--TATA C-------TT TTAGTTCTTG ATAAATCTTT GTGTTT---- ---------- ---------- ---------- ----------
Lti02         CATACGATGG TATG--TATA C-------TT TTAATTCTTG ATAAATCTTT GTGTTT---- ---------- ---------- ---------- ----------
Lti03         CATACGATGG TATG--TATA C-------TT TTAGTTCTTG ATAAATCTTT GTGTTT---- ---------- ---------- ---------- ----------
Lti04         CATACGATGG TATG--TATA C-------TT TTAGTTCTTG ATAAATCTTT GTGTTT---- ---------- ---------- ---------- ----------
Lti05         CATACGATGG TATG--TATA C-------TT TTAGTTCTTG ATAAATCTTT GTGTTT---- ---------- ---------- ---------- ----------
Lti06         CATACGATGG TATG--TATA C-------TT TTAGTTCTTG ATAAATCTTT GTGTTT---- ---------- ---------- ---------- ----------
Lti07         CATACGATGG TATG--TATA C-------TT TTAGCTCTTG ATAAATCTTT GTGTTT---- ---------- ---------- ---------- ----------
Lti08         CATACGATGG TATG--TATA C-------TT TTAGTTCTTG ATAAATCTTT GTGTTT---- ---------- ---------- ---------- ----------
Lti09         CATACGATGG TATG--TATA C-------TT TTAGTTCTTG ATAAATCTTT GTGTTT---- ---------- ---------- ---------- ----------
Mhi01         CATACGACGG TATG--CATA C-------TT TTAGTCCTTA ATAAATC--T GTGTTTTCCA AATGCTTGTT TGATTTCCCA -------TGA AAAGAAGAAA
Mhi02         CATACGACGG TATG--CATG C-------TT TTAGTCCTTA ATAAATC--T GTGTTTTCCA AATGCTTGTT TGATTTCCCA -------TGA AAAGAAGAAA
Mhi03         CATACGACGG TATG--CATA C-------TT TTAGTCCTTA ATAAATC--T GTGTTTTCCA AATGCTTGTT TGATTTCCCA -------TGA AAAGAAGAAA
Mhi04         CATACGACGG TATG--CATA C-------TT TTAGTCCTTA ATAAATC--T GTGTTTTCCA AATGCTTGTT TGATTTCCCA -------TGA AAAGAAGAAA
Mhi05         CATACGACGG TATG--CATA C-------TT TTAGTCCTTA ATAAATC--T GTGTTTTCCA AATGCTTGTT TGATTTCCCA -------TGA AAAGAAGAAA
Mhi06         CATACGACGG TATG--CATA C-------TT TTAGTCCTTA ATAAATC--T GTGTTTTCCA AATGCTTGTT TGATTTCCCA -------TGA AAAGAAGAAA
Mhi07         CATACGACGG TATG--CATA C-------TT TTAGTCCTTA ATAAATC--T GTGTTTTCCA AATGCTTGTT TGATTTCCCA -------TGA AAAGAAGAAA
Lth01         CATACGATGG TATG--TATA T-------TT TTATTTCTTG ATAAATCTTT GTGTTTTCCA AATGCTTGTT TGATTTCCCA -------TGT AAAGAAAAA-
Lth02         CATACGATGG TATG--TATA T-------TA TTATTTCTTG ATAAATCTTT GTGTTTTCCA AATGCTTGTT TGATTTCCCA -------TGA AAAGAAAAA-
Lth03         CATACGATGG TATG--TATA T-------TT TTATTTCTTG ATAAATCTTT GTGTTTTCCA AATGCTTGTT TGATTTCCCA -------TGA AAAGAAAAA-
Lth04         CATACGATGG TATG--TATA T-------TT TTATTTCTTG ATAAATCTTT GTGTTTTCCA AATGCTTGTT TGATTTCCCA -------TGT AAAGAAAAA-
Lth05         CATACGATGG TATG--TATA T-------TT TTATTTCTTG ATAAATCTTT GTGTTTTCCA AATGCTTGTT TGATTTCCCA -------TGT AAAGAAAAA-
Lth06         CATACGATGG TATG--TATA T-------TT TTATTTCTTG ATAAATCTTT GTGTTTTCCA AATGCTTGTT TGATTTCCCA -------TGA AAAGAAAAA-
Lth07         CATACGATGG TATG--TATA T-------TT TTATTTCTTG ATAAATCTTT GTGTTTTCCA AATGCTTGTT TGATTTCCCA -------TGA AAAGAAAAA-
Lth08         CATACGATGG TATG--TATA T-------TA TTATTTCTTG ATAAATCTTT GTGTTTTCCA AATGCTTGTT TGATTTCCCA -------TGA AAAGAAAAA-
Lth09         CATACGATGG TATG--TATA T-------TA TTATTTCTTG ATAAATCTTT GTGTTTTCCA AATGCTTGTT TGATTTCCCA -------TGA AAAGAAAAA-
Lth10         CATACGATGG TATG--TATA T-------TT TTATTTCTTG ATAAATCTTT GTGTTTTCCA AATGCTTGTT TGATTTCCCA -------TGA AAAGAAAAA-
Lth11         CATACGATGG TATG--TATA T-------TT TTATTTCTTG ATAAATCTTT GTGTTTTCCA AATGCTTGTT TGATTTCCCA -------TGA AAAGAAAAA-
Lth12         CATACGATGG TATG--TATA T-------TT TTATTTCTTG ATAAATCTTT GTGTTTTCCA AATGCTTGTT TGATTTCCCA -------TGA AAAGAAAAA-
Lth13         CATACGATGG TATG--TATA T-------TT TTATTTCTTG ATAAATCTTT GTGTTTTCCA AATGCTTGTT TGATTTCCCA -------TGA AAAGAAAAA-
Mal01         CATACGATGG TATG--TATA T-------TT TTATTTCTTG ATAAATCTTT GTGTTTTCCA AATGCTTGTT TGATTTCCCA -------TGA AAAGAAAAA-
Mal02         CATACGATGG TATG--TATA T-------TT TTATTTCTTG ATAAATCTTT GTGTTTTCCA AATGCTTGTT TGATTTCCCA -------TGA AAAGAAAAA-
Mal03         CATACGATGG TATG--TATA T-------TT TTATTTCTTG ATAAATCTTT GTGTTTTCCG AATGCTTGTT TGATTTCCCA -------TGA AAAGAAAAA-
Mal04         CATACGATGG TATG--TATA T-------TT TTATTTCTTG ATAAATCTTT GTGTTTTCCA AATGCTTGTT TGATTTCCCA -------TGA AAAGAAAAA-
Mal05         CATACGATGG TATG--TATA T-------TT TTATTTCTTG ATAAATCTTT GTGTTTTCCA AATGCTTGTT TGATTTCCCA -------TGA AAAGAAAAA-
Mal06         CATACGATGG TATG--TATA T-------TT TTATTTCTTG ATAAATCTTT GTGTTTTCCA AATGCTTGTT TGATTTCCCA -------TGA AAAGAAAAA-
Mal07         CATACGATGG TATG--TATA T-------TT TTATTTCTTG ATAAATCTTT GTGTTTTCCA AATGCTTGTT TGATTTCCCA -------TGA AAAGAAAAA-
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Mal08       CATACGATGG TATG--TATA T-------TT TTATTTCTTG ATAAATCTTT GTGTTTTCCA AATGCTTGTT TGATTTCCCA -------TGA AAAGAAAAA-
Mal09       CATACGATGG TATG--CATA CAGCATACTT ATAGTTCTTG ATAAATCTTT GTGTTT-CCA AATGCTTGTT TGATTTCCCA -------TGA AAGAAAAAAA
Ltr01       CATACGATGG TATG--TATA C-------TT TTATTTCTTG ATAAATCTTG GTGTTTTCGA AATGCTTGTT TGATTTCCCA -------TGA AAAGAAAAAA
Ltr02       CATACGATGG TATG--TATA C-------TT TTATTTCTTG ATAAATCTTG GTGTTTTCGA AATGCTCGTT TGATTTCCCA -------TGA AAAGAAAAAA
Ltr03       CATACGATGG TATG--TATA C-------TT TTATTTCTTG ATAAATCTTG GTGTTTTCGA AATGCTTGTT TGATTTCCCA -------TGA AAAGAAAAAA
Ltr04       CATACGATGG TATG--TATA C-------TT TTATTTCTTG ATAAATCTTG GTGTTTTCGA AATGCTTGTT TGATTTCCCA -------TGA AAAGAAAAAA
Ltr05       CATACGATGG TATG--TATA C-------TT TTATTTCTTG ATAAATCTTG GTGTTTTCGA AATGCTTGTT TGGTTTCCCA -------TGA AAAGAAAAAA
Ltr06       CATACGATGG TATG--TATA C-------TT TTATTTCTTG ATAAATCTTG GTGTTTTCGA AATGCTTGTT TGATTTCCCA -------TGA AAAGAAAAAA
Ltr07       CATACGATGG TATG--TATA C-------TT TTATTTCTTG ATAAATCTTG GTGTTTTCGA AATGCTTGTT TGATTTCCCA -------TGA AAAGAAAAAA
Lag01       CATACGATGG TATG--TATA C-------TT TTATTTCTTG ATAAATCTTG GTGTTTTCGA AATGCTTGTT TGATTTCCCA -------TGA AAAGAAAAAA
Lag02       CATACGATGG TATG--TATA C-------TT TTATTTCTTG ATAAATCTTG GTGTTTTCGA AATGCTTGTT TGATTTCCCA -------TGA AAAGAAAAAA
Lag03       CATACGATGG TATG--TATA C-------TT TTATTTCTTG ATAAATCTTG GTGTTTTCGA AATGCTTGTT TGATTTCCCA -------TGA AAAGAAAAAA
Lag04       CATACGATGG TATG--TATA C-------TT TTATTTCTTG ATAAATCTTG GTGTTTTCGA AATGCTTGTT TGATTTCCCA -------TGA AAAGAAAAAA
Lag05       CATACGATGG TATG--TATA C-------TT TTATTTCTTG ATAAATCTTG GTGTTTTCGA AATGCTTGTT TGATTTCCCA -------TGA AAAGAAAAAA
Lfl01       CATACGATGG TATG--TATA C-------TT TTATTTCTTG ATAAATCTTG GTGTTTTCGA AATGCTTGTT TGATTTCCCA -------TGA AAAGAAAAAA
Lfl02       CATACGATGG TATG--TATA C-------TT TTATTTCTTG ATAAATCTTG GTGTTTTCGA AATGCTTGTT TGATTTCCCA -------TGA AAAGAAAAAA
Ltp01       CATACGATGG TATG--TATA C-------TT TTATTTCTTG ATAAATCTTG GTGTTTTCGA AATGCTTGTT TGATTTCCCA -------TGA AAAGAAAAAA
Lbr01       CATACGATGG TATG--TATA C-------TT TTATTTCTTG ATAAATCTTG GTGTTTTTGA AATGCTTGTT TGATTTCCCA ATTCCCATGA AAAGAAAAAA
Lbr02       CATACGATGG TATG--TATA C-------TT TTATTTCTTG ATAAATCTTG GTGTTTTTGA AATGCTTGTT TGATTTCCCA ATTCCCATGA AAAGAAAAAA
Lbr03       CATACGATGG TATG--TATA C-------TT TTATTTCTTG ATAAATCTTG GTGTTTTTGA AATGCTTGTT TGATTTCCCA ATTCCCATGA AAAGAAAAAA
Lob01       CATACGATGG TATG--TATA C-------TT TTATTTCTTG ATAAATCTTG GTGTTTTCGA AATGCTTGTT TGATTTCCCA -------TGA AAAGAAAAAA
Lob02       CATACGATGG TATG--TATA C-------TT TTATTTCTTG ATAAATCTTG GTGTTTTCGA AATGCTTGTT TGATTTCCCA -------TGA AAAGAAAAAA
Lob03       CATACGATGG TATG--TATA C-------TT TTATTTCTTG ATAAATCTTG GTGTTTTCGA AATGCTTGTT TGATTTCCCA -------TGA AAAGAAAAAA
Lob04       CATACGATGG TATG--TATA C-------TT TTATTTCTTG ATAAATCTTG GTGTTTTCGA AATGCTTGTT TGATTTCCCA -------TGA AAAGAAAAAA
Lob05       CATACGATGG TATG--TATA C-------TT TTATTTCTTG ATAAATCTTG GTGTTTTCGA AATGCTTGTT TGATTTCCCA -------TGA AAAGAAAAAA
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Lol02       CATACGATGG TATG--TATA C-------TT TTATTTCTTG ATAAATCTTG GTGTTTTCGA AATGCTTGTT TGATTTCCCA -------TGA AAAGAAAAAA
Lol03       CATACGATGG TATG--TATA C-------TT TTATTTCTTG ATAAATCTTG GTGTTTTCGA AATGCTTGTT TGATTTCCCA -------TGA AAAGAAAAAA
Lol04       CATACGATGG TATG--TATA C-------TT TTATTTCTTG ATAAATCTTG GTGTTTTCGA AATGCTTGTT TGATTTCCCA -------TGA AAAGAAAAAA
Mae01       CATACGATGG TATG--TATA C-------GT TTAGTCCTTG ATAAATCTTT GTGTTTTCCA ACTGCTTGTT TGATTT---- ---------- ----------
Mae02       CATACGATGG TATG--TATA C-------GT TTAGTCCTTG ATAAATCTTT GTGTTTTCCA ACTGCTTGTT TGATTT---- ---------- ----------
Mae03       CATACGATGG TATG--TATA C-------GT TTAGTCCTTG ATAGATCTTT GTGTTTTCCA ACTGCTTGTT TGATTT---- ---------- ----------
Mae04       CATACGATGG TATG--TATA C-------GT TTAGTCCTTG ATAAATCTTT GTGTTTTCCA ACTGCTTGTT TGATTT---- ---------- ----------
Mae05       CATACGATGG TATG--TATA C-------GT TTAGTCCTTG ATAAATCTTT GTGTTTTCCA ACTGCTTGTT TGATTT---- ---------- ----------
Mae06       CATACGATGG TATG--TATA C-------GT TTAGTCCTTG ATAAATCTTT GTGTTTTCCA ACTGCTTGTT TGATTT---- ---------- ----------
Mae07       CATACGATGG TATG--TATA C-------GT TTAGTCCTTG ATAAATCTTT GTGTTTTCCA ACTGCTTGTT TGATTT---- ---------- ----------
Mae08       CATACGATGG TATG--CATA C-------TT TTATTTCTTG ATAAATC--T GT-------- ---------- ---------- ---------- ----------
Mmo01       CATACGATGG TATG--CATA CAGCATACTT ATAGTTCTTG ATAAATCTGT GTGTTTTCCA AATGCTTGTT TGATTTCCCA -------TGA AAAGAAAAAA
Mmo02       CATACGATGG TATG--CATA CAGCATACTT ATAGTTCTTG ATAAATCTGT GTGTTTTCCA AATGCTTGTT TGATTTCCCA -------TGA AAAGAAAAAA
Mmo03       CATACGATGG TATG--CATA CAGCATACTT ATAGTTCTTG ATAAATCTGT GTGTTTTCCA AATGCTTGTT TGATTTCCCA -------TGA AAAGAAAAAA
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Mmo04          CATACGATGG TATG--CATA CAGCATACTT ATAGTTCTTG ATAAATCTGT GTGTTTTCCA AATGCTTGTT TGATTTCCCA -------TGA AAAGAAAAAA
Mmo05          CATACGATGG TATG--CATA CAGCATACTT ATAGTTCTTG ATAAATCTTT GTGTTTTCCA AATGCTTGTT TGAATTCCCA -------TGA AAAGAAAAAA
Mmo06          CATACGATGG TATG--CATA CAGCATACTT ATAGTTCTTG ATAAATCTTT GTGTTTTCCA AATGCTTGTT TGAATTCCCA -------TGA AAAGAAAAAA
Mmo07          CATACGATGG TATG--CATA CAGCATACTT ATAGTTCTTG ATAAATCTGT GTGTTTTCCA AATGCTTGTT TGATTTCCCA -------TGA AAAGAAAAAA
Mmo08          CATACGATGG TATG--CATA CAGCATACTT ATAGTTCTTG ATAAATCTTT GTGTTTTCCA AATGCTTGTT TGAATTCCCA -------TGA AAAGAAAAAA
Mmo09          CATACGATGG TATG--CATA CAGCATACTT ATAGTTCTTG ATAAATCTTT GTGTTTTCCA AATGCTTGTT TGAATTCCCA -------TGA AAAGAAAAAA
Mmo10          CATACGATGG TATG--CATA CAGCATACTT ATAGTTCTTG ATAAATCTGT GTGTTTTCCA AATGCTCGTT TGATTTCCCA -------TGA AAAGAAAAAA
Mto01          CATACGATGG TATG--CATA CAGCATACTT ATAGTTCTTG ATAAATCTTT GTGTTTTCCA AATGCTTGTT TGATTTCCCA -------TGA AAAGAAAAAA
Mto02          CATACGATGG TATG--CATA CAGCATACTT ATAGTTCTTG ATAAATCTTT GTGTTTTCCA AATGCTTGTT TGATTTCCCA -------TGA GAAGAAAAAA
Mto03          CATACGATGG TATG--CATA CAGCATACTT ATAGTTCTTG ATAAATCTTT GTGTTTTCCA AATGCTTGTT TGATTTCCCA -------TGA AAAGAAAAAA
Mto04          CATACGATGG TATG--CATA CAGCATACTT ATAGTTCTTG ATAAATCTTT GTGTTTTCCA AATGCTTGTT TGATTTCCCA -------TGA AAAGAAAAAA
Mto05          CATACGATGG TATG--CATA CAGCATACTT ATAGTTCTTG ATAAATCTTT GTGTTTTCCA AATGCTTGTT TGATTTCCCA -------TGA AAAGAAAAAA
Mto06          CATACGATGG TATG--CATA C-------TT TTAGTTCTTG ATAAATCTTG GTGTTTTCGA AATGCTTGTT TGATTTCCCA -------TGA AAAGAAAAAA
Mto07          CATACGATGG TATG--TATG C-------TT TTACTTCTTG ATGAATCTTT GTGTCTTCCA AATGCTTGT- ---------- ---------- ----------
Ahi01          CATACGATGG TATG--TATA C------TTT TTAGTTCTTG ATAAATCTTT GTGTTCTCCA AATGTTTGTT TTATTTCCCC -------TGA AAAGAAAAA-
Ahi02          CATACGATGG TATG--TATA C------TTT TTAGTTCTTG ATAAATCTTT GTGTTCTCCA AATGTTTGTT TTATTTCCCC -------TGA AAAGAAAAA-
Ahi03          CATACGATGG TATG--TATA C------TTT TTAGTTCTTG ATAAATCTTT GTGTTCTCCA AATGTTTGTT TTATTTCCCC -------TGA AAAGAAAAA-
Ahi04          CATACGATGG TATG--TATA C------TTT TTAGTTCTTG ATAAATCTTT GTGTTCTCCA AATGTTTGTT TTATTTCCCC -------TGA AAAGAAAAA-
Ahi05          CATACGATGG TATGTGTATA C------TTT TTAC------ --------TT GTGTTCTCCA AATGCTTGTT T--------- ---------- ----------
Ahi06          CATACGATGG TATG--TATA C------TTT TTAGTTCTTG ATAAATCTTT GTGTTCTCCA AATGTTTGTT TTATTTCCCC -------TGA AAAGAAAAA-
Ahi07          CATACGATGG TATG--TATA C------TTT TTAGTTCTTG ATAAATCTTT GTGTTCTCCA AATGTTTGTT TTATTTCCCC -------TGA AAAGAAAAA-
Ahi08          CATACGATGG TATGTGTATA C------TTT TTAC------ --------TT GTGTTCTCCA AATGCTTGTT T--------- ---------- ----------
Alo01          CATACGATGG TATG--TATA C------TTT TTAGTTCTTG ATAAATCTTT GTGTTCTCCA AATGTTTGTT TTATTTCCCC -------TGA AAAGAAAAA-
Alo02          CATACGATGG TATG--TATA C------TTT TTAGTTCTTG ATAAATCTTT GTGTTCTCCA AATGTTTGTT TTATTTCCCC -------TGA AAAGAAAAA-
Alo03          CATACGATGG TATG--TATA C------TTT TTAGTTCTTG ATAAATCTTT GTGTTCTCCA AATGTTTGTT TTATTTCCCC -------TGA AAAGAAAAA-
Alo04          CATACGATGG TATG--TATA C------TTT TTAGTTCTTG ATAAATCTTT GTGTTCTCCA AATGTTTGTT TTATTTCCCC -------TGA AAAGAAAAA-
Alo05          CATACGATGG TATG--TATA C------TTT TTAGTTCTTG ATAAATCTTT GTGTTCTCCA AATGTTTGTT TTATTTCCCC -------TGA AAAGAAAAA-
Alo06          CATACGATGG TATG--TATA C------TTT TTAGTTCTTG ATAAATCTTT GTGTTCTCCA AATGTTTGTT TTATTTCCCC -------TGA AAAGAAAAA-
Alo07          CATACGATGG TATG--TATA C------TTT TTAGTTCTTG ATAAATCTTT GTGTTCTCCA AATGTTTGTT TTATTTCCCC -------TGA AAAGAAAAA-
Alo08          CATACGATGG TATG--TATA C------TTT TTAGTTCTTG ATAAATCTTT GTGTTCTCCA AATGTTTGTT TTATTTCCCC -------TGA AAAGAAAAA-
Alo09          CATACGATGG TATG--TATA C------TTT TTAGTTCTTG ATAAATCTTT GTGTTCTCCA AATGTTTGTT TTATTTCCCC -------TGA AAAGAAAAA-
Alo10          CATACGATGG TATG--TATA C------TTT TTAGTTCTTG ATAAATCTTT GTGTTCTCCA AATGTTTGTT TTATTTCCCC -------TGA AAAGAAAAA-
Mca01          CATACGATGG TATGTGTATA C-------TT TTACTCCTTC ATAAATCTTT GTGTTCTCCA AATGCTTGTT T--------- ---------- ----------
Mca02          CATACGATGG TATGTGTATA C-------TT TTACTCCTTC ATAAATCTTT GTGTTCTCCA AATGCTTGTT T--------- ---------- ----------
Mca03          CATACGATGG TATGTGTATA C-------TT TTACTCCTTC ATAAATCTTT GTGTTCTCCA AATGCTTGTT TGATT----- ---------- ----------
Mca04          CATACGATGG TATGTGTATA C-------TT TTACTCCTTC ATAAATCTTT GTGTTCTCCA AATGCTTGTT TGATT----- ---------- ----------
Mtf01          CATACGATGG TATGTGTATA C-------TT TTAGTTCTTT ---------T GTGTTCTCCA AATGCTTGT- ---------- ---------- ----------
Mtf02          CATACGATGG TATGTGTATA C-------TT TTAGTTCTTT ---------T GTGTTCTCCA AATGCTTGT- ---------- ---------- ----------
Mtf03          CATACGATGG TATGTGTATA C-------TT TTAGTTCTTT ---------T GTGTTCTCCA AATGCTTGTT ---------- ---------- ----------
Mtf04          CATACGATGG TATGTGTATA C-------TT TTAGTTCTTT ---------T GTGTTCTCCA AATGCTTGTT ---------- ---------- ----------
Mtf05          CATACGATGG TATGTGTATA C-------TT TTAGTTCTTG ACAAACCTTT GTGTTCTCCA AATACTTGTT T--------- ---------- ----------
Mma01          CATACGATGG TATGTGTATA C-------TT TTAGTTCTTG ATAAATCTTT GTGTTCTCCA ATTGCTTGTT T--------- ---------- ----------
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Mma02        CATACGATGG TATGTGTATA C-------TT TTAGTTCTTG ATAAATCTTT GTGTTCTCCA ATTGCTTGTT T--------- ---------- ----------
Mma03        CATACGATGG TATGTGTATA C-------TT TTAGTTCTTG ATAAATCTTT GTGTTCTCCA ATTGCTTGTT T--------- ---------- ----------
Mma04        CATACGATGG TATGTGTATA C-------TT TTAGTTCTTG ATAAATCTTT GTGTTCTCCA ATTGCTTGTT T--------- ---------- ----------
Mma05        CATACGATGG TATGTGTATA C-------TT TTAGTTCTTG ATAAATCTTT GTGTTCTCCA ATTGCTTGTT T--------- ---------- ----------
Las01        CATACGATGG TATG--TATA C-------TT TTAGTACTTG ATAAATCTTT GTGTTTTCCA AATGTTTGTT TGATTTCCCA -------TGA AAAGAAAAAA
Las02        CATACGATGG TATG--TATA C-------TT TTAGTTCTTG ATAAATCTTT GTGTTTTCCA AATGTTTGTT TGATTTCCCA -------TGA AAAGAAAAAA
Las03        CATACGATGG TATG--TATA C-------TT TTAGTTCTTG ATAAATCTTT GTGTTTTCCA AATGTTTGTT TGATTTCCCA -------TGA AAAGAAAAAA
Las04        CATACGATGG TATG--CATA C-------TT TTAGTTCTTG ATGAATCTTT GTGCTTTCCA AATGCTTGTT TTATTTCCCA -------TGA AAAGAAAAAA
Las05        CATACGATGG TATG--CATA C-------TT TTAGTTCTTG ATAAATCTTT GTGCTTTCCA AATGCTTGTT TTATTTCCCA -------TGA AAAGAAAAAA
Las06        CATACGATGG TATG--CATA C-------TT TTAGTTCTTG ATAAATCTTT GTGCTTTCCA AATGCTTGTT TTATTTCCCA -------TGA AAAGAAAAAA
Las07        CATACGATGG TATG--CATA C-------TT TTAGTTCTTG ATAAATCTTT GCGCTTTCCA AATGCTTGTT TTATTTCCCA -------TGA AAAGAAAAAA
Las08        CATACGATGG TATG--CATA C-------TT TTAGTTCTTG ATAAATCTTT GTGCTTTCCA AATGCTTGTT TTATTTCCCA -------TGA AAAGAAAAAA
Lpe01        CATACGATGG TATG--CATA C-------TT TTAGCTCTTG ATAAATCTTT GTGCTTTCCA AATGCTTGTT TTATTTCCCA -------TGA AAAGAAAAAA
Lpe02        CATACGATGG TATG--CATA C-------TT TTAGTTCTTG ATAAATCTTT GTGCTTTCCA AATGCTTGTT TTATTTCCCA -------TGA AAAGAAAAAA
Lpe03        CATACGATGG TATG--CATA C-------TT TTAGTTCTTG ATAAATCTTT GTGCTTTCCA AATGCTTGTT TTATTTCCCA -------TGA AAAGAAAAAA
Lpe04        CATACGATGG TATG--TATA C-------TT TTAGTTCTTG ATAAATCTTT GTGTTTTCCA AATGCTTGTT TGATTTCCCA -------TGA AAAGAAAAAA
Lac01        CATACGATGG TATG--TATA C-------TT TTAGTTCTTG ATAAATCTTT GTGTTTTCCA AATGCTTGTT TTATTTCCCA -------TGA AAAGAAAAA-
Lac02        CATACGATGG TATG--TATA C-------TT TTAGTTCTTG ATAAATCTTT GTGTTTTCCA AATGCTTGTT TTATTTCCCA -------TGA AAAGAAAAA-
Lac03        CATACGATGG TATG--TATA C-------TT TTAGTTCTTG ATAAATCTTT GTGTTTTCCA AATGCTTGTT TTATTTCCCA -------TGG AAAGAAAAA-
Lac04        CATACGATGG TATG--TATA C-------TT TTAGTTCTTG ATAAATCTTT GTGTTTTCCA AATGCTTGCT TTATTTCCCA -------TGA AAAGAAAAA-
Lac05        CATACGATGG TATG--TATA C-------TT TTAGTTCTTG ATAAATCTTT GTGTTTTCCA AATGCTTGTT TTATTTCCCA -------TGA AAAGAAAAA-
Lac06        CATACGATGG TATG--TATA C-------TT TTAGTTCTTG ATAAATCTTT GTGTTTTCCA AATGCTTGTT TTATTTCCCA -------TGA AAAGAAAAA-
Lac07        CATACGAT-- ---------A C-------TT TTAGTTCTTG ATAAATCTTT GTGTTTTCCA AATGCTTGTT TTATTTCCCA -------TGA AAAGAAAAA-
Lac08        CATACGATGG TATG--TATA C-------TT TTAGTTCTTG ATAAATCTTT GTGTTTTCCA AATGCTTGTT TTATTTCCCA -------TGA AAAGAAAAA-
Lma01        CATTCGATGG TATG--TATA C-------TT TTAGTTCTTG ATAAATCTTT GTGTTTTCCA AATGCTTGTT TTATTTCCCA -------TGA AAAGAAAAA-
Lma02        CATTCGATGG TATG--TATA C-------TT TTAGTTCTTG ATAAATCTTT GTGTTTTCCA AATGCTTGTT TTATTTCCCA -------TGA AAAGAAAAA-
Lcr01        CATACGATGG TATG--CATA C-------TT TTAGTTCTTG ATAAATCTTT GTGCTTTCCA AATGCTTGTT TTATTTCCCA -------TGA AAAGAAAAAA
Lcr02        CATACGATGG TATG--CATA C-------TT TTAGTTCTTG ATAAATCTTT GTGCTTTCCA AATGCTTGTT TTATTTCCCA -------TGA AAAGAAAAAA
Msy01        CATACGATGG TATG--CATA C-------TT TTAGTTCTTG ATAAATCTTT GTGCTTTCCA AATGCTTGTT TTATTTCCCA -------TGA AAAGAAAAAA
Msy02        CATACGATGG TATG--CATA C-------TT TTAGTTCTTG ATAAATCTTT GTGCTTTCCA AATGCTTGTT TTATTTCCCA -------TGA AAAGAAAAAA
Msy03        CATACGATGG TATG--CATA C-------TT TTAGTTCTTG ATAAATCTTT GTGCTTTCCA AATGCTTGTT TTATTTCCCA -------TGA AAAGAAAAAA
Msy04        CATACGATGG TATG--CATA C-------TT TTAGTTCTTG ATAAATCTTT GTGCTTTCCA AATGCTTGTT TTATTTCCCA -------TGA AAAGAAAAAA
Msy05        CATACGATGG TATG--CATA C-------TT TTAGTTCTTG ATAAATCTTT GTGCTTTCCA GATGCTTGTT TTATTTCCCA -------TGA AAAGAAAAAA
Lmu01        CATACGATGG TATC--CATA C-------TT TTAGTTCTTG ATAAATCTTT GTGCTTTCCA AATGCTTGTT TTATTTCCCA -------TGA AAAGAAAAAA
Lmu02        CATACGATGG TATC--CATA C-------TT TTAGTTCTTG ATAAATCTTT GTGCTTTCCA AATGCTTGTT TTATTTCCCA -------TGA AAAGAAAAAA
Lmu03        CATACGATGG TATG--CATA C-------TT TTAGTTCTTG ATAAATCTTT GTGCTTTCCA AATGCTTGTT TTATTTCCCA -------TGA AAAGAAAAAA
Lmu04        CATACGATGG TATC--CATA C-------TT TTAGTTCTTG ATAAATCTTT GTGCTTTCCA AATGCTTGTT TTATTTCCCA -------TGA AAAGAAAAAA
Lmu05        CATACGATGG TATC--CATA C-------TT TTAGTTCTTG ATAAATCTTT GTGCTTTCCA AATGCTTGTT TTATTTCCCA -------TGA AAAGAAAAAA
Lmu06        CATACGATGG TATC--CATA C-------TT TTAGTTCTTG ATAAATCTTT GTGCTTTCCA AATGCTTGTT TTATTTCCCA -------TGA AAAGAAAAAA
Lmu07        CATACGATGG TATC--CATA C-------TT TTAGTTCTTG ATAAATCTTT GTGCTTTCCA AATGCTTGTT TTATTTCCCA -------TGA AAAGAAAAAA
Lmu08        CATACGATGG TATC--CATA C-------TT TTAGTTCTTG ATAAATCTTT GTGCTTTCCA AATGCTTGTT TTATTTCCCA -------TGA AAAGAAAAAA
Lmu09        CATACGATGG TATC--CATA C-------TT TTAGTTCTTG ATAAATCTTT GTGCTTTCCA AATGCTTGTT TTATTTCCCA -------TGA AAAGAAAAAA
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Mpa01         CATACGATGG TGTC--CATA C-------TT TTAGTTCTTG ATAAATCTTT GTGCTCTCCA AATGCTTGTT TTATTTCCCA -------TGA AAAGAAAAAA
Mpa02         CATACGATGG TATC--CATA C-------TT TTAGTTCTTG ATAAATCTTT GTGCTTTCCA AATGCTTGTT TTATTTCCCA -------TGA AAAGAAAAAA
Mpa03         CATACGATGG TATC--CATA C-------TT TTAGTTCTTG ATAAATCTTT GTGCTTTCCA AATGCTTGTT TTATTTCCCA -------TGA AAAGAAAAAA
Mpa04         CATACGATGG TATC--CATA C-------TT TTAGTTCTTG ATAAATCTTT GTGCTTTCCA AATGCTTGTT TTATTTCCCA -------TGA AAAGAAAAAA
Mpa05         CATACGATGG TATC--CATA C-------TT TTAGTTCTTG ATAAATCTTT GTGCTTTCCA AATGCTTGTT TTATTTCCCA -------TGA AAAGAAAAAA
Mpa06         CATACGATGG TATC--CATA C-------TT TTAGTTCTTG ATAAATCTTT GTGCTTTCCA AATGCTTGTT TTATTTCCCA -------TGA AAAGAAAAAA
Mve01         CATACGATGG TATC--CATA C-------TT TTAGTTCTTG ATAAATCTTT GTGCTTTCCA AATGCTTGTT TTATTTCCCA -------TGA AAAGAAAAAA
Mve02         CATACGATGG TATC--CATA C-------TT TTAGTTCTTG ATAAATCTTT GTGCTTTCCA AATGCTTGTT TTATTTCCCA -------TGA AAAGAAAAAA
Mve03         CATACGATGG TATC--CATA C-------TT TTAGTTCTTG ATAAATCTTT GTGCTTTCCA AATGCTTGTT TTATTTCCCA -------TGA AAAGAAAAAA
Mni01         CATACGATGG TATG--CATA C-------TT TTAGTTCTTG ATAAATCTTT GTGCTTTCCA GATGCTTGTT TTATTTCCCA -------TGA AAAGAAAAAA
Mni02         CATACGATGG TATG--CATA C-------TT TTAGTTCTTG ATAAATCTTT GTGCTTTCCA GATGCTTGTT TTATTTCCCA -------TGA AAAGAAAAAA
Mni03         CATACGATGG TATG--CATA C-------TT TTAGTTCTTG ATAAATCTTT GTGCTTTCCA GATGCTTGTT TTATTTCCCA -------TGA AAAGAAAAAA
Mni04         CATACGATGG TATG--CATA C-------TT TTAGTTCTTG ATAAATCTTT GTGCTTTCCA GATGCTTGTT TTATTTCCCA -------TGA AAAGAAAAAA
Mni05         CATACGATGG TATG--CATA C-------TT TTAGTTCTTG ATAAATCTTT GTGCTTTCCA GATGCTTGTT TTATTTCCCA -------TGA AAAGAAAAAA
Mni06         CATACGATGG TATG--CATA C-------TT TTAGTTCTTG ATAAATCTTT GTGCTTTCCA GATGCTTGTT TTATTTCCCA -------TGA AAAGAAAAAA
Mne01         CATACGATGG TATG--CATA C-------TT TTAGTTCTTG ATAAATCTTT GTGCTTTCCA AATGCTTGTT TTATTTCCCA -------TGA AAAGAAAAAA
Aof01         CATACGATGG TATG--TATA C-------TT TTAGTTCTTG ATAAATCTTT GTGCTTTCCA AATGCTTGTT TGATTTCCCA -------TGA AAAGAAAAA-
Aca01         CATACGATGG TATG--TATA C-------TT TTAGTTCTTG ATAAATCTTT GTGCTTTCCA AATGCTTGTT TGATTTCCCA -------TGA AAAGAAAAA-
Aca02         CATACGATGG TATG--TATA C-------TT TTTGTTCTTG ATAAATCTTT GTGCTTTCCA AATGCTTGTT TGATTTCCCA -------TGA AAAGAAAAA-
Ani40         CATACGATGG TATG--TATA C-------TT TTAGTTCTTG ATAAATCTTT GTGTTTTCCA AATGCTTGTT TGATTTCCCA -------TGA AAAGAAAAA-


              ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     210        220        230        240        250        260        270        280        290        300
Lmo01         ---------- ---------- ---------- ---------- -ACTGCTTAG ACTGACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
Lmo02         ---------- ---------- ---------- ---------- -ACTGCTTAG ACTGACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
Lmo03         ---------- ---------- ---------- ---------- -ACTGCTTAG ACTGACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
Lmo04         ---------- ---------- ---------- ---------- -ACTGCTTAG ACTGACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
Lmo05         ---------- ---------- ---------- ---------- -ACTGCTTAG ACTGACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
Lmo06         ---------- ---------- ---------- ---------- -ACTGCTTAG ACTGACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
Lmo07         ---------- ---------- ---------- ---------- -ACTGCTTAG ACTGACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
Lmo08         ---------- ---------- ---------- ---------- -ACTGCTTAG ACTGACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
Lmo09         ---------- ---------- ---------- ---------- -ACTGCTTAG ACTGACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
Lmo10         ---------- ---------- ---------- ---------- -ACTGCTTAG ACTGACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
Lmo11         ---------- ---------- ---------- ---------- -ACTGCTTAG ACTGACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
Lmo12         ---------- ---------- ---------- ---------- -ACTGCTTAG ACTGACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
Lmo13         ---------- ---------- ---------- ---------- -ACTGCTTAG ACTGACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
Lti01         ---------- ---------A TGGACTGCTT AA-------- -AATGCTTAG ATTGACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
Lti02         ---------- ---------A TGGACTGCTT AA-------- -AATGCTTAG ATTGACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
Lti03         ---------- ---------A TGGACTGCTT AA-------- -AATGCTTAG ATTGACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
Lti04         ---------- ---------A TGGACTGCTT AA-------- -AATGCTTAG ATTGACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
Lti05         ---------- ---------A TGGACTGCTT AA-------- -AATGCTTAG ATAGACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
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Lti06            ---------- ---------A TGGACTGCTT AA-------- -AATGCTTAG ATTGACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
Lti07            ---------- ---------A TGGACTGCTT AA-------- -AATGCTTAG ATTGACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
Lti08            ---------- ---------A TGGACTGCTT AA-------- -AATGCTTAG ATTGACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
Lti09            ---------- ---------A TGGACTGCTT AA-------- -AATGCTTAG ATTGACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
Mhi01            AAAA-TGATA -GATATGTGG TGAACTGCTT AA-------- -ACTGCTTAG ACTGACCACT TTGAACTCCT CCAGAGAACC TGTTGGACGA TGTCGAAAAG
Mhi02            AAAA-TGATA -GATATGTGG TGAACTGCTT AA-------- -ACTGCTTAG ACTGACCACT TTGAACTCCT CCAGAGAACC TGTTGGACGA TGTCGAAAAG
Mhi03            AAAA-TGATA -GATATGTGG TGAACTGCTT AA-------- -ACTGCTTAG ACTGACCACT TTGAACTCCT CCAGAGAACC TGTTGGACGA TGTCGAAAAG
Mhi04            AAAA-TGATA -GATATGTGG TGAACTGCTT AA-------- -ACTGCTTAG ACTGACCACT TTGAACTCCT CCAGAGAACC TGTTGGACGA TGTCGAAAAG
Mhi05            AAAA-TGATA -GATATGTGG TGAACTGCTT AA-------- -ACTGCTTAG ACTGACCACT TTGAACCCCT CCAGAGAACC TGTTGGACGA TGTCGAAAAG
Mhi06            AAAA-TGATA -GATATGTGG TGAACTGCTT AA-------- -ACTGCTTAG ACTGACCACT TTGAACTCCT CCAGAGAACC TGTTGGACGA TGTCGAAAAG
Mhi07            AAAA-TGATA -GATATGTGG TGAACTGCTT AA-------- -ACTGCTTAG ACTGACCACT TTGAACTCCT CCAGAGAACC TGTTGGACGA TGTCGAAAAG
Lth01            ---------- -GAGATGTGG TGAACTGCTT AA-------- -ACTGCTTAG ACTGACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
Lth02            ---------- -GAGATGTGG TGAACTGCTT AA-------- -ACTGCTTAG ACTGACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
Lth03            ---------- -GAGATGTGG TGAACTGCTT AA-------- -ACTGCTTAG ACTGACCACT TTGAACTTCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
Lth04            ---------- -GAGATGTGG TGAACTGCTT AA-------- -ACTGCTTAG ACTGACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
Lth05            ---------- -GAGATGTGG TGAACTGCTT AA-------- -ACTGCTTAG ACTGACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
Lth06            ---------- -GAGATGTGG TGAACTGCTT AA-------- -ACTGCTTAG ACTGACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
Lth07            ---------- -GAGATGTGG TGAACTGCTT AA-------- -ACTGCTTAG ACTGACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
Lth08            ---------- -GAGATGTGG TGAACTGCTT AA-------- -ACTGCTTAG ACTGACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
Lth09            ---------- -GAGATGTGG TGAACTGCTT AA-------- -ACTGCTTAG ACTGACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
Lth10            ---------- -GAGATGTGG TGAACTGCTT AA-------- -ACTGCTTAG ACTGACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
Lth11            ---------- -GAGATGTGG TGAACTGCTT AA-------- -ACTGCTTAG ACTGACCACT TTGAACTTCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
Lth12            ---------- -GAGATGTGG TGAACTGCTT AA-------- -ACTGCTTAG ACTGACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
Lth13            ---------- -GAGATGTGG TGAACTGCTT AA-------- -ACTGCTTAG ACTGACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
Mal01            ---------- -GAGATGTGG TGAACTGCTT AA-------- -ACTGCTTAG ACTGACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
Mal02            ---------- -GAGATGTGG TGAACTGCTT AA-------- -ACTGCTTAG ACTGACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
Mal03            ---------- -GAGATGTGG TGAACTGCTT AA-------- -ACTGCTTAG ACTGACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
Mal04            ---------- -GAGATGTGG TGAACTGCTT AA-------- -ACTGCTTAG ACTGACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
Mal05            ---------- -GAGATGTGG TGAACTGCTT AA-------- -ACTGCTTAG ACTGACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
Mal06            ---------- -GAGATGTGG TGAACTGCTT AA-------- -ACTGCTTAG ACTGACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
Mal07            ---------- -GAGATGTGG TGAACTGCTT AA-------- -ACTGCTTAG ACTGACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
Mal08            ---------- -GAGATGTGG TGAACTGCTT AA-------- -ACTGCTTAG ACTGACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
Mal09            AAA---GATA AGTGATGTAG TGAACTGCTT GA-------- -ACTGCTTAG ACTCACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
Ltr01            A-----GATA -GAGATTTAG TGAACTGTTT AA-------- -ACTGCTTAG ACTGACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
Ltr02            A-----GATA -GAGATTTAG TGAACTGTTT AA-------- -ACTGCTTAG ACTGACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
Ltr03            A-----GATA -GAGATTTAG TGAACTGTTT AA-------- -ACTGCTTAG ACTGACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAGG
Ltr04            ------GATA -GAGATTTAG TGAACTGTTT AA-------- -ACTGCTTAG ACTGACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
Ltr05            ------GATA -GAGATTTAG TGAACTGTTT AA-------- -ACTGCTTAG ACTGACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
Ltr06            ------GATA -GAGATTTAG TGAACTGTTT AA-------- -ACTGCTTAG ACTGACCACT TTGAACTCCT TCAGAGAACC TGTTGGGCGA TGTCGAAAAG
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Lag01            ------GATA -GAGATTTAA TGAACTGTTT AA-------- -ACTGCTTAG ACTGACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
Lag02            ------GATA -GAGATTTAA TGAACTGTTT AA-------- -ACTGCTTAG ACTGACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
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Lag03          ------GATA -GAGATTTAA TGAACTGTTT AA-------- -ACTGCTTAG ACTGACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
Lag04          ------GATA -GAGATTTAA TGAACTGTTT AA-------- -ACTGCTTAG ACTGACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
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Lfl02          ------GATA -GAGATTTAG TGAACTGTTT AA-------- -ACTGCTTAG ACTGACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
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Lob01          ------GATA -GAGATGTAG TGAACTGTTT AA-------- -ACTTCTTAG ACTGACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
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Mto03          AAAAAAGATA AGTGATGTAG TGAACTGCTT AA-------- -ACTGCTTAG ACTCACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
Mto04          AAAAA-GATA AGTGATGTAG TGAACTGCTT AA-------- -ACTGCTTAG ACTCACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
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Mto05      AAAAA-GATA AGTGATGTAG TGAACTGCTT AA-------- -ACTGCTTAG ACTCACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
Mto06      AAAAA-GATA AGTGATGTAG TGAACTGCTT AA-------- -ACTGCTTAG ACTCACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
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Ahi08      ---------- ---------- ---------- ---------- ---------G ATTGACCACT TTGAACTCCT TCAGAGAACC TGTTAGACGA TGTCGAAAAG
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Alo02      ------GATA -GATATGTAG TGA------- ---------- -ACTGCTTAG ACTAACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
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Mca03      ---------- ---------- ---------- ---------- ---------- ---GACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
Mca04      ---------- ---------- ---------- ---------- ---------- ---GACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
Mtf01      ---------- ---------- ---------- --------TA AACTTCTTAG ACTGACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
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Mtf04      ---------- ---------- ---------- ---------A AACTTCTTAG ACTGACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
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Las03      ------AATA -GAGATGTAG TGA------- ---------- -ACTGCTTAG ACTGACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
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Las08       ------GATA -GAGATGTAG TGAACTGCTT AAACTGCTTA GACTGCTTAG ACTGACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
Lpe01       ------GATA -GAGATGTAG TGAACTGCTT AAACTGCTTA GACTGCTTAG ACTGACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGG TGTCGAAAAG
Lpe02       ------GATA -GAGATGTAG TGAACTGCTT AAACTGCTTA GACTGCTTAG ACTGACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
Lpe03       ------GATA -GAGATGTAG TGAACTGCTT AG-------- -ACTGCTTAG ACTGACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
Lpe04       ------AATA -GAGATGTAG TGA------- ---------- -ACTGCTTAG ACTGACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
Lac01       -----CGATA -GACATGTAG TGAACTGCTT AA-------- -ACTGCTTAG ACTGACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
Lac02       -----CGATA -GACATGTAG TGAACTGCTT AA-------- -ACTGCTTAG ACTGACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
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Lac06       -----CGATA -GACATGTAG TGAACTGCTT AA-------- -ACTGCTTAG ACTGACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
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Msy04       ------GATA -GAGATGTAG TGATCTGCTT AAGCTGCTTA GACTGCTTAG ACTGACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
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Mpa01       ------GATA -GAGATGTAG TGAACTGCTT AAACTGCTTA GACTGCTTAG ACTGACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
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Mpa03       ------GATA -GAGATGTAG TGAACTGCTT AAACTGCTTA GACTGCTTAG ACTGACCACT TTGAACTCCT TCAGAGAACC TGTTGGACGA TGTCGAAAAG
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                     310        320        330        340        350        360        370        380        390        400
Lmo01         GCATCAGGCG AACAATCCAT GATGGCTGCA CATTCGAACA AGTCTCAGGT ACTGTTTT-- ---------C GAAAGGTTTT TAGTTATGAT T-AAAGATC-
Lmo02         GCATCTGGCG AACAATCCAT GATGGCTGCA CATTCGAACA AGTCTCAGGT ACTGTTTT-- ---------C GAAAGGTTTT TAGTTATGAT T-AAAGATC-
Lmo03         GCATCAGGCG AACAATCCAT GATGGCTGCA CATTCGAACA AGTCTCAGGT ACTGTTTT-- ---------C GAAAGGTTTT TAGTTATGAT T-AAAGATC-
Lmo04         GCATCAGGCG AACAATCCAT GATGGCTGCA CATTCGAACA AGTCTCAGGT ACTGTTTT-- ---------C GAAAGGTTTT TAGTTATGAT T-AAAGATC-
Lmo05         GCATCAGGCG AACAATCCAT GATGGCTGCA CATTCGAACA AGTCTCAGGT ACTGTTTT-- ---------C GAAAGGTTTT TAGTTATGAT T-AAAGATC-
Lmo06         GCATCAGGCG AACAATCCAT GATGGCTGCA CATTCGAACA AGTCTCAGGT ACTGTTTT-- ---------C GAAAGGTTTT TAGTTATGAT T-AAAGATC-
Lmo07         GCATCAGGCG AACAATCCAT GATGGCTGCA CATTCGAACA AGTCTCAGGT ACTGTTTT-- ---------C GAAAGGTTTT TAGTTATGAT T-AAAGATC-
Lmo08         GCATCTGGCG AACAATCCAT GATGGCTGCA CATTCGAACA AGTCTCAGGT ACTGTTTT-- ---------C GAAAGGTTTT TAGTTATGAT T-AAAGATC-
Lmo09         GCATCTGGCG AACAATCCAT GATGGCTGCA CATTCGAACA AGTCTCAGGT ACTGTTTT-- ---------C GAAAGGTTTT TAGTTATGAT T-AAAGATC-
Lmo10         GCATCAGGCG AACAATCCAT GATGGCTGCA CATTCGAACA AGTCTCAGGT ACTGTTTT-- ---------C GAAAGGTTTT TAGTTATGAT T-AAAGATC-
Lmo11         GCATCAGGCG AACAATCCAT GATGGCTGCA CATTCGAACA AGTCTCAGGT ACTGTTTT-- ---------C GAAAGGTTTT TAGTTATGAT T-AAAGATC-
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Lmo13         GCATCAGGCG AACAATCCAT GATGGCTGCA CATTCGAACA AGTCTCAGGT ACTGTTTT-- ---------C GAAAGGTTTT TAGTTATGAT T-AAAGATC-
Lti01         GCATCTGGCG AACAATCCAT GATGGCTGCA CATTCGAATA AGTCTCAGGT ACTGTTTT-- ---------C GAAAGGTTTT TAGTTATGAT T-AAAGATC-
Lti02         GCATCTGGCG AACAATCCAT GATGGCTGCA CATTCGAATA AGTCTCAGGT ACTGTTTT-- ---------C GAAAGGTTTT TAGTTATGAT T-AAAGATC-
Lti03         GCATCTGGCG AACAATCCAT GACGGCTGCA CATTCGAATA AGTCTCAGGT ACTGTTTT-- ---------C GAAAGGTTTT TAGTTATGAT T-AAAGATC-
Lti04         GCATCTGGCG AACAATCCAT GATGGCTGCA CATTCGAATA AGTCTCAGGT ACTGTTTT-- ---------C GAAAGGTTTT TAGTTATGAT T-AAAGATC-
Lti05         GCATCTGGCG AACAATCCAT GATGGCTGCA CATTCGAATA AGTCTCAGGT ACTGTTTT-- ---------C GAAAGGTTTT TAGTTATGAT T-AAAGATC-
Lti06         GCATCTGGCG AACAATCCAT GATGGCTGCA CATTCGAATA AGTCTCAGGT ACTGTTTT-- ---------C GAAAGGTTTT TAGTTATGAT T-AAAGATC-
Lti07         GCATCTGGCG AACAATCCAT GATGGCTGCA CATTCGAATA AGTCTCAGGT ACTGTTTT-- ---------C GAAAGGTTTT TAGTTATGAT T-AAAGATC-
Lti08         GCATCTGGCG AACAATCCAT GATGGCTGCA CATTCGAATA AGTCTCAGGT ACTGTTTT-- ---------C GAAAGGTTTT TAGTTATGAT T-AAAGATC-
Lti09         GCATCTGGCG AACAATCCAT GATGGCTGCA CATTCGAATA AGTCTCAGGT ACTGTTTT-- ---------C GAAAGGTTTT TAGTTATGAT T-AAAGATC-
Mhi01         GCATCAGTCG AACAATCCAT GATGGCTGCA CATTCGAATA AGTCTCAGGT ACTGTTTT-- ---------C GAAAGGTTTT TAGTTATGCT T-AAAGATC-
Mhi02         GCATCAGTCG AACAATCCAT GATGGCTGCA CATTCGAATA AGTCTCAGGT ACTGTTTT-- ---------C GAAAGGTTTT TAGTTATGCT T-AAAGATC-
Mhi03         GCATCAGTCG AACAATCCAT GATGGCTGCA CATTCGAATA AGTCTCAGGT ACTGTTTT-- ---------C GAAAGGTTTT TAGTTATGCT T-AAAGATC-
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Mhi06         GCATCAGTCG AACAATCCAT GATGGCTGCA CATTCGAATA AGTCTCAGGT ACTGTTTT-- ---------C GAAAGGTTTT TAGTTATGCT T-AAAGATC-
Mhi07         GCATCAGTCG AACAATCCAT GATGGCTGCA CATTCGAATA AGTCTCAGGT ACTGTTTT-- ---------C GAAAGGTTTT TAGTTATGCT T-AAAGATC-
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Lth02     GCATCTGGCG AACAATCCAT GATGGCTGCA CATTCGAATA AGTCTCAGGT ACTGTTTTT- ---------- GAAAGGTTTT TAGTTATGAT T-AAAGATC-
Lth03     GCATCTGGCG AACAATCCAT GATGGCTGCA CATTCGAGTA AGTCTCAGGT ACTGTTTTT- ---------- GAAAGGTTTT TAGTTATGAT T-AAAGATC-
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Mto07        GCGTCCATCG AACAATCCAC GATGGCTGCA CACTCGAATA AGTCCCAGGT AC-------- ---------- ---------- ---------- ----------
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Ahi02        GCATCTGGCG AACAATCCAC GATGGCTGCA CATTCGAATA AGTCTCAGGT ACTGTTT--- --------CT GAAAGGTTTT TAGTTATGAT T-AAAGATC-
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Ahi07        GCATCTGGCG AACAATCCAC GATGGCTGCA CATTCGAATA AGTCTCAGGT ACTGTTT--- --------CT GAAAGGTTTT TAGTTATGAT T-AAAGATC-
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Alo04      GCATCTGGCG AACAATCCAC GATGGTTGCA CATTCGAATA AGTCTCAGGT ACTGTTTTTT TGCTGTT--- ---------- ------TGTT T---------
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Alo07      GCATCTGGCG AACAATCCAC GATGGTTGCG CATTCGAATA AGTCTCAGGT ACTGTTTTTT TGCTGTT--- ---------- ------TGTT T---------
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Mpa06        GCATCTGGTG AACAATCCAT GATGGCTGCA CATTCGAATA AGTCTCAGGT A--------- ---------- ---------- ------TGAT T-AAAGATC-
Mve01        GCATCTGGTG AACAATCCAT GATGGCTGCA CATTCGAATA AGTCTCAGGT A--------- ---------- ---------- ------TGAT T-AAAGATC-
Mve02        GCATCTGGTG AACAATCCAT GATGGCTGCA CATTCGAATA AGTCTCAGGT A--------- ---------- ---------- ------TGGT T-AAAGATC-
Mve03        GCATCTGGTG AACAATCCAT GATGGCTGCA CATTCGAATA AGTCTCAGGT A--------- ---------- ---------- ------TGGT T-AAAGATC-
Mni01        GCATCTGGCG AACAATCCAT GATGGCTGCA CAATCGAATA AGTCTCAGGT A--------- ---------- ---------- ------TGAT T-AAAGATC-
Mni02        GCATCTGGCG AACAATCCAT GATGGCTGCA CAATCGAATA AGTCTCAGGT A--------- ---------- ---------- ------TGAT T-AAAGATC-
Mni03        GCATCTGGCG AACAATCCAT GATGGCTGCA CAATCGAATA AGTCTCAGGT A--------- ---------- ---------- ------GGAT T-AAAGATC-
Mni04        GCATCTGGCG AACAATCCAT GATGGCTGCA CAATCGAATA AGTCTCAGGT A--------- ---------- ---------- ------TGAT T-AAAGATC-
Mni05        GCATCTGGCG AACAATCCAT GATGGCTGCA CAATCGAATA AGTCTCAGGT A--------- ---------- ---------- ------TGAT T-AAAGATC-
Mni06        GCATCTGGCG AACAATCCAT GATGGCTGCA CAATCGAATA AGTCTCAGGT A--------- ---------- ---------- ------TGAT T-AAAGATC-
Mne01        GCATCTGGCG AACAATCCAT GATGGCTGCA CAATCGAATA AGTCTCAGGT A--------- ---------- ---------- ------TGAT T-AAAGATC-
Aof01        GCATCCGGTG AACAATCCAT GATGGCTGCA CATTCGAATA AGTCCCAGGT ACTGTTTTTT -GCTGTCTTT GGAAGGTTTT TAGTTATGAT T-AAAGATC-
Aca01        GCATCCGGTG AACAATCCAT GATAGCTGCA CATTCGAATA AGTCCCAGGT ACTGTTTTTT -GCTGTCTTT GGAAGGGTTT TAGTTATGAT T-AAAGATC-
Aca02        GCATCCGGTG AACAATCCAT GATGGCTGCA CATTCGAATA AGTCCCAGGT ACTGTTTTTT -GCTGTCTTT GGAAGGTTTT TAGTTATGAT T-AAAGATC-
Ani40        GCATCCGGCG AGCAATCCAT GATGGCTGCA CATTCGAATA AGTCCCAGGT ACTGTTTTTT -GCTGTCTTT GAAAGGTTTT TAATTATGAT T-AAAGATC-
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                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                       410        420        430        440        450        460        470        480        490        500
Lmo01           ATTAGTGTTT -AGAGATTGA GAGCTCTT-- --TGTTATTC GTGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Lmo02           ATTAGTGTTT -AGAGATTGA GAGCTCTT-- --TGTTATTC GTGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Lmo03           ATTAGTGTTT -AGAGATTGA GAGCTCTT-- --TGTTATTC GTGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Lmo04           ATTAGTGTTT -AGAGATTGA GAGCTCTT-- --TGTTATTC GTGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Lmo05           ATTAGTGTTT -AGAGATTGA GAGCTCTT-- --TGTTATTC GTGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Lmo06           ATTAGTGTTT -AGAGATTGA GAGCTCTT-- --TGTTATTC GTGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Lmo07           ATTAGTGTTT -AGAGATTGA GAGCTCTT-- --TGTTATTC GTGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Lmo08           ATTAGTGTTT -AGAGATTGA GAGCTCTT-- --TGTTATTC GTGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Lmo09           ATTAGTGTTT -AGAGATTGA GAGCTCTT-- --TGTTATTC GTGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Lmo10           ATTAGTGTTT -AGAGATTGA GAGCTCTT-- --TGTTATTC GTGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Lmo11           ATTAGTGTTT -AGAGATTGA GAGCTCTT-- --TGTTATTC GTGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Lmo12           ATTAGTGTTT -AGAGATTGA GAGCTCTT-- --TGTTATTC GTGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Lmo13           ATTAGTGTTT -AGAGATTGA GAGCTCTT-- --TGTTATTC GTGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Lti01           ATTAGTGTTT TAGAGATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Lti02           ATTAGTGTTT TAGAGATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Lti03           ATTAGTGTTT TAGAGATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Lti04           ATTAGTGTTT TAGAGATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Lti05           ATTAGTGTTT TAGAGATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Lti06           ATTAGTGTTT TAGAGATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Lti07           ATTAGTGTTT TAGAGATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Lti08           ATTAGTGTTT TAGAGATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Lti09           ATTAGTGTTT TAGAGATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Mhi01           ATTAGTGTTT -AGAAATTGA GAGCTCTC-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Mhi02           ATTAGTGTTT -AGAAATTGA GAGCTCTC-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Mhi03           ATTAGTGTTT -AGAAATTGA GAGCTCTC-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Mhi04           ATTAGTGTTT -AGAAATTGA GAGCTCTC-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Mhi05           ATTAGTGTTT -AGAAATTGA GAGCTCTC-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Mhi06           ATTAGTGTTT -AGAAATTGA GAGCTCTC-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Mhi07           ATTAGTGTTT -AGAAATTGA GAGCTCTC-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Lth01           ATTAGTGTTT -AGAAATTGA GAGTTACT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Lth02           ATTAGTGTTT -AGAAATCGA GAGTTACT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Lth03           ATTAGTGTTT -AGAAATTGA GAGTTACT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Lth04           ATTAGTGTTT -AGAAATTGA GAGTTACT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Lth05           ATTAGTGTTT -AGAAATTGA GAGTTACT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Lth06           ATTAGTGTTT -AGAAATTGA GAGTTACT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Lth07           ATTAGTGTTT -AGAAATTGA GAGTTACT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Lth08           ATTAGTGTTT -AGAAATCGA GAGTTACT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Lth09           ATTAGTGTTT -AGAAATCGA GAGTTACT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Lth10           ATTAGTGTTT -AGAAATTGA GAGTTACT-- --TGTTATTC ATGTTGGTTT T--ACACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
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Lth11         ATTAGTGTTT -AGAAATTGA GAGTTACT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Lth12         ATTAGTGTTT -AGAAATTGA GAGTTACT-- --TGTTATTC ATGTTGGTTT ---ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Lth13         ATTAGTGTTT -AGAAATTGA GAGTTACT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Mal01         ATTAGTGTTT -AGAAATTGA GAGTTACT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Mal02         ATTAGTGTTT -AGAAATTGA GAGTTACT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Mal03         ATTAGTGTTT -AGAAATTGA GAGTTACT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Mal04         ATTAGTGTTT -AGAAATTGA GAGTTACT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Mal05         ATTAGTGTTT -AGAAATTGA GAGTTACT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGCGTCTAC
Mal06         ATTAGTGTTT -AGAAATTGA GAGTTACT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Mal07         ATTAGTGTTT -AGAAATTGA GAGTTACT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Mal08         ATTAGTGTTT -AGAAATTGA GAGTTACT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Mal09         ATTAGTGTTT -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTCGGTTC T--ATACAGG ATGTTGGAGT TCATGCAAGA CATACCAGCA GTGTGTCTAC
Ltr01         ATTAGTGTCT -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Ltr02         ATTAGTGTCT -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Ltr03         ATTAGTGTCT -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Ltr04         ATTAGTGTCT -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Ltr05         ATTAGTGTCT -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Ltr06         ATTAGTGTCT -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Ltr07         ATTAGTGTCT -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Lag01         ATTAGTGTCT -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Lag02         ATTAGTGTCT -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Lag03         ATTAGTGTCT -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Lag04         ATTAGTGTCT -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Lag05         ATTAGTGTCT -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Lfl01         ATTAGTGTCT -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Lfl02         ATTAGTGTCT -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCACGCAAGA CATATCAGCA GTGTGTCTAC
Ltp01         ATTAGTGTCT -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Lbr01         ATTAGTGTCT -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--ATAAAGG ATGTTGGAGT TCATGGAAGA CATATCAGCA GTGTGTCTAC
Lbr02         ATTAGTGTCT -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--ATAAAGG ATGTTGGAGT TCATGGAAGA CATATCAGCA GTGTGTCTAC
Lbr03         ATTAGTGTCT -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGGAAGA CATATCAGCA GTGTGTCTAC
Lob01         ATTAGTGTCT -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Lob02         ATTAGTGTCT -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Lob03         ATTAGTGTCT -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTCGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Lob04         ATTAGTGTCT -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Lob05         ATTAGTGTCT -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Lob06         ATTAGTGTCT -AGAAATTGA GAGCTCTT-- --TGTTAT-C ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Lob07         ATTAGTGTCT -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Lol01         ATTAGTGTCT -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCGAGA CATATCAGCA GTGTGTCTAC
Lol02         ATTAGTGTCT -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Lol03         ATTAGTGTCT -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Lol04         ATTAGTGTCT -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Mae01         ATTAGCGTTT -AGAAGTTGA GAGCTCTTTG TTTGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
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Mae02        ATTAGCGTTT -AGAAGTTGA GAGCTCTTTG TTTGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Mae03        ATTAGCGTTT -AGAAGTTGA GAGCTCTTTG TTTGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Mae04        ATTAGCGTTT -AGAAGTTGA GAGCTCTTTG TTTGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Mae05        ATTAGCGTTT -AGAAGTTGA GAGCTCTTTG TTTGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Mae06        ATTAGCGTTT -AGAAGTTGA GAGCTCTTTG TTTGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Mae07        ATTAGCGTTT -AGAAGTTGA GAGCTCTTTG TTTGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Mae08        ATTAGCGTTT -AGAAGTTGA GAGCTCTTTG TTTGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Mmo01        ATTAGTGTTT -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTCGGTTC T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Mmo02        ATTAGTGTTT -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTCGGTTC T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Mmo03        ATTAGTGTTT -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTCGGTTC T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Mmo04        ATTAGTGTTT -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTCGGTTC T--ATACAGG ATGTTGGAGT TCATGCAAGG CATATCAGCA GTGTGTCTAC
Mmo05        ATTAGTGTTT -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTCGGTTC T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
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Mmo07        ATTAGTGTTT -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTCGGTTC T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Mmo08        ATTAGTGTTT -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTCGGTTC T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Mmo09        ATTAGTGTTT -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTCGGTTC T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Mmo10        ATTAGTGTTT -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTCGGTTC T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Mto01        ATTAGTGTTT -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTCGGTTC T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCACCA TTGTGTCTAC
Mto02        ATTAGTGTTT -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTCGGTTC T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCACCA TTGTGTCTAC
Mto03        ATTAGTGTTT -AGAAATTGA GAGCTCTT-- --TGTTATTC ACGTCGGTTC T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Mto04        ATTAGTGTTT -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTCGGTTC T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Mto05        ATTAGTGTTT -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTCGGTTC T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
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Mto07        ---------- ---------- ---------- ---------- ---------- -------AGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Ahi01        ATTAGTGTTT -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
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Ahi03        ATTAGTGTTT -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Ahi04        ATTAGTGTTT -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Ahi05        ATTCGTGTTT -ATAAATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
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Ahi07        ATTAGTGTTT -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Ahi08        ATTCGTGTTT -ATAAATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Alo01        ---------- -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--GTACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Alo02        ---------- -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--GTACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Alo03        ---------- -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--GTACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Alo04        ---------- -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--GTACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Alo05        ---------- -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--GTACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Alo06        ---------- -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--GTACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Alo07        ---------- -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--GTACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Alo08        ---------- -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--GTACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Alo09        ---------- -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--GTACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Alo10        ---------- -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--GTACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
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Mca01        ATTCGTGTTT -AGAAATTGA GACCTCTT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Mca02        ATTAGTGTTT -AGAAATTGA GACCTCTT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCACCA GTGTGTCTAC
Mca03        ATTAGTGTTT -AGAAATTGA GACCTCTT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Mca04        ATTCGTGTTT -AGAAATTGA GACCTCTT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Mtf01        ---------- ---------- ---------- ---------C ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Mtf02        ---------- ---------- ---------- ---------C ATGTTGGTTT TT-ATACAGG ATGTTGGAGT TCGTGCAAGA CATATCAGCA GTGTGTCTAC
Mtf03        ---------- ---------- ---------- --------TC ATGTTGGTTT TT-ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Mtf04        ---------- ---------- ---------- --------TC ATGTTGGTTT TT-ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Mtf05        -TTAGTGTTT -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT TTTATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Mma01        ---------- ---------- ---------- ---------C ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Mma02        ---------- ---------- ---------- ---------C ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Mma03        ---------- ---------- ---------- ---------C ATGTTGGTTT T--ATACGGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Mma04        ---------- ---------- ---------- ---------C ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Mma05        ---------- ---------- ---------- ---------C ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Las01        ATTAGTGTTT -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
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Lpe03        ATTAGTGTTT -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT ---ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Lpe04        ATTAGTGTTT -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Lac01        ATTAGTGTTT -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--ATTCAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Lac02        ATTAGTGTTT -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Lac03        ATTAGTGTTT -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
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Msy04        ATTAGCGTTT -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATGAGCA GTGTGTCTAC
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Lmu03       ATTAGTGTTT -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
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Mpa01       ATTAGTGTTT -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
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Mpa03       ATTAGTGTTT -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Mpa04       ATTAGTGTTT -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Mpa05       ATTAGTGTTT -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Mpa06       ATTAGTGTTT -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Mve01       ATTAGTGTTT -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Mve02       ATTAGTGTTT -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
Mve03       ATTAGTGTTT -AGAAATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
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Aca02       ACTAGTGTTT -AGAGATTGA GAGCTCTT-- --TGTTATTC ATGTTGGTTT T--ATACAGG ATGTTGGAGT TCATGCAAGA CATATCAGCA GTGTGTCTAC
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                   510        520        530        540        550        560        570        580        590        600
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Lmo08       ATTGGATAGT GGTATGTAAT AATCTCAATT TATATTTCTT CAATGTTCCT TCAAGAAAGA AAAATAATTA ATTCTAGAGA TCTAATTG-T CTGGTTTGAT
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Lth13        ATTGGATAGT GGTATGTAAT AATATCAATT TTTCTTTCTT CAATGTTCCT TCAAGAAAGA AAAAA--TCA ATTCTAGATA TCTAATAG-T ATGGTTTGAT
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Mal02        ATTGGATAGT GGTATGTAAT AATATCAATT TTTCTTTCTT CAATGTTCCT TCAAGAAAGA AAAAA--TCA ATTCTAGATA TCTAATAG-T ATGGTTTGAT
Mal03        ATTGGATAGT GGTATGTAAT AATATCAATT TTTCTTTCTT CAATGTTCCT TCAAGAAAGA AAAAA--TCA ATTCTAGATA TCTAATAG-T ATGGTTTGAT
Mal04        ATTGGATAGT GGTATGTAAT AATATCAATT TTTCTTTCTT CAATGTTCCT TCAAGAAAGA AAAAA--TCA ATTCTAGATA TCTAATAG-T ATGGTTTGAT
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Mal07        ATTGGATAGT GGTATGTAAT AATATCAATT TTTCTTTCTT CAATGTTCCT TCAAGAAAGA AAAAA--TCA ATTCTAGATA TCTAATAG-T ATGGTTTGAT
Mal08        ATTGGATAGT GGTATGTAAT AATATCAATT TTTCTTTCTT CAATGTTCCT TCAAGAAAGA AAAAA--TCA ATTCTAGATA TCTAATAG-T ATGGTTTGAT
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Ltr03        ATTGGATAGT GGTATGTAAC AATATCAATT -ATCTTTCTT CAATGACCCT TCAAGAAAAA AATA---TCA ATTCTAGAGA ACTAATTG-T CTGGTTCGAT
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Ltr06        ATTGGATAGT GGTATGTAAC AATATCAATT -ATCTTCCTT CAATGACCCT TCAAGAAAAA AATA---TCA ATTCTAGAGA TCTAATTG-T CTGGTTCGAT
Ltr07        ATTGGATAGT GGTATGTAAC AATATCAATT -ATCTTCCTT CAATGACCCT TCAAGAAAAA AATA---TCA ATTCTAGAGA TCTAATTG-T CTGGTTCGAT
Lag01        ATTGGATAGT GGTATGTAAC AATATCAATT -ATCTTTCTT CAATGACCCT TCAAGAAAAA AATA---TCA ATTCTAGAGA TCTAATTG-T CTGGTTCGAT
Lag02        ATTGGATAGT GGTATGTAAC AATATCAATT -ATCTTTCTT CAATGACCCT TCAAGAAAAA AATA---TCA ATTCTAGAGA TCTAATTG-T CTGGTTCGAT
Lag03        ATTGGATAGT GGTATGTAAC AATATCAATT -ATCTTTCTT CAATGACCCT TCAAGAAAAA AATA---TCA ATTCTAGAGA TCTAATTG-T CTGGTTCGAT
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Mae07        ATTGGATAGT GGTATGTAAC AATATCAATT TATCTTTCTT CAATGTTCCT TCAAGAAAAA AAT----TCA ATTCTATAGA TCTAATTG-T CTTGTTCGAT
Mae08        ATTGGATAGT GGTATGTAAC AATATCAATT TATCTTTCTT CAATGTTCCT TCAAGAAAAA AAT----TCA ATTCTATAGA TCTAATTG-T CTTGTTCGAT
Mmo01        ATTGGATAGT GGTATGTAAT AATATCAATT TATCTTTCTT CAATGTTCCT TCAAGAAAAA AAAAA-CTCA ATTCTAGAGA TTTAATTG-T CTGGTTCGAT
Mmo02        ATTGGATAGT GGTATGTAAT AATATCAATT TATCTTTCTT CAATGTTCCT TCAAGAAAAA AAAAA-CTCA ATTCTAGAGA TTTAATTG-T CTGGTTCGAT
Mmo03        ATTGGATAGT GGTATGTAAT AATATCAATT TATCTTTCTT CAATGTTCCT TCAAGAAAAA AAAAA-CTCA ATTCTAGAGA TTTAATTG-T CTGGTTCGAT
Mmo04        ATTGGATAGT GGTATGTAAT AATATCAATT TATCTTTCTT CAATGTTCCT TCAAGAAAAA AAAA--CTCA ATTCTAGAGA TTTAATTG-T CTGGTTCGAT
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Mmo05          ATTGGATAGT GGTATGTAAT AATATCAATT TATCTTTCTT CAATGTTCCT TCAAGAAAAA AAAA--CTCA ATTCTAGAGA TTTAATTG-T CTGGTTCGAT
Mmo06          ATTGGATAGT GGTATGTAAT AATATCAATT TATCTTTCTT CAATGTTCCT TCAAGAAAAA AAA---CTCA ATTCTAGAGA TTTAATTG-T CTGGTTCGAT
Mmo07          ATTGGATAGT GGTATGTAAT AATATCAATT TATCTTTCTT CAATGTTCCT TCAAGAGAAA AAAAA-CTCA ATTCTAGAGA TTTAATTG-T CTGGTTCGAT
Mmo08          ATTGGATAGT GGTATGTAAT AATATCAATT TATCTTTCTT CAATGTTCCT TCAAGAAAAA AAAA--CTCA ATTCTAGAGA TTTAATTG-T CTGGTTCGAT
Mmo09          ATTGGATAGT GGTATGTAAT AATATCAATT TATCTTTCTT CAATGTTCCT TCAAGAAAAA AAAA--CTCA ATTCTAGAGA TTTAATTG-T CTGGTTCGAT
Mmo10          ATTGGATAGT GGTATGTAAT AATATCAATT TATCTTTCTT CAATGTTCCT TCAAGAAAAA AAAAA-CTCA ATTCTAGAGA TTTAATTG-T CTGGTTCGAT
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Mto02          ATTGGATAGT GGTATGTAAT AATATCAATT TATCTTTCTT CACCGTTCCT TCAAGAAAAA AAAAAACTCA ATTCTAGAGA TCTAATTG-T CTGGTTCGAT
Mto03          ATTGGATAGT GGTATGTAAT AATATCAATT TATCTTTCTT CAATGTTCCT TCAAGAAAAA AAAAA-CTCA ATTCTAGAGA TCTAATTG-T CTGGTTCGAT
Mto04          ATTGGATAGT GGTATGTAAT AATATCAATT TATCTTTCTT CAATGTTCCT TCAAGAAAAA AAAAAACTCA ATTCTAGAGA TCTAATTG-T CTGGTTCGAT
Mto05          ATTGGATAGT GGTATGTAAT AATATCAATT TATCTTTCTT CAATGTTCCT TCAAGAAAAA AAAAA-CTCA ATTCTAGAGA TCTAATTG-T CTGGTTCGAT
Mto06          ATTGGATAGT GGTATGTAAT AATATCAATT TATCTTTCTT CAATGTTCCT TCAAGAAAAA AAAAA-CTCA ATTCTAGAGA TCTAATTG-T CTGGTTCGAT
Mto07          ATTGGATAGT GGTATGTAAT A---TCAATT TCTA------ ---------T TCAAGAAAAA AGAG---TCT ATTATAAAGC TCTAACTGCC CTCCTTGGAT
Ahi01          ATTAGATAGT GGTATGTAAT AATCTCAATT CATCTTTCTT CAATGTTCCC TCAAGAAAAA AAAA----CA ATTCTA---- --TAATTG-T CTGGTTCGAT
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Ahi08          ATTGGATAGT GGTATGTAAT AATCTCAATT TATCTTTCTT CAA------- ----GAAAAA AAA---TTCA ATTCTAGAGA TCTAATTT-T CTGGTTTGAT
Alo01          ATTGGATAGT GGTATGTAAT AATCTCAATT CATCTTTCTT CAATGTTCCT TCAAGAAAAA AAAG----CA ATTCTA---- --TAATTG-T CTGGTTCGAT
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Alo03          ATTGGATAGT GGTATGTAAT AATCTCAATT CATCTTTCTT CAATGTTCCT TCAAGAAAAA AAAG----CA ATTCTA---- --TAATTG-T CTGGTTCGAT
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Alo06          ATTGGATAGT GGTATGTAAT AATCTCAATT CATCTTTCTT CAATGTTCCT TCAAGAAAAA AAAG----CA ATTCTA---- --TAATTG-T CTGGTTCGAT
Alo07          ATTGGATAGT GGTATGTAAT AATCTCAATT CATCTTTCTT CAATGTTCCT TCAAGAAAAA AAAG----CA ATTCTA---- --TAATTG-T CTGGTTCGAT
Alo08          ATTGGATAGT GGTATGTAAT AATCTCAATT CATCTTTCTT CAATGTTCCT TCAAGAAAAA AAAG----CA ATTCTA---- --TAATTG-T CTGGTTCGAT
Alo09          ATTGGATAGT GGTATGTAAT AATCTCAATT CATCTTTCTT CAATGTTCCT TCAAGAAAAA AAAG----CA ATTCTA---- --TAATTG-T CTGGTTCGAT
Alo10          ATTGGATAGT GGTATGTAAT AATCTCAATT CATCTTTCTT CAATGTTCCT TCAAGAAAAA AAAG----CA ATTCTA---- --TAATTG-T CTGGTTCGAT
Mca01          ATTGGATAGT GGTATGTAAT AATCTCAATT TATCTTTCTT CAATGTTCCT TCAAGAAA-- ---------- ---CTAGAGA TCTAATTG-T CTGGTTCGAT
Mca02          ATTGGATAGT GGTATATAAT AATCTCAATT TATCTTTCTT CAATGTTCCT TCAAGAAAAA AAT----TCA ATTCTAGAGA TCTAATTG-T CTGGTTCTAT
Mca03          ATTGGATAGT GGTATGTAAT GATCTCAATT TATCTTTCTT CAATGTTCCT TCAAGAAA-- ---------- ---CTAGAGA TCTAATTG-T CTGGTTCGAT
Mca04          ATTGGATAGT GGTATGTAAT AATCTCAATT TATCTTTCTT CAATGTTCCT TCAAGAAA-- ---------- ---CTAGAGA TCTAATTG-T CTGGTTCGAT
Mtf01          ATTGGATAGT GGTATGTAGT AATATCAATT T-CTTTTCTT CAATGTTCTT TCAAGAACAA CAAA---TCA ATTCTAGAGA TCTAATTG-T CTGGTTGGAT
Mtf02          ATTGGATAGT GGTATGTAGT AATATCAATT TATCTTTCTT CAATGTTCTC TCAAGAACAA CAAA---TCA ATTCTAGAGA TCTAATTG-T CTGGTTTGAT
Mtf03          ATTGGATAGT GGTATGTAGT AATATCAATT TATCTTTCTT CAATGTTCTT TCAAGAACAA CAAA---TCA ATTCTAGAGA TCTAATTG-T CTGGTTTGAT
Mtf04          ATTGGATAGT GGTATGTAGT AATATCAATT TATCTTACTT CAACGTTCTT TCAAGAACAA CAAA---TCA ATTCTAGAGA TCTAATTG-T CTGGTTTGAT
Mtf05          ATTGGATAGT GGTATGTAGT AATATCAATT TATCTTACTT CAATGTTCTT TCAAGAACAA CAAA---TCA ATTCTAGAGA TCTAATTG-T CTGGTTTGAT
Mma01          ATTGGATAGT GGTATGTAGT AATATCAATG T-TCTTTCTT CAATGTTCTT TCAAGAACAA CAAA---TCA ATTCTAGAGA TCTAATTG-T CTGGTTTGAT
Mma02          ATTGGATAGT GGTATGTAGT AATATCAATG T-TCTTTCTT CAATGTTCTT TCAAGAACAA CAAA---TCA ATTCTAGAGA TCTAATTG-T CTGGTTTGAT
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Mma03       ATTGGATAGT GGTATGTAGT AATATCAATG T-TCTTTCTT CAATGTTCTT TCAAGAACAA CAAA---TCA ATTCTAGAGA TCTAATTG-T CTGGTTTGAT
Mma04       ATTAGATAGT GGTATGTAGT AATATCAATG T-TCTTTCTT CAATGTTCTT TCAAGAACAA CAAA---TCA ATTCTAGAGA TCTAATTG-T CTGGTTTGAT
Mma05       ATTGGATAGT GGTATGTAGT AATATCAATG T-TCTTTCTT CAATGTTCTT TCAAGAACAA CAAA---TCA ATTCTAGAGA TCTAATTG-T CTGGTTTGAT
Las01       ATTGGATAGT GGTATGTAAT ACTATCAATT TATCTTTCTT CAATGTTCCT TCAAGAAACA GAAA---TCA ATTCTAGAGA TCTAATTG-T CTGGTTCGAT
Las02       ATTGGATAGT GGTATGTAAT ACTATCAATT TATCTTTCTT CAATGTTCCT TCAAGAAACA GAAA---TCA ATTCTAGAGA TCTAATTG-T CTGGTTCGAT
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Lpe03       ATTGGATAGT GGTATGTAAT ACTATCAATT TATCTTTCTT CAATGTTCCT TCAAGAAAGA AAGAAA-TCA GTTCTACAGA TCTAATTG-T CTGGTTCGAT
Lpe04       ATTGGATAGT GGTATGTAAT ACTATCAATT TATCTTTCTT CAATGTTCCT TCAAGAAACA GAAA---TCA ATTCTAGAGA TCTAATTG-T CTGGTTCGAT
Lac01       ATTGGATAGT GGTATGTAAT ACTATCAATT TATATTTCTT CAATGTTCCT TCAAGAAAAA AAAA---TCA ATTCTAGATA TCTAATTG-T CTGGTTCGAT
Lac02       ATTGGATAGT GGTATGTAAT ACTATCAATT TATATTTCTT CAATGTTCCT TCAAGAAAAA AAAA---TCA ATTCTAGATA TCTAATTG-T CTGGTTCGAT
Lac03       ATTGGATAGT GGTATGTAAT ACTATCAATT TATATTTCTT CAATGTTCCT TCAAGAAAAA AAAA---TCA ATTCTAGATA TCTAATTG-T CTGGTTCGAT
Lac04       ATTGGATAGT GGTATGTAAT ACTATCAATT TATATTTCTT CAATGTTCCT TCAAGAAAAA AAAA---TCA ATTCTAGATA TCTAATTG-T CTGGTTCGAT
Lac05       ATTGGATAGT GGTATGTAAT ACTATCAATT TATATTTCTT CAATGTTCCT TCAAGAAAAA AAAA---TCA ATTCTAGATA TCTAATTG-T CTGGTTCGAT
Lac06       ATTGGATAGT GGTATGTAAT ACTATCAATT TATATTTCTT CAATGTTCCT TCAAGAAAAA AAAA---TCA ATTCTAGATA TCTAATTG-T CTGGTTCGAT
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Lma02       ATTGGATAGT GGTATGTAAT ACTATCAATT TATCTTTCTT CAATGTTCCT TCAAGAAAAA AAA----TCA ATTCTAGAGA TCTAATTG-C CTGGTTCGAT
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Msy01       ATTGGATAGT GGTATGTAAT ACTATCAATT TATCTTTCTT CAATGTTCCT TCAAGAAAGA AAGAAA-TCA ATTCTAGAGA TCTAATTG-T CTGGTTCGAT
Msy02       ATTGGATAGT GGTATGTAAT ACTATCAATT TATCTTTCTT CAATGTTCCT TCAAGAAAGA AAGAAA-TCA ATTCTAGAGA TCTAATTG-T CTGGTTCGAT
Msy03       ATTGGATAGT GGTATGTAAT ACTATCAATT TATCTTTCTT CAATGTTCCT TCAAGAAAGA AAGAAA-TCA ATTCTAGAGA TCTAATTG-T CTGGTTCGAT
Msy04       ATTGGATAGT GGTATGTAAT ACTATCAATT TATCTTTCTT CAATGTTCCT TCAAGAAAGA AAGAAA-TCA ATTCTAGAGA TCTAATTG-T CTGGTTCGAT
Msy05       ATTGGATAGT GGTATGTAAT ACTATCAATT TATCTTTCTT CAGTGTTCCT TCAAGAAAGA AAGAAA-TCA ATTCTAGAGA TCTAATTG-T CTGGTTCGAT
Lmu01       ATTGGATAGT GGTATGTAAT ACTATCAATT TATCTTTCTT CAATGTTCCT TCAAGAAAGA AAGAAA-TCA ATTCTAGAGA TCTAATTG-T CCGGTTCGAT
Lmu02       ATTGGATAGT GGTATGTAAT ACTATCAATT TATCTTTCTT CAATGTTCCT TCAAGAAAGA AAGAAA-TCA ATTCTAGAGA TCTAATTG-T CCGGTTCGAT
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Lmu06       ATTGGATAGT GGTATGTAAT ACTATCAATT TATCTTTCTT CAATGTTCCT TCAAGAAAGA AAGAAA-TCA ATTCTAGAGA TCTAATTG-T CCGGTTCGAT
Lmu07       ATTGGATAGT GGTATGTAAT ACTATCAATT TATCTTTCTT CAATGTTCCT TCAAGAAAGA AAGAAA-TCA ATTCTAGAGA TCTAATTG-T CCGGTTCGAT
Lmu08       ATTGGATAGT GGTATGTAAT ACTATCAATT TATCTTTCTT CAATGTTCCT TCAAGAAAGA AAGAAA-TCA ATTCTAGAGA TCTAATTG-T CCGGTTCGAT
Lmu09       ATTGGATAGT GGTATGTAAT ACTATCAATT TATCTTTCTT CAATGTTCCT TCAAGAAAGA AAGAAA-TCA ATTCTAGAGA TCTAATTG-T CCGGTTCGAT
Mpa01       ATTGGATAGT GGTATGTAAT ACTATCAATT TATCTTTCTT CAATGTTCCT TCAAGAAAGA AAGAAA-TCA ATTCTAGAGA TCTAATTG-T CCGGTTCGAT
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Mpa03           ATTGGATAGT GGTATGTAAT ACTATCAATT TATCTTTCTT CAATGTTCCT TCAAGAAAGA AAGAAA-TCA ATTCTAGAGA TCTAATTG-T CCGGTTCGAT
Mpa04           ATTGGATAGT GGTATGTAAT ACTATCAATT TATCTTTCTT CAATGTTCCT TCAAGAAAGA AAGAAA-TCA ATTCTAGAGA TCTAATTG-T CCGGTTCGAT
Mpa05           ATTGGATAGT GGTATGTAAT ACTATCAATT TATCTTTCTT CAATGTTCCT TCAAGAAAGA AAGAAA-TCA ATTCTAGAGA TCTAATTG-T CCGGTTCGAT
Mpa06           ATTGGATAGT GGTATGTAAT ACTATCAATT TATCTTTCTT CAATGTTCCT TCAAGAAAGA AAGAAA-TCA ATTCTAGAGA TCTAATTG-T CCGGTTCGAT
Mve01           ATTGGATAGT GGTATGTAAT ACTATCAATT TATCTTTCTT CAATGTTCCT TCAAGAAAGA AAGAAA-TCA ATTCTAGAGA TCTAATTG-T CCGGTTCGAT
Mve02           ATTGGATAGT GGTATGTAAT ACTATCAATT TATCTTTCTT CAATGTTCCT TCAAGAAAGA AAGAAA-TCA ATTCTAGAGA TCTAATTG-T CCGGTTCGAT
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Mni02           ATTGGATAGT GGTATGTAAT ACTATCAATT TATCTTTCTT CAGTGTTCCT TCAAGAAAGA AAGAAA-TCA ATTCTAGAGA TCTAATTG-T CTGGTTCGAT
Mni03           ATTGGATAGT GGTATGTAAT ACTATCAATT TATCTTTCTT CAGTGTTCCT TCAAGAAAGA AAGAAA-TCA ATTCTAGAGA TCTAATTG-T CTGGTTCGAT
Mni04           ATTGGATAGT GGTATGTAAT ACTATCAATT TATCTTTCTT CAGTGTTCCT TCAAGAAAGA AAGAAA-TCA ATTCTAGAGA TCTAATTG-T CTGGTTCGAT
Mni05           ATTGGATAGT GGTATGTAAT ACTATCAATT TATCTTTCTT CAGTGTTCCT TCAAGAAAGA AGGAAA-TCA ATTCTAGAGA TCTAATTG-T CTGGTTCGAT
Mni06           ATTGGATAGT GGTATGTAAT ACTATCAATT TATCTTTCTT CAGTGTTCCT TCAAGAAAGA AAGAAA-TCA ATTCTAGAGA TCTAATTG-T CTGGTTCGAT
Mne01           ATTGGATAGT GGTATGTAAT ACTATCAATT TATCTTTCTT CAATGTTCCT TCAAGAAAGG AAGAAA-TCA GTTCTAGAGA TCTAATTG-T CTGGTTCGAT
Aof01           ATTGGATAGT GGTATGCA-- -CTATCAATT TATCTTTCTT CAATGTTACT TCAAGAAAAA AA-----TCA ATTCTAGAGA TCTAATTG-T CTGGTTTCAT
Aca01           ATTGGATAGT GGTATGCA-- -CTATCAATT TATCTTTCTT CAATGTTACT TCAAGAAAAA AA-----TCA ATTCTAGAGA TCTAATTG-T CTGGTTTGAT
Aca02           ATTGGATAGT GGTATGCA-- -CTATCAATT TATCTTTCTT CAATGTTACT TCAAGAAAAA AAA----TCA ATTCTGGAGA TCTAATTG-T CTGGTTTGAT
Ani40           ATTGGATAGT GGTATGTA-- -ATATCAATT TATCTTTCTT CAATGTTCCT TCAAGAAAAA AA-----TCA ATTTTAGAGA TCTAATTG-T CTGGTTTGAT


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                       610        620        630        640        650        660        670        680        690        700
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Lmo03           GTTTT-CGTG AAGAAATGAC CGAAGACAAT GGGAACCCTA TTTGGAAGAA CCGGGTGGAA AGTTGGAAGG AAAAGAAGAA CAAGAAGAAG AAGCCT---G
Lmo04           GTTTT-CGTG AAGAAATGAC CGAAGACAAT GGGAACCCTA TTTGGAAGAA CCGGGTGGAA AGTTGGAAGG AAAAGAAGAA CAAGAAGAAG AAGCCT---G
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Lmo13           GTTTT-CGTG AAGAAATGAC CGAAGACAAT GGGAACCCTA TTTGGAAGAA CCGGGTGGAA AGTTGGAAGG AAAAGAAGAA CAAGAAGAAG AAGCCT---G
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Lti02           GTTTT-CATG AAGAAATGAC TGAAGACAAC GGGAACCCGA TTTGGAAGAA CCGGGTGGAA AGTTGGAAGG AAAAGAAGAA CAAGAAGAAA AAGCCT---G
Lti03           GTTTT-CATG AAGAAATGAC TGAAGACAAC GGGGACCCGA TTTGGAAGAA CCGGGTGGAA AGTTGGAAGG AAAAGAAGAA CAAGAAGAAA AAGCCT---G
Lti04           GTTTT-CATG AAGAAATGAC TGAAGACAAC GGGAACCCGA TTTGGAAGAA CCGGGTGGAA AGTTGGAAGG AAAAGAAGAA CAAGAAGAAA AAGCCT---G
Lti05           GTTTT-CATG AAGAAATGAC TGAAGACAAC GGGAACCCGA TTTGGAAGAA CCGGGTGGAA AGTTGGAAGG AAAAGAAGAA CAAGAAGAAA AAGCCT---G
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Lti09         GTTTT-CATG AAGAAATGAC TGAAGACAAC GGGAACCCGA TTTGGAAGAA CCGGGTGGAA AGTTGGAAGG AAAAGAAGAA CAAGAAGAAA AAGCCT---G
Mhi01         GTTTT-CATA AAGAAATGAC CGAAGAAAAT GGGAACCCGA TTTGGAAGAA CCGGGTGGAA AGTTGGAAGG AAAAGAAGAA CAAGAAGAAA AAGCCT---G
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Mhi05         GTTTT-CATA AAGAAATGAC CGAAGAAAAT GGGAACCCGA TTTGGAAGAA CCGGGTGGAA AGTTGGAAGG AAAAGAAGAA CAAGAAGAAA AAGCCT---G
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Mhi07         GTTTT-CATA AAGAAATGAC CGAAGAAAAT GGGAACCCGA TTTGGAAGAA CCGGGTGGAA AGTTGGAAGG AAAAGAAGAA CAAGAAGAAA AAGCCT---G
Lth01         GTTTT-CGTG AAGAAATGAC CGAAGACAAT GGGAACCCGA TTTGGAAGAA CAGGGTGGAA AGTTGGAAGG AAAAGAAGAA CAAGAAGAAA AAGCCT---G
Lth02         GTTTT-CGTG AAGAAATGAC CGAAGACAAT GGGAACCCGA TTTGGAAGAA CAGGGTGGAA AGTTGGAAGG AAAAGAAGAA CAAGAAGAAA AAGCCT---G
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Mpa03          GTTTT-CGTG AAGAAATGAC CGAAGACAAT GGGAACCCGA TTTGGAAGAA CAGGGTGGAA AGTTGGAAGG AAAAGAAGAA CAAGAAGAAA AAGCCTACTG
Mpa04          GTTTT-CGTG AAGAAATGAC CGAAGACAAT GGGAACCCGA TTTGGAAGAA CAGGGTGGAA AGTTGGAAGG AAAAGAAGAA CAAGAAGAAA AAGCCTACTG
Mpa05          GTTTT-CGTG AAGAAATGAC CGAAGACAAT GGGAACCCGA TTTGGAAGAA CAGGGTGGAA AGTTGGAAGG AAAAGAAGAA CAAGAAGAAA AAGCCTACTG
Mpa06          GTTTT-CGTG AAGAAATGAC CGAAGACAAT GGGAACCCGA TTTGGAAGAA CAGGGTGGAA AGTTGGAAGG AAAAGAAGAA CAAGAAGAAA AAGCCTACTG
Mve01          GTTTT-CGTG AAGAAATGAC CGAAGACAAT GGGAACCCGA TTTGGAAGAA CAGGGTGGAA AGTTGGAAGG AAAAGAAGAA CAAGAAGAAA AAGCCTACTG
Mve02          GTTTT-CGTG AAGAAATGAC CGAAGACAAT GGGAACCCGA TTTGGAAGAA CAGGGTGGAA AGTTGGAAGG AAAAGAAGAA CAAGAAGAAA AAGCCTACTG
Mve03          GTTTT-CGTG AAGAAATGAC CGAAGACAAT GGGAACCCGA TTTGGAAGAA CAGGGTGGAA AGTTGGAAGG AAAAGAAGAA CAAGAAGAAA AAGCCTACTG
Mni01          ATTTT-CGTG AAGAAATGAC CGAAGACAAT GGGAACCCGA TTTGGAAGAA CAGGGTGGAA AGTTGGAAGG AAAAGAAGAA CAAGAAGAAA AAGCCTACTG
Mni02          ATTTT-CGTG AAGAAATGAC CGAAGACAAT GGGAACCCGA TTTGGAAGAA CAGGGTGGAA AGTTGGAAGG AAAAGAAGAA CAAGAAGAAA AAGCCTACTG
Mni03          ATTTT-CGTG AAGAAATGAC CGAAGACAAT GGGAACCCGA TTTGGAAGAA CAGGGTGGAA AGTTGGAAGG AAAAGAAGAA CAAGAAGAAA AAGCCTACTG
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Mni04           ATTTT-CGTG AAGAAATGAC CGAAGACAAT GGGAACCCGA TTTGGAAGAA CAGGGTGGAA AGTTGGAAGG AAAAGAAGAA CAAGAAGAAA AAGCCTACTG
Mni05           ATTTT-CGTG AAGAAATGAC CGAAGACAAT GGGAACCCGA TTTGGAAAAA CGGGGTGGAA AGTTGGAAGG AAAAGAAGAA CAAGAAGAAA AAGCCTACTG
Mni06           ATTTT-CGTG AAGAAATGAC CGAAGACAAT GGGAACCCGA TTTGGAAGAA CAGGGTGGAA AGTTGGAAGG AAAAGAAGAA CAAGAAGAAA AAGCCTACTG
Mne01           GTTTT-CGTG AAGAAATGAC CGAAGACAAT GGGAACCCGA TTTGGAAGAA CAGGGTGGAA AGTTGGAAGG AAAAGAAGAA CAAGAAGAAA AAGCCTACTG
Aof01           GTTTTACGTG AAGAAATGAC CGAAGACAAC GGGAACCCGA TTTGGAAGAA CAGGGTGGAA AGTTGGAAGG AAAAGAAGAA CAAGAAGAAA AAGCCT---G
Aca01           GTTTTACGTG AAGAAATGAC CGAAGACAAC GGGAACCCGA TTTGGAAGAA CAGGGTGGAA AGTTGGAAGG AAAAGAAGAA CAAGAAGAAA AAGCCT---G
Aca02           GTTTTTCGTG AAGAAATGAC CGAAGACAAC AGGAACCCGA TTTGGAAGAA CAGGGTGGAA AGTTGGAAGG AAAAGAAGAA CAAGAAGAAA AAGCCT---G
Ani40           GTTTT-CGTG AAGAAATGAC TGAAGACAAT GGGAACCCGA TTTGGAAGAA CAGGGTGGAA AGTTGGAAGG AAAAGAAGAA CAAGAAGAAA AAGCCT---G


                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                       710        720        730        740        750        760        770        780        790        800
Lmo01           CAAAAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTGTA TATATATAC- ---------- ----------
Lmo02           CAAAAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTGTA TATATATAC- ---------- ----------
Lmo03           CAAAAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTGTA TATATATAC- ---------- ----------
Lmo04           CAAAAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTGTA TATATATAC- ---------- ----------
Lmo05           CAAAAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTGTA TATATATAC- ---------- ----------
Lmo06           CAAAAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTGTA TATATATAC- ---------- ----------
Lmo07           CAAAAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTGTA TATATATAC- ---------- ----------
Lmo08           CAAAAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTGTA TATATATAC- ---------- ----------
Lmo09           CAAAAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTGTA TATATATAC- ---------- ----------
Lmo10           CAAAAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTGTA TATATATAC- ---------- ----------
Lmo11           CAAAAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTGTA TATATATAC- ---------- ----------
Lmo12           CAAAAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGCGTA TATATATAC- ---------- ----------
Lmo13           CAAAAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTGTA TATATATAC- ---------- ----------
Lti01           CAAAAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA TATATAC--- ---------- ----------
Lti02           CAAAAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA TATATAC--- ---------- ----------
Lti03           CAAAAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA TATATAC--- ---------- ----------
Lti04           CAAAAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA TATATAC--- ---------- ----------
Lti05           CAAAAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA TATATAC--- ---------- ----------
Lti06           CAAAAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA TATATAC--- ---------- ----------
Lti07           CAAAAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA TATATAC--- ---------- ----------
Lti08           AAAAAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAGTG GAAGATAAAC CGTAAGTATA TATATAC--- ---------- ----------
Lti09           CAAAAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA TATATAC--- ---------- ----------
Mhi01           CTAAAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGCATA TATATATAC- ---------- ----------
Mhi02           CTAAAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGCATA TATATATAC- ---------- ----------
Mhi03           CTAAAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGCATA TATATATAC- ---------- ----------
Mhi04           CTAAAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGCATA TATATATAC- ---------- ----------
Mhi05           CTAAAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGCATA TATATATAC- ---------- ----------
Mhi06           CTAAAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGCATA TATATATAC- ---------- ----------
Mhi07           CTAAAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGCATA TATATATAC- ---------- ----------
Lth01           CAAAAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTGTG TATATATATA CAC------- ----------
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Lth02        CAAAAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTGTG TATATATATA CAC------- ----------
Lth03        CAAAAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTGTG TATATATATA CAC------- ----------
Lth04        CAAAAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTGTG TATATATATA CAC------- ----------
Lth05        CAAAAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTGTG TATATATATA CAC------- ----------
Lth06        CAAAAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTGTG TATATATATA CAC------- ----------
Lth07        CAAAAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTAA GCAACAAATG GAAGATAAAC CGTAAGTGTG TATATATATA CAC------- ----------
Lth08        CAAAAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTGTG TATATATATA CAC------- ----------
Lth09        CAAAAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTGTG TATATATATA CAC------- ----------
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Lth13        CAAAAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTGTG TATATATATA CAC------- ----------
Mal01        CAAAAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTGTG TATATATATA CAC------- ----------
Mal02        CAAAAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTGTG TATATATATA CAC------- ----------
Mal03        CAAAAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTGTG TATATATATA CAC------- ----------
Mal04        CAAAAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTGTG TATATATATA CAC------- ----------
Mal05        CAAAAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTGTG TATATATATA CAC------- ----------
Mal06        CAAAAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTGTG TATATATATA CAC------- ----------
Mal07        CAAAAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTGTG TATATATATA CAC------- ----------
Mal08        CAAAAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTGTG TATATATATA CAC------- ----------
Mal09        CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA TATATAC--- ---------- ----------
Ltr01        CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA TATATATACA CACAC----- ----------
Ltr02        CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA TATATATATA CACACAC--- ----------
Ltr03        CAACAACTAA GGCTGA---- --------AG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA TATATATATA CACACAC--- ----------
Ltr04        CAACAACTAA GGCTGA---- --------AG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA TATATATATA CACACAC--- ----------
Ltr05        CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA TATATATACA CACAC----- ----------
Ltr06        CAACAACTAA GGCTGA---- --------AG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA TATATATATA CACACAC--- ----------
Ltr07        CAACAACTAA GGCTGA---- --------AG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA TATATATATA CACACAC--- ----------
Lag01        CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA TATATACACA CAC------- ----------
Lag02        CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA TATATACACA CAC------- ----------
Lag03        CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA TATATACACA CAC------- ----------
Lag04        CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA TATATACACA CAC------- ----------
Lag05        CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA TATATGCACA CAC------- ----------
Lfl01        CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA TATATATACA CACAC----- ----------
Lfl02        CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA TATATATACA CACACAC--- ----------
Ltp01        CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA TATATACACA CAC------- ----------
Lbr01        CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA TATATACACA CAC------- ----------
Lbr02        CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA TATATACACA CAC------- ----------
Lbr03        CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA TATATATACA CACAC----- ----------
Lob01        CAACAACTAA GGCTGACATA GAAGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTGTA TATATATATA TACAC----- ----------
Lob02        CAACAACTAA GGCTGACATA GAAGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTGTA TATATATATA CAC------- ----------
Lob03        CAACAACTAA GGCTGACATA GAAGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTGTA TATATATATA TACAC----- ----------
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Lob04         CAACAACTAA GGCTGACATA GAAGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTGTA TATATATACA TACAC----- ----------
Lob05         CAACAACTAA GGCTGACATA GAAGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTGTA TATATATATA TACAC----- ----------
Lob06         CAACAACTAA GGCTGACATA GAAGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTGTA TATATATATA TACAC----- ----------
Lob07         CAACAACTAA GGCTGACATA GAAGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTGTA TATATATATA TACAC----- ----------
Lol01         CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTGTA TATATATATA TACACACACA C---------
Lol02         CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTGTA TATATATATA CACACACAC- ----------
Lol03         CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTGTA TATATATATA CACACACAC- ----------
Lol04         CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTGTA TATATATATA TACACACACA C---------
Mae01         CAACAACTAA GGCTGACATA GAGGCTGAAG TTCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGCGCG TATATATATA TATATATATA CACACATATG
Mae02         CAACAACTAA GGCTGACATA GAGGCTGAAG TTCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGCGCG TATATATATA TATATATACA CACATATGC-
Mae03         CAACAACTAA GGCTGACATA GAGGCTGAAG TTCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGCGCG TATATATATA CATATATACA CACATATGC-
Mae04         CAACAACTAA GGCTGACATA GAGGCTGAAG TTCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGCGCG TATATATATA TATATATACA CACATATGC-
Mae05         CAACAACTAA GGCTGACATA GAGGCTGAAG TTCCACCTGA GCAACAAATG GAAGATAGAC CGTGAGCGCG TATATATATA TATATATACA CACATATGC-
Mae06         CAACAACTAA GGCTGACATA GAGGCTGAAG TTCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGCGCG TATATATATA TATATATACA CACATATGC-
Mae07         CAACAACTAA GGCTGACATA GAGGCTGAAG TTCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGCGCG TATATATATA TATATATACA CACATATGC-
Mae08         CAACAACTAA GGCTGACATA GAGGCTGAAG TTCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGCGCG TATATATATA TATATATACA CACATATGC-
Mmo01         CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA TATATAC--- ---------- ----------
Mmo02         CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA TATATAC--- ---------- ----------
Mmo03         CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA TATATAC--- ---------- ----------
Mmo04         CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA TATATAC--- ---------- ----------
Mmo05         CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA TATATAC--- ---------- ----------
Mmo06         CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA TATATAC--- ---------- ----------
Mmo07         CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA TATATAC--- ---------- ----------
Mmo08         CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA TATATAC--- ---------- ----------
Mmo09         CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA TATATAC--- ---------- ----------
Mmo10         CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA TATATAC--- ---------- ----------
Mto01         CAACAACTAA GGGTGACATA GAGGGGGAAG TCCCACTTGA GCAACAAATG GAAGATAAAC CGTAAGTATA TATATAC--- ---------- ----------
Mto02         CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACTTGA GCAACAAATG GAAGATAAAC CGTAAGTATA TATATAC--- ---------- ----------
Mto03         CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA TATATAC--- ---------- ----------
Mto04         CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA TATATAC--- ---------- ----------
Mto05         CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA TATATAC--- ---------- ----------
Mto06         CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA TATATAC--- ---------- ----------
Mto07         CAACAACTAA GGTTGACAGA GAGGCTCAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGCACG AAAAC----- ---------- ----------
Ahi01         CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GACGATAAAC CGTAAGCGCA TATATAC--- ---------- ----------
Ahi02         CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GACGATAAAC CGTAAGCGCA TATATAC--- ---------- ----------
Ahi03         CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GACGATAAAC CGTAAGCGCA TATATAC--- ---------- ----------
Ahi04         CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GACGATAAAC CGTAAGCGCA TATATATATA TATATATATA TACAC-----
Ahi05         CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GACGATAAAC CGTAAGCGCA TATATAC--- ---------- ----------
Ahi06         CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GACGATAAAC CGTAAGCGCA TATATAC--- ---------- ----------
Ahi07         CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GACGATAAAC CGTAAGCGCA TATATAC--- ---------- ----------
Ahi08         CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GACGATAAAC CGTAAGCGCA TATATATATA TATATATATA TACAC-----
Alo01         CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCGGA GCAACAAATG GACGATAAAC CGTAAGCGTA TATATAC--- ---------- ----------
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Alo02        CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCGGA GCAACAAATG GACGATAAAC CGTAAGCGTA TATATAC--- ---------- ----------
Alo03        CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCGGA GCAACAAATG GACGATAAAC CGTAAGCGTA TATATAC--- ---------- ----------
Alo04        CAACAACTAA GGCTGACATA GAGGCAGAAG TCCCACCGGA GCAACAAATG GACGATAAAC CGTAAGCGTA TATATAC--- ---------- ----------
Alo05        CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCGGA GCAACAAATG GACGATAAAC CGTAAGCGTA TATATAC--- ---------- ----------
Alo06        CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCGGA GCAACAAATG GACGATAAAC CGTAAGCGTA TATATAC--- ---------- ----------
Alo07        CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCAGA GCAACAAATG GACGATAAAC CGTAAGCGTA TATATAC--- ---------- ----------
Alo08        CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCGGA GCAACAAATG GACGATAAAC CGTAAGCGTA TATATAC--- ---------- ----------
Alo09        CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCGGA GCAACAAATG GACGATAAAC CGTAAGCGTA TATATAC--- ---------- ----------
Alo10        CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCGGA GCAACAAATG GACGATAAAC CGTAAGCGTA TATATAC--- ---------- ----------
Mca01        CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GACGATAAAC CGTAAGC--- ---------- ---------- ----------
Mca02        CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGC--- ---------- ---------- ----------
Mca03        CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GACGATAAAC CGTAA----- ---------- ---------- ----------
Mca04        CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GACGATAAAC CGTAA----- ---------- ---------- ----------
Mtf01        CAACAACTAA GGCCGACAAA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTACGTGTG TATATATATA TATATATAC- ----------
Mtf02        CAACAACTAA GGCCGACAAA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTACGTGTG TATATATATA TATATATAC- ----------
Mtf03        CAACAACTAA GGCCGACAAA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTACGTGTG TATATATATA TATATATAC- ----------
Mtf04        CAACAACTAA GGCCGACAAA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTACGTGTG TATATATATA TATATATAC- ----------
Mtf05        CAACAACTAA GGCCGACAAA GAGGGTGAAG TCCCACCCGA GCAACAAATG GAAGATAAAC CGTGCGTGTG TGTGTATATA TATATATATA TATATATATA
Mma01        CAACAACTAA GGCCGACAAA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTACGTGTA TATATATAT- ---------- ----------
Mma02        CAACAACTAA GCCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAGC CGTAAGTGTA TATATATACA CGATAATAC- ----------
Mma03        CAACAACTAA GGCCGACAAA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTACGTGTA TATATATAT- ---------- ----------
Mma04        CAACAACTAA GGCCGACAAA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTACGTGTA TATATATAT- ---------- ----------
Mma05        CAACAACTAA GGCCGACAAA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTACGTGTA TATATATAT- ---------- ----------
Las01        CAACAACAAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GGAGATAAAC CGTAAGTATA TATATATATA TATA------ ----------
Las02        CAACAACAAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA TATATATATA TATA------ ----------
Las03        CAACAACAAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA TATATATATA TATA------ ----------
Las04        CAACAACTAA GGCTGACATA GAGGCKGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA CATATATATA TATATATACA CACAC-----
Las05        CAACAACAAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA TATATATATA TATATTA--- ----------
Las06        CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA CATATATATA TATATATACA CACAC-----
Las07        CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA CATATATATA TATATATACA CACAC-----
Las08        CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA CATATATATA TATATATACA CACAC-----
Lpe01        CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA CATATATATA TATATATATA TATATATATA
Lpe02        CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA CATATATATA TATATATATA TATATATATA
Lpe03        CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA CACATATATA TATATATATA TATATATATA
Lpe04        CAACAACAAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTGTA TATATATATA TATATT---- ----------
Lac01        CAACAACTAA GGCTGACATA GCGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA TATAA----- ---------- ----------
Lac02        CAACAACTAA GGCTGACATA GCGGCTGAAG TCCCACCTGG GCAACAAATG GAAGATAAAC CGTAAGTATA TATAA----- ---------- ----------
Lac03        CAACAACTAA GGCTGACATA GCGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA TATAA----- ---------- ----------
Lac04        CAACAACTAA GGCTGACATA GCGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA TATAA----- ---------- ----------
Lac05        CAACAACTAA GGCTGACATA GCGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA TATAA----- ---------- ----------
Lac06        CAACAACTAA GGCTGACATA GCGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA TATAA----- ---------- ----------
Lac07        CAACAACTAA GGCTGACATA GCGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA TATAA----- ---------- ----------
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Lac08            CAACAACTAA GGCTGACATA GCGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA TATAA----- ---------- ----------
Lma01            CAACAACTAA GGCTGACATA GGGGCTGAAG TCCCCCCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA TATATATGTA A--------- ----------
Lma02            CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCCCCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA TATATATGTA A--------- ----------
Lcr01            CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA CATATATATA TATATATATA TATATACGC-
Lcr02            CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA CATATATATA TATATATATA CAC-------
Msy01            CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA CATATATATA TATACACA-- ----------
Msy02            CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA CGTATATATA TATACACA-- ----------
Msy03            CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA CATATATATA TATACACA-- ----------
Msy04            CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA CATATATATA TATACACA-- ----------
Msy05            CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA CATATATATA TATATATACA C---------
Lmu01            CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA TATATATATG TATATAC--- ----------
Lmu02            CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA TATATATATG TATATAC--- ----------
Lmu03            CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA CATATATATA TACAC----- ----------
Lmu04            CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA CATATATATA TACAC----- ----------
Lmu05            CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA CATATATATA TACAC----- ----------
Lmu06            CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA CATATATATA TACAC----- ----------
Lmu07            CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA CATATATATA TACAC----- ----------
Lmu08            CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA CATATATATA TACAC----- ----------
Lmu09            CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA CATATATATA TACAC----- ----------
Mpa01            CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA CATATATATA TACAC----- ----------
Mpa02            CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA CATATATATA TACAC----- ----------
Mpa03            CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA CATATATATA TACAC----- ----------
Mpa04            CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA CATATATATA TACAC----- ----------
Mpa05            CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA CATATATATA TACAC----- ----------
Mpa06            CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA CATATATATA TACAC----- ----------
Mve01            CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA CATATATATA TACAC----- ----------
Mve02            CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA CATATATATA TACAC----- ----------
Mve03            CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA CATATATATA TACAC----- ----------
Mni01            CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA CATATATATA TATATATATA CAC-------
Mni02            CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGCAAGTATA CATATATATA TATATATATA TACAC-----
Mni03            CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA CATATATATA TATATGTATA TACAC-----
Mni04            CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA CATATATATA TATATATATA CAC-------
Mni05            CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTGTA CATATATATA TATATATATA CAC-------
Mni06            CAACAACTAA GGCTGACATA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA CATATATATA TATATATATA CAC-------
Mne01            CAACAACTAA GGCTGACATA GAGGCAGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA CATATATATA TATATATATA TATATATACA
Aof01            CAACAACTAA GGCTGACAGA GAGGCTGAAG TCCCACCTGA GCAACAGATG GAAGATAAAC CGTAAGTATA TATAC----- ---------- ----------
Aca01            CAACAACTAA GGCTGACAGA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA TATAC----- ---------- ----------
Aca02            CAACAACTAA GGCTGACAGA GAGGCTGAAG TCCCACCTGA GCAACATATG GAAGATAAAC CGTAAGTATA TATAC----- ---------- ----------
Ani40            CAACAACTAA GGCTGACAGA GAGGCTGAAG TCCCACCTGA GCAACAAATG GAAGATAAAC CGTAAGTATA TATAC----- ---------- ----------

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                        810        820        830        840        850        860        870        880        890        900
Lmo01           ---------- ---------- ---GAAGCA- GAT------- --------TC TACTTGGTGC AATGT----- ------TTTT TGTTTATG-T TAAGTCTCAC
Lmo02           ---------- ---------- ---GAAGCA- GAT------- --------TC TACTTGGTGC AATGT----- ------TTTT TGTTTATG-T TAAGTCTCAC
Lmo03           ---------- ---------- ---GAAGCA- GAT------- --------TC TACTTGGTGC AATGT----- ------TTTT TGTTTATG-T TAAGTCTCAC
Lmo04           ---------- ---------- ---GAAGCA- GAT------- --------TC TACTTGGTGC AATGT----- ------TTTT TGTTTATG-T TAAGTCTCAC
Lmo05           ---------- ---------- ---GAAGCA- GAT------- --------TC TACTTGGTGC AATGT----- ------TTTT TGTTTATG-T TAAGTCTCAC
Lmo06           ---------- ---------- ---GAAGCA- GAT------- --------TC TACTTGGTGC AATGT----- ------TTTT TGTTTATG-T TAAGTCTCAC
Lmo07           ---------- ---------- ---GAAGCA- GAT------- --------TC TACTTGGTGC AATGT----- ------TTTT TGTTTATG-T TAAGTCTCAC
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Lmo11           ---------- ---------- ---GAAGCA- GAT------- --------TC TACTTGGTGC AATGT----- ------TTTT TGTTTATG-T TAAGTCTCAC
Lmo12           ---------- ---------- ---GAAGCA- GAT------- --------TC TACTTGGTGC AATGT----- ------TTTT TGTTTATG-T TAAGTCTCAC
Lmo13           ---------- ---------- ---GAAGCA- GAT------- --------TC TACTTGGTGC AATGT----- ------TTTT TGTTTATG-T TAAGTCTCAC
Lti01           ---------- ---------- ---GAAGCA- GAT------- --------TC TACTTAGTGC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Lti02           ---------- ---------- ---GAAGCA- GAT------- --------TC TACTTAGTGC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Lti03           ---------- ---------- ---GAAGCA- GAT------- --------TC TACTTAGTGC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Lti04           ---------- ---------- ---GAAGCA- GAT------- --------TC TACTTAGTGC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Lti05           ---------- ---------- ---GAAGCA- GAT------- --------TC TACTTAGTGC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Lti06           ---------- ---------- ---GAAGCA- GAT------- --------TC TACTTAGTGC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Lti07           ---------- ---------- ---GAAGCA- GAT------- --------TC TACTTAGTGC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Lti08           ---------- ---------- ---GAAGCA- GAT------- --------TC TACTTAGTGC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Lti09           ---------- ---------- ---GAAGCA- GAT------- --------TC TACTTAGTGC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Mhi01           ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATTC TACTTGGTGC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAG
Mhi02           ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATTC TACTTGGTGC AATGT----- -------CTT TGTTTATG-T TAAGTCTCAG
Mhi03           ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATTC TACTTGGTGC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAG
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Mhi07           ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATTC TACTTGGTGC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAG
Lth01           ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATTC TACTTAGTCC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Lth02           ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATTC TACTTAGTCC AATGT----- -------TTT TGTT-ATG-C TAAGTCTCAC
Lth03           ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATTC TACTTAGTCC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Lth04           ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATTC TACTTAGTCC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Lth05           ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATTC TACTTAGTCC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Lth06           ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATTC TACTTAGTCC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Lth07           ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATTC TACTTAGTCC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Lth08           ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATTC TACTTAGTCC AATGT----- -------TTT TGTT-ATG-C TAAGTCTCAC
Lth09           ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATTC TACTTAGTCC AATGT----- -------TTT TGTT-ATG-C TAAGTCTCAC
Lth10           ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATTC TACTTAGTCC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Lth11           ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATTC TACTTAGTCC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Lth12           ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATTC TACTTAGTCC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
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Lth13         ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATTC TACTTAGTCC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Mal01         ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATTC TACTTAGTCC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Mal02         ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGGTTC TACT-AGTCC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Mal03         ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATTC TACTTAGTCC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Mal04         ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATTC TACTTAGTCC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Mal05         ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATTC TACTTAGTCC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Mal06         ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATTC TACTTAGTCC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Mal07         ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATTC TACTTAGTCC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Mal08         ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATTC TACTTAGTCC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Mal09         ---------- ---------- ---GAAGCA- GATCAATGA- --TATGATTC TATTTGGTGC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Ltr01         ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATTC TACTTAGTGC AGTGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Ltr02         ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATTC TACTTAGTGC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Ltr03         ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATTC TACTTAGTGC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Ltr04         ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATTC TACTTAGTGC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Ltr05         ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATTC TACTTAGTGC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Ltr06         ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATTC TACTTAGTGC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Ltr07         ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATTC TACTTAGTGC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Lag01         ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATTC TACTTAGTGC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Lag02         ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATTC TACTTAGTGC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Lag03         ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATTC TACTTAGTGC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Lag04         ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATTC TACTTAGTGC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Lag05         ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATTC TACTTAGTGC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Lfl01         ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATTC TACTTAGTGC AATGT----- -------TTT AGTTTATG-T TAAGTCTCAC
Lfl02         ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATTC TACTTAGTGC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Ltp01         ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATTC TACTTAGTGC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Lbr01         ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATTC TACTTAGTGC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Lbr02         ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATTC TACTTAGTGC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Lbr03         ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATTC TACTTAGTGC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Lob01         ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATTC TACTTAGTGC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Lob02         ---------- ---------- ---GAAGCA- GATCAATGA- --TACGATTC TACTTAGTGC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Lob03         ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATTC TACTTAGTGC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Lob04         ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATTC TACTTAGTGC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Lob05         ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATTC TACTTAGTGC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Lob06         ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATTC TACTTAGTGC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
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Lol01         ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATTC TACTTAGTGC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Lol02         ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATTC TACTTAGTGC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Lol03         ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATTC TACTTAGTGC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Lol04         ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATTC TACTTAGTGC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Mae01         C--------- ---------- ---GAAGCA- GATCAATGAG ---AAGATTC GACTTAGTGC AATGT----- -------TTT TGATTATG-T TAAGTCTCAC
Mae02         ---------- ---------- ---GAAGCA- GATCAATGAG ---AAGATTC GACTTAGTGC AATGT----- -------TTT TGATTATG-T TAAGTCTCAC
Mae03         ---------- ---------- ---GAAGCA- GATCAATGAG ---AAGATTC GACTTAGTGC AATGT----- -------TTT TGATTATG-T TAAGTCTCAC
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Mae04        ---------- ---------- ---GAAGCA- GATCAATGAG ---AAGATTC GACTTAGTGC AATGT----- -------TTT TGATTATG-T TAAGTCTCAC
Mae05        ---------- ---------- ---GAAGCA- GATCAATGAG ---AAGATTC GACTTAGTGC AATGT----- -------TTT TGATTATG-T TAAGTCTCAC
Mae06        ---------- ---------- ---GAAGCA- GATCAATGAG ---AAGATTC GACTTAGTGC AATGT----- -------TTT TGATTATG-T TAAGTCTCAC
Mae07        ---------- ---------- ---GAAGCA- GATCAATGAG ---AAGATTC GACTTAGTGC AATGT----- -------TTT TGATTATG-T TAAGTCTCAC
Mae08        ---------- ---------- ---GAAGCA- GATCAATGAG ---AAGATTC GACTTAGTGC AATGT----- -------TTT TGATTATG-T TAAGTCTCAC
Mmo01        ---------- ---------- ---GAAGCA- GATCAATGA- --TATGATTC TATTTGGTGC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Mmo02        ---------- ---------- ---GAAGCA- GATCAATGA- --TATGATTC TATTTGGTGC AATGT----- -------GTT TGTTTATG-T TAAGTCTCAC
Mmo03        ---------- ---------- ---GAAGCA- GATCAATGA- --TATGATTC TATTTGGTGC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Mmo04        ---------- ---------- ---GAAGCA- GATCAATGA- --TATGATTC TATTTGGTGC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Mmo05        ---------- ---------- ---GAAGCA- GATCAATGA- --TATGATTC TATTTGGTGC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Mmo06        ---------- ---------- ---GAAGCA- GATCAATGA- --TATGATTC TATTTGGTGC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
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Mmo09        ---------- ---------- ---GAAGCA- GATCAATGA- --TATGATTC TATTTGGTGC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
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Mto01        ---------- ---------- ---GAAGCA- GATCAATGA- --TATGATTC TATTTGGTGC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Mto02        ---------- ---------- ---GAAGCA- GATCAATGA- --TATGATTC TATTTGGTGC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Mto03        ---------- ---------- ---GAAGCA- GATCAATGA- --TATGATTC TATTTGGTGC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Mto04        ---------- ---------- ---GAAGCA- GATCAATGA- --TATGATTC TATTTGGTGC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Mto05        ---------- ---------- ---GAAGCA- GATCAATGA- --TATGATTC TATTTGGTGC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Mto06        ---------- ---------- ---GAAGCA- GATCAATGA- --TATGATTC TATTTGGTGC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Mto07        ---------- ---------- ---GAAGCAA GATCAATGA- --TAAGATTC TACT-AGTGC AATGT----- -----TTTTT TGTTTACATT CAAGTCTTAC
Ahi01        ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATT- ---------- ---------- ---------- -----ATG-T TAAGCCTCAA
Ahi02        ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATT- ---------- ---------- ---------- -----ATG-T TAAGTCTCAA
Ahi03        ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATT- ---------- ---------- ---------- -----ATG-T TAAGTCTCAA
Ahi04        ---------- ---------- ---GAAGCA- GATCAATGA- --TACGATTC TACTTAGTGC AATGT----- -------TTT TGTTTATG-T TAAGTCTCGC
Ahi05        ---------- ---------- ---GAAACA- GATCAATGA- --TAAGATT- ---------- ---------- ---------- -----ATG-T TAAGTCTCAA
Ahi06        ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATT- ---------- ---------- ---------- -----ATG-T TAAGTCTCAA
Ahi07        ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATT- ---------- ---------- ---------- -----ATG-T TAAGTCTCAA
Ahi08        ---------- ---------- ---GAAGCA- GATCAATGA- --TACGATTC TACTTAGTGC AATGT----- -------TTT TGTTTATG-T TAAGTCTCGC
Alo01        ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATTC TACTTGGTGC AATGT----- -------TTT TGTTTATG-T TGAGTCTCAC
Alo02        ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATTC TACTTGGTGC AATGT----- -------TTT TGTTTATG-T TGAGTCTCAC
Alo03        ---------- ---------- ---GAGGCA- GATCAATGA- --TAAGATTC TACTTGGTGC AATGT----- -------TTT TGTTTATG-T TGAGTCTCAC
Alo04        ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATTC TACTTGGTGC AATGT----- -------TTT TGTTTATG-T TGAGTCTCAC
Alo05        ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATTC TACTTGGTGC AATGT----- -------TTT TGTTTATG-T TGAGTCTCAC
Alo06        ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATTC TACTTGGTGC AATGT----- -------TTT TGTTTATG-T TGAGTCTCAC
Alo07        ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATTC TACTTGGTGC AATGT----- -------TTT TGTTTATG-T TGAGTCTCAC
Alo08        ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATTC TACTTGGTGC AATGT----- -------TTT TGTTTATG-T TGAGTCTCAC
Alo09        ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATTC TACTTGGTGC AATGT----- -------TTT TGTTTATG-T TGAGTCTCAC
Alo10        ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATTC TACTTGGTGC AATGT----- -------TTT TGTTTATG-T TGAGTCTCAC
Mca01        ---------- ---------- ---------- --TCAATGA- --TACGATTC TACTTAGTGC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Mca02        ---------- ---------- ---------- --TCAATGA- --TACGATTC TACTTGGTGC AATGT----- -------TTT TGGTTAAGGT TAAGTCTCAC
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Mca03        ---------- ---------- ---------- GCTCAATGA- --TACGATTC TACTTAGTGC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Mca04        ---------- ---------- ---------- GCTCAATGA- --TACGATTC TACTTAGTGC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Mtf01        ---------- ---------- ---GAAGCA- GATCGATGA- --TACGATTC GACTTAGTGC AATGC----- -------TTA TGTTTATG-T TAAGTCTAAA
Mtf02        ---------- ---------- ---GAAGCA- GATCGATGA- --TACGATTC GACTTAGTGC AATGC----- -------TTA TGTTTATG-T TAAGTCTAAA
Mtf03        ---------- ---------- ---GAAGCA- GATCGATGA- --TACGATTC GACTTAGTGC AATGC----- -------TTA TGTTTATG-T TAAGTCTAAA
Mtf04        ---------- ---------- ---GAAGCA- GATCGATGA- --TACGATTC GACTTAGTGC AATGC----- -------TTA TGTTTATG-T TAAGTCTAAA
Mtf05        C--------- ---------- ---GAAGCA- GATCGATGA- --TACGATTC GACTTAGTGC AATGC----- -------TTA TGTTTATG-T TAAGTCTAAA
Mma01        ---------- ---------- ---GAAGCA- GATCGATGA- --TAAGATTC GACTTAGTGC AATGCTTATG TTTATGTTTA TGTTTATG-T TAAGTCTCAT
Mma02        ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATTC TACTTAGTGC AAGGT----- -------TTT TGTTTATG-T CAAGTCTTAC
Mma03        ---------- ---------- ---GAAGCA- GATCGATGA- --TAAGATTC GACTTAGTGC AATGCTTATG TTTATGTTTA TGTTTATG-T TAAGTCTCAT
Mma04        ---------- ---------- ---GAAGCA- GATCGATGA- --TAAGATTC GACTTAGTGC AATGCTTATG TTTATGTTTA TGTTTATG-T TAAGTCTCAT
Mma05        ---------- ---------- ---GAAGCA- GATCGATGA- --TAAGATTC GACTTAGTGC AATGCTTATG TTTATGTTTA TGTTTATG-T TAAGTCTCAT
Las01        ---------- ---------- ---------- ---------- ---------- ---TTAGTGC AATGT----- -------TTT TGTTTACG-T TAAGTCTCAC
Las02        ---------- ---------- ---------- ---------- ---------- ---TTAGTGC AATGT----- -------TTT TGTTTATG-- TAAGTCTCAC
Las03        ---------- ---------- ---------- ---------- ---------- ---TTAGTGC AATGT----- -------TTT TGTTTACG-T TAAGTCTCAC
Las04        ---------- ---------- ---GAAGCA- TATCAATTA- --TAAGATTC TACTTAGTGC AATGT----- -------TTT TGTTTATG-- TAAGTCTCAC
Las05        ---------- ---------- ---GTGCAA- ---------- ---------- ---------- --TGT----- -------TTT TGTTTACG-T TAAGTCTCAA
Las06        ---------- ---------- ---GAAGCA- TATCAATTA- --TAAGATTC TACTTAGTGC AATGT----- -------TTT TGTTTATG-- TAAGTCTCAC
Las07        ---------- ---------- ---GAAGCA- TATCAATTA- --TAAGATTC TACTTAGTGC AATGT----- -------TTT TGTTTATG-- TAAGTCTCAC
Las08        ---------- ---------- ---GAAGCA- TATCAATTA- --TAAGATTC TACTTAGTGC AATGT----- -------TTT TGTTTATG-- TAAGTCTCAC
Lpe01        TATATACACA CACACACACA C--GAAGCA- TATCAATTA- --TAAGATTC TACTTAGTGC AATGT----- -------TTT TGTTTATG-- TAAGTCTCAC
Lpe02        TATATATACA CACACACACA CACGAAGCA- TATCAATTA- --TAAGATTC TACTTAGTGC AATGT----- -------TTT TGTTTATG-- TAAGTCTCAC
Lpe03        TATATACACA CACACACAC- ---GAAGCA- TATCAATTA- --TAAGATTC TACTTAGTGC AATGT----- -------TTT TGTTTATG-- TAAGTCTCAC
Lpe04        ---------- ---------- ---AGTGCA- ---------- ---------- ---------- -GTGT----- -------TTT TGTTTACG-T TAAGTCTCAC
Lac01        ---------- ---------- ---GAAGCA- GATCAATTA- --TAAGAGTC TACTTAGTGC AATGT----- -------TTT TGTTTACG-T TAAGTCTCAC
Lac02        ---------- ---------- ---GAAGCA- GATCAATTA- --TAAGAGTC TACTTAGTGC AATGT----- -------TTT TGTTTACG-T TAAGTCTCAC
Lac03        ---------- ---------- ---GAAGCA- GATCAATTA- --TAAGAGTC TACTTAGTGC AATGT----- -------TTT TGTTTACG-T TAAGTCTCAC
Lac04        ---------- ---------- ---GAAGCA- GATCAATTA- --TAAGAGTC TACTTAGTGC AATGT----- -------TTT TGTTTACG-T TAAGTCTCAC
Lac05        ---------- ---------- ---GAAGCA- GATCAATTA- --TAAGAGTC TACTTAGTGC AATGT----- -------TTT TGTTTACG-T TAAGTCTCAC
Lac06        ---------- ---------- ---GAAGCA- GATCAATTA- --TAAGAGTC TACTTAGTGC AATGT----- -------TTT TGTTTACG-T TAAGTCTCAC
Lac07        ---------- ---------- ---GAAGCA- GATCAATTA- --TAAGAGTC TACTTAGTGC AATGT----- -------TTT TGTTTACG-T TAAGTCTCAC
Lac08        ---------- ---------- ---GAGGCA- GATCAATTA- --TAAGAGTC TACTTAGTGC AATGT----- -------TTT TGTTTACG-T TAAGTCTCAC
Lma01        ---------- ---------- ---GAAGCA- GATCAATTA- --TAAGAGTC TACTTAGTGC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Lma02        ---------- ---------- ---GAAGCA- GATCAATTA- --TAAGAGTC TACTTAGTGC AATGT----- -------TTT TGTTTATG-T TAAGTCTCAC
Lcr01        ---------- ---------- ---GAAGCA- TATCAATTA- --TAAGATTC TACTTAGTGC AATGT----- -------TTT TGTTTATG-- TAAGTCTCAC
Lcr02        ---------- ---------- ---GTAGCA- GATCAATGA- --TAAGATTC TACTTAGTGC AAGGT----- -------TTT TATTTACC-- CAAGTCTTAC
Msy01        ---------- ---------- ---GAAGCA- TATCAATTA- --TAAGATTC TACTTAGTGC AATGT----- -------TTT TGTTTATG-- TAAGTCTCAC
Msy02        ---------- ---------- ---GAAGCA- TATCAATTA- --TAAGATTC TACTTAGTGC AATGT----- -------TTT TGTTTATG-- TAAGTCTCAC
Msy03        ---------- ---------- ---GAAGCA- TATCAATTA- --TAAGATTC TACTTAGTGC AATGT----- -------TTT TGTTTATG-- TAAGTCTCAC
Msy04        ---------- ---------- ---GAAGCA- TATCAATTA- --TAAGATTC TACTTAGTGC AATGT----- -------TTT TGTTTATG-- TAAGTCTCAC
Msy05        ---------- ---------- ---GAAGCA- TATCAATTA- --TAAGATTC TACTTAGTGC AATGT----- -------TTT TGTTTATG-- TAAGTCTCAC
Lmu01        ---------- ---------- ---GTAGCA- GATCGATGT- --TAAGATTC TACTTAGTGC AAGGT----- -------TTT TATTTACC-- AAAGTCTTAC
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Lmu02        ---------- ---------- ---GTAGCA- GATCGATGT- --TAAGATTC TACTTAGTGC AAGGT----- -------TTT TATTTACC-- AAAGTCTTAC
Lmu03        ---------- ---------- ---GAAGCA- TATCAATTA- --TAAGATTC TACTTAGTGC AATGT----- -------TTT TGTTTATG-- TAAGACTCAC
Lmu04        ---------- ---------- ---GAAGCA- TATCAATTA- --TAAGATTC TACTTAGTGC AATGT----- -------TTT TGTTTATG-- TCAGACTCAC
Lmu05        ---------- ---------- ---GAAGCA- TATCAATTA- --TAAGATTC TACTTAGTGC AATGT----- -------TTT TGTTTATG-- TAAGACTCAC
Lmu06        ---------- ---------- ---GAAGCA- TATCAATTA- --TAAGATTC TACTTAGTGC AATGT----- -------TTT TGTTTATG-- TAAGACTCAC
Lmu07        ---------- ---------- ---GAAGCA- TATCAATTA- --TAAGATTC TACTTAGTGC AATGT----- -------TTT TGTTTATG-- TAAGACTCAC
Lmu08        ---------- ---------- ---GAAGCA- TATCAATTA- --TAAGATTC TACTTAGTGC AATGT----- -------TTT TGTTTATG-- TAAGACTCAC
Lmu09        ---------- ---------- ---GAAGCA- TATCAATTA- --TAAGATTC TACTTAGTGC AATGT----- -------TTT TGTTTATG-- TAAGACTCAC
Mpa01        ---------- ---------- ---GAAGCA- TATCAATTA- --TAAGATTC TACTTAGTGC AATGT----- -------TTT TGTTTATG-- TAAGACTCAC
Mpa02        ---------- ---------- ---GAAGCA- TATCAATTA- --TAAGATTC TACTTAGTGC AATGT----- -------TTT TGTTTATG-- TAAGACTCAC
Mpa03        ---------- ---------- ---GAAGCA- TATCAATTA- --TAAGATTC TACTTAGTGC AATGT----- -------TTT TGTTTATG-- TAAGACTCAC
Mpa04        ---------- ---------- ---GAAGCA- TATCAATTA- --TAAGATTC TACTTAGTGC AATGT----- -------TTT TGTTTATG-- TAAGACTCAC
Mpa05        ---------- ---------- ---GAAGCA- TATCAATTA- --TAAGATTC TACTTAGTGC AATGT----- -------TTT TGTTTATG-- TAAGACTCAC
Mpa06        ---------- ---------- ---GAAGCA- TATCAATTA- --TAAGATTC TACTTAGTGC AATGT----- -------TTT TGTTTATG-- TAAGACTCAC
Mve01        ---------- ---------- ---GAAGCA- TATCAATTA- --TAAGATTC TACTTAGTGC AATGT----- -------TTT TGTTTATG-- TAAGACTCAC
Mve02        ---------- ---------- ---GAAGCA- TATCAATTA- --TAAGATTC TACTTAGTGC AATGT----- -------TTT TGTTTATG-- TAAGACTCAC
Mve03        ---------- ---------- ---GAAGCA- TATCAATTA- --TAAGATTC TACTTAGTGC AATGT----- -------TTT TGTTTATG-- TAAGACTCAC
Mni01        ---------- ---------- ---GAAGCA- TATCAATTA- --TAAGATTC TACTTAGTGC AATGT----- -------TTT TGTTTACG-- TAAGTCTCAC
Mni02        ---------- ---------- ---GAAGCA- TATCAATTA- --TAAGATTC TACTTAGTGC AATGT----- -------TTT TGTTTACG-- TAAGTCTCAC
Mni03        ---------- ---------- ---GAAGCA- TATCAATTA- --TAAGATTC TACTTAGTGC AATGT----- -------TTT TGTTTACG-- TAAGTCTCAC
Mni04        ---------- ---------- ---GAAGCA- TATCAATTA- --CAAGATTC TACTTAGTGC AATGT----- -------TTT TGTTTACG-- TAAGTCTCAC
Mni05        ---------- ---------- ---GAAGCA- TATCAATTA- --TAAGATTC TACTTAGTGC AATGT----- -------TTT TGTTTACG-- TAAGTCTCAC
Mni06        ---------- ---------- ---GAAGCA- TATCAATTA- --TAAGATTC TACTTAGTGC AATGT----- -------TTT TGTTTACG-- TAAGTCTCAC
Mne01        C--------- ---------- ---GAAGCA- TATCAATTAC TATAAGATTC TACTTAGTGC AATGT----- -------TTT TGTTTATG-- TAAGTCTCAC
Aof01        ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATTC TACTTAGTGC TATGT----- -------TTT TGTTTATG-T TAAGTCTTAC
Aca01        ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATTC TACTTAGTGC TATGT----- -------TTT TGTTTATG-T TAAGTCTTAC
Aca02        ---------- ---------- ---GAAGCA- GATCAATGA- --TAAGATTC TACTTAGTGC TATGT----- -------TTT TGTTTATG-T TAAGTCTTAC
Ani40        ---------- ---------- ---AAAGCA- TATCAATGA- --TAAGATTC TACTTAGTGC AATGT----- -------TTT TGTTTATG-T TAAGTCTTAC


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                    910        920        930        940        950        960        970        980        990       1000
Lmo01        --TGATATGT AAAA-TTTGG TTTTGC---- AGGGCACCG- --GATGCTTC TCAGCCCCTC TCAACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lmo02        --TGATATGT AAAA-TTTGG TTTTGC---- AGGGCACCG- --GATGCTTC TCAGCCCCTC TCAACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lmo03        --TGATATGT AAAA-TTTGG TTTTGC---- AGGGCACCG- --GATGCTTC TCAGCCCCTC TCAACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lmo04        --TGATATGT AAAA-TTTGG TTTTGC---- AGGGCACCG- --GATGCTTC TCAGCCCCTC TCAACTATAA TTCCAATTCC GAGAAGCAAA CTTGCACCAT
Lmo05        --TGATATGT AAAA-TTTGG TTTTGC---- AGGGCACCG- --GATGCTTC TCAGCCCCTC TCAACTATAA TTCCAATTCC GAGAAGCAAA CTTGCACCAT
Lmo06        --TGATATGT AAAA-TTTGG TTTTGC---- AGGGCACCG- --GATGCTTC TCAGCCCCTC TCAACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lmo07        --TGATATGT AAAA-TTTGG TTTTGC---- AGGGCACCG- --GATGCTTC TCAGCCCCTC TCAACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lmo08        --TGATATGT AAAA-TTTGG TTTTGC---- AGGGCACCG- --GATGCTTC TCAGCCCCTC TCAACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lmo09        --TGATATGT AAAA-TTTGG TTTTGC---- AGGGCACCG- --GATGCTTC TCAGCCCCTC TCAACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lmo10        --TGATATGT AAAA-TTTGG TTTTGC---- AGGGCACCG- --GATGCTTC TCAGCCCCTC TCAACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
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Lmo11        --TGATATGT AAAA-TTTGG TTTTGC---- AGGGCACCG- --GATGCTTC TCAGCCCCTC TCAACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lmo12        --TGATATGT AAAA-TTTGG TTTTGC---- AGGGCACCG- --GATGCTTC TCAGCCCCTC TCAACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lmo13        --TGATATGT AAAA-TTTGG TTTTGC---- AGGGCACCG- --GATGCTTC TCAGCCCCTC TCAACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lti01        --TGATATGT AAAA-TTTGG TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lti02        --TGATATGT AAAA-TTTGG TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lti03        --TGATATGT AAAA-TTTGG TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lti04        --TGATATGT AAAA-TTTGG TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lti05        --TGATATGT AAAA-TTTGG TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lti06        --TGATATGT AAAA-TTTGG TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lti07        --TGATATGT AAAA-TTTGG TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lti08        --TGATATGT AAAA-TTTGG TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lti09        --TGATATGT AAAA-TTTGG TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Mhi01        --TGATATGT AAAA-TTTGG TTTTGC---- AGGGCTCCA- --GATGCTTC CCAGCCCCTC TCTACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Mhi02        --TGATATGT AAAA-TTTGG TTTTGC---- AGGGCTCCA- --GATGCTTC CCAGCCCCTC TCTACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Mhi03        --TGATATGT AAAA-TTTGG TTTTGC---- AGGGCTCCA- --GATGCTTC CCAGCCCCTC TCTACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Mhi04        --TGATATGT AAAA-TTTGG TTTTGC---- AGGGCTCCA- --GATGCTTC CCAGCCCCTC TCTACTATAA TTCCAATTCC GAAAGGCAAA CTTGCACCAT
Mhi05        --TGATATGT AAAA-TTTGG TTTTGC---- AGGGCTCCA- --GATGCTTC CCAGCCCCTC TCTACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Mhi06        --TGATATGT AAAA-TTTGG TTTTGC---- AGGGCTCCA- --GATGCTTC CCAGCCCCTC TCTACTTTAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Mhi07        --TGATATGT AAAA-TTTGG TTTTGC---- AGGGCTCCA- --GATGCTTC CCAGCCCCTC TCTACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lth01        --TGATATGT AAAC-TTTGG TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lth02        --TGATATGT AAAC-TTTGG TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lth03        --TGATATGT AAAC-TTTGG TTTTGC---- AGGGCACCA- --GATGCCTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lth04        --TGATATGT AAAC-TTTGG TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lth05        --TGATATGT AAAC-TTTGG TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lth06        --TGATATGT AAAC-TTTGG TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lth07        --TGATATGT AAAC-TTTGG TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lth08        --TGATATGT AAAC-TTTGG TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lth09        --TGATATGT AAAC-TTTGG TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lth10        --TGATATGT AAAC-TTTGG TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lth11        --TGATATGT AAAC-TTTGG TTTTGC---- AGGGCACCA- --GATGCCTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lth12        --TGATATGT AAAC-TTTGG TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCTT
Lth13        --TGATATGT AAAC-TTTGG TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Mal01        --TGATATGT AAAC-TTTGG TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Mal02        --TGATATGT AAAC-TTTGG TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Mal03        --TGATATGT AAAC-TTTGG TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Mal04        --TGATATGT AAAC-TTTGG TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Mal05        --TGATATGT AAAC-TTTGG TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Mal06        --TGATATGT AAAC-TTTGG TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCAATATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Mal07        --TGATATGT AAAC-TTTGG TTTTGC---- AGGGTACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Mal08        --TGATATGT AAAC-TTTGG TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Mal09        --TGATATGT AAAT-TTTGG TTTTGC---- GGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Ltr01        --TGATATGT AAAA-TTTGG TTTTGC---- AGGACACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
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Ltr02          --TGATATGT AAAA-TTTGG TTTTGC---- AGGACACGA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Ltr03          --TGATATGT AAAA-TTTGG TTTTGC---- AGGACACGA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Ltr04          --TGATATGT AAAA-TTTGG TTTTGC---- AGGACACGA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Ltr05          --TGATATGT AAAA-TTTGG TTTTGC---- AGGACACCA- --GATGCTTC TCAGCCCCTC TCCACTATAG TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Ltr06          --TGATATGT AAAA-TTTGG TTTTGC---- AGGACACGA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Ltr07          --TGATATGT AAAA-TTTGG TTTTGC---- AGGACACGA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lag01          --TGATATGT AAAA-TTTGG TTTTGC---- AGGACACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lag02          --TGATATGT AAAA-TTTGG TTTTGC---- AGGACACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lag03          --TGATATGT AAAA-TTTGG TTTTGC---- AGGACACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lag04          --TGATATGT AAAA-TTTGG TTTTGC---- AGGACACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lag05          --TGATATGT AAAA-TTTGG TTTTGC---- AGGACACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lfl01          --TGATATGT AAAA-TTTGG TTTTGC---- AGGACACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lfl02          --TGATATGT AAAA-TTTGG TTTTGC---- AGGACACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Ltp01          --TGATATGT AAAA-TTTGG TTTTGC---- AGGACACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCTT
Lbr01          --TGATATGT AAAA-TTTGG TTTTGC---- AGGACACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCATCAT
Lbr02          --TGATATGT AAAA-TTTGG TTTTGC---- AGGACACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lbr03          --TGATATGT AAAA-TTTGG TTTTGC---- AGGACACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lob01          --TGATATGT AAAA-TTTGG TTTTTC---- AGGACACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lob02          --TGATATGT AAAA-TTTGG TTTTTC---- AGGACACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAC
Lob03          --TGATATGT AAAA-TTTGG TTTTTC---- AGGACACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lob04          --TGATATGT AAAA-TTTGG CTTTTC---- AGGACACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lob05          --TGATATGT AAAA-TTTGG TTTTTC---- AGGACACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lob06          --TGATATGT AAAA-TTTGG TTTTTC---- AGGACACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lob07          --TGATATGT AAAA-TTTGG TTTTTC---- AGGACACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lol01          --TGATATGT AAAA-TTTGG TTTTGC---- AGGACACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lol02          --TGATATGT AAAA-TTTGG TTTTGC---- AGGACACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lol03          --TGATACGT AAAA-TTTGG TTTTGC---- AGGACACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lol04          --TGATATGT AAAA-TTTGG TTTTGC---- AGGACACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Mae01          --TGATATGT AAAA-TTTGT TTTTGC---- AGGGCACCA- --GATGCTTC ACAGCCCCTA TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Mae02          --TGATATAT AAAA-TTTGT TTTTGC---- AGGGCACCA- --GATGCTTC ACAGCCCCTA TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Mae03          --TGATATGT AAAA-TTTGT TTTTGC---- AGGGCACCA- --GATGCTTC ACAGCCCCTA TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Mae04          --TGATATGT AAAA-TTTGT TTTTGC---- AGGGCACCA- --GATGCTTC ACAGCCCCTA TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Mae05          --TGATATGT AAAA-TTTGT TTTTGC---- AGGGCACCA- --GATGCTTC ACAGCCCCTA TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Mae06          --TGATATGT AAAA-TTTGT TTTTGC---- AGGGCACCA- --GATGCTTC ACAGCCCCTA TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Mae07          --TGATATGT AAAA-TTTGT TTTTGC---- TGGGCACCA- --GATGCTTC ACAGCCCCTA TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Mae08          --TGATATGT AAAA-TTTGT TTTTGC---- AGGGCACCA- --GATGCTTC ACAGCCCCTA TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Mmo01          --TGATATGT AAAT-CTTGA TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Mmo02          --TGATATGT AAAT-TTTGG TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Mmo03          --TGATATGT AAAT-CTTGG TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Mmo04          --TGATATGT AAAT-TTTGG TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAGTTCC GAAAAGCAAA CTTGCACCAT
Mmo05          --TGAKATGT AAAT-TTTGG TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Mmo06          --TGATATGT AAAT-CTTGG TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
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Mmo07        --TGATATGT AAAT-CTTGG TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Mmo08        --TGATATGT AAAT-TTTGG TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Mmo09        --TGATATGT AAAT-TTTGG TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Mmo10        --TGATGTGT AAAT-CTTGG TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TCCCAATTCC GAAAAGCAAA CTTGCACCAT
Mto01        --TGATATGT AAAT-TTTGG TTATGC---- AGGGCACCA- --GATGCTTC TCAGCCCCCC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Mto02        --TGATATGT AAAT-TTTGG TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Mto03        --TGATATGT AAAT-TTTGG TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Mto04        --TGATATGT AAAT-TTTGG TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Mto05        --TGATATGT AAAT-TTTGG TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Mto06        --TGATATGT AAAT-TTTGG TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Mto07        --TGATATGT AAAA-TTTGC ATTTGC---- AGATCACCA- --GATGCTTC CCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCGT
Ahi01        --TCATATGT AAAA-TTTGC TATTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTT TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Ahi02        --TCATATGT AAAA-TTTGC TATTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTT TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Ahi03        --TCATATGT AAAA-TTTGC TATTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTT TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Ahi04        --TGATATGT AAAA-TTTGG CTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC TAAAAGCAAA CTTGCACCAT
Ahi05        --TCATATGT AAAA-TTTGC TATTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTT TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Ahi06        --TCATATGT AAAA-TTTGC TATTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTT TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Ahi07        --TCATATGT AAAA-TTTGC TATTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTT TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Ahi08        --TGATATGT AAAA-TTTGG CTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC TAAAAGCAAA CTTGCACCAT
Alo01        --TGATATGT AAAA-TTTGC TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTCGCACCAT
Alo02        --TGATATGT AAAA-TTTGC TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTCGCACCAT
Alo03        --TGATATGT AAAA-TTTGC TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTCGCACCAT
Alo04        --TGATATGT AAAA-TTTGC TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTCGCACCAT
Alo05        --TGATATGT AAAA-TTTGC TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTCGCACCAT
Alo06        --TGATATGT AAAA-TTTGC TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTCGCACCAT
Alo07        --TGATATGT AAAA-TTTGC TTTTGC---- AGGGCACCA- --GATGSTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTCGCACCAT
Alo08        --TGATATGT AAAA-TTTGC TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCGCTATAA TTCCAATTCC GAAAAGCAAA CTCGCACCAT
Alo09        --TGATATGT AAAA-TTTGC TTTTGC---- AGGGCGCCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTCGCACCAT
Alo10        --TGATATGT AAAA-TTTGC TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTCGCACCAT
Mca01        --TGATATGT GAAA-TTTGG TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCGATTCC TAAAAGCAAA CTTGCACCAT
Mca02        --TGATATGT GAAA-TTTGG TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCGATTCC TAAAAGCAAA CTTGCACCAT
Mca03        --TGATATGT GAAA-TTTGG TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCGATTCC TAAAAGCAAA CTTGCACCAT
Mca04        --TGATATGT GAAA-TTTGG TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCGATTCC TAAAAGCAAA CTTGCACCAT
Mtf01        --TTATATGT AAAA-CTTGG TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTG TCCGCTATAA TTCCAATTCC GAAAAGCAAG CTTGCACCAT
Mtf02        --TTATATGT AAAA-CTTGG TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTG TCCGCTATAA TTCCAATTCC GAAAAGCAAG CTTGCACCAT
Mtf03        --TTATATGT AAAA-CTTGG TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTG TCCGCTATAA TTCCAATTCC GAAAAGCAAG CTTGCACCAT
Mtf04        --TTATATGT AAAA-CTTGG TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTG TCCGCTATAA TTCCAATTCC GAAAAGCAAG CTTGCACCAT
Mtf05        --TTATATGT AAAA-CTTGG TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTG TCCACTATAA TTCCAATTCC GAAAAGCAAG CTTGCACCAT
Mma01        --TGATATGT AAAA-CTTGG TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTG TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Mma02        --TGATATGT AAAA-CTTGC ATTTGC---- AGGGCACCAC CAGATGCTTC CCAGCCCCTC TCCGCTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Mma03        --TGATATGT AAAA-CTTGG TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTG TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Mma04        --TGATATGT AAAA-CTTGG TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTG TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
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Mma05        --TGATATGT AAAA-CTTGG TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTG TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Las01        ACTGATATGT AAAT-TTTGC TTT-GC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Las02        --TGATATGT AAAA-TTTGC TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Las03        ACTGATATGT AAAT-TTTGC TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Las04        --TGATATGT AAAA-TTTGC TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATGA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Las05        -CTGATATGT AAAT-TTTGC TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Las06        --TGATATGT AAAA-TTTGC TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Las07        --TGATATGT AAAA-TTTGC TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Las08        --TGATATGT AAAA-TTTGC TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCGAA CTTGCACCAT
Lpe01        --TGATATGT AAAA-TTTGC TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lpe02        --TGATATGT AAAA-TTTGC TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lpe03        --TAATATGT AAAA-TTTGC TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lpe04        ACTGATATGT AAAT-TTTGC TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lac01        --TGATATGT AAAA-TTTGC TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lac02        --TGATATGT AAAA-TTTGC TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lac03        --TGATATGT AAAA-TTTGC TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCGT
Lac04        --TGATATGT AAAA-TTTGC TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lac05        --TGATATGT AAAA-TTTGC TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lac06        --TGATATGT AAAA-TTTGC TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lac07        --TGATATGT AAAA-TTTGC TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAACTCC GAAAAGCAAA CTTGCACCAT
Lac08        --TGATATGT AAAA-TTTGC TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lma01        --TGATATGT AAAA-TTTGC TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lma02        --TGATATGT AAAA-TTTGC TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lcr01        --TGATATGT AAAA-TTTGC TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lcr02        --TGATATGT AAAAACTTGC ATTTGCTTGC AGGGCAGCA- --GATGCTTC CCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCGT
Msy01        --TGATATGT AAAA-TTTGC TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCCATTCC GAAAAGCAAA CTTGCACCAT
Msy02        --TGATATGT AAAA-TTTGC TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Msy03        --TGATATGT AAAA-TTTGC TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Msy04        --TGATATGT AAAA-TTTGC TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Msy05        --TGATATGT AAAA-TTTGC TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lmu01        --TGATATGT AAAA-CTTGC ATTTGCTTGC AGGGCAGCA- --GATGCTTC CCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCGT
Lmu02        --TGATATGT AAAA-CTTGC ATTTGCTTGC AGGGCAGCA- --GATGCTTC CCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCGT
Lmu03        --TGATATGT AAAA-TTTGC TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCGT
Lmu04        --TGATATGT AAAA-TTTGC TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lmu05        --TGATATGT AAAA-TTTGC TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lmu06        --TGATATGT AAAA-TTTGC TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lmu07        --TGATATGT AAAA-TTTGC TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lmu08        --TGATATGT AAAA-TTTGC TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Lmu09        --TGATATGT AAAA-TTTGC TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Mpa01        --TGATATGT AAAA-TTTGC TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Mpa02        --TGATATGT AAAA-TTTGC TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Mpa03        --TGATATGT AAAA-TTTGC TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
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Mpa04        --TGATATGT AAAA-TTTGC TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Mpa05        --TGATATGT AAAA-TTTGC TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Mpa06        --TGATATGT AAAA-TTTGC TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Mve01        --TGATATGT AAAA-TTTGC TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Mve02        --TGATATGT AAAA-TTTGC TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Mve03        --TGATATGT AAAA-TTTGC TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Mni01        --TGATATCT AAAA-TTTGC TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Mni02        --TGATATCT AAAA-TTTGC TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Mni03        --TGATATCT AAAA-TTTGC TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Mni04        --TGATATCT AAAA-TTTGC TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Mni05        --TGATATCT AAAA-TTTGC TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Mni06        --TGATATCT AAAA-TTTGC TTTTGC---- AGGGCACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Mne01        --TGATATGT AAAA-TTTGC TTTTGC---- AGGGAACCA- --GATGCTTC TCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Aof01        --TGATATGT AAAA-TTTGC TTTTGC---- AGGATACCA- --GATGCTTC CCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCGT
Aca01        --TGATATGT AAAA-TTTGC TTTTGC---- AGGATACCA- --GATGCTTC CCAGCCCCTC TCCACTATAA TTCCAATTCC GAGAAGCAAA CTTGCACCAT
Aca02        --TGATATGT AAAA-TTTGC TTTTGC---- AGGATACCA- --GATGCTTC CCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
Ani40        --TGATATGT AAAA-TTTGC TTTTGC---- AGGGCACCA- --GATGCTTC CCAGCCCCTC TCCACTATAA TTCCAATTCC GAAAAGCAAA CTTGCACCAT
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             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|
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Lmo02        ACCGAACCGT GATTATTATG CGTCTGATCA TTCTCGGTCT TTTCTTCCAT TACCGAGTAA CAAACCCTGT CGACA
Lmo03        ACCGAACCGT GATCATTATG CGTCTGATCA TTCTCGGTCT TTTCTTCCAT TACCGAGTAA CAAACCCCGT CGACA
Lmo04        ACCGAACCGT GATCATTATG CGTCTGATCA TTCTCGGTCT TTTCTTCCAT TACCGAGTAA CAAACCCTGT CGACA
Lmo05        ACCGAACCGT GATCATTATG CGTCTGATCA TTCTCGGTCT TTTCTTCCAT TACCGAGTAA CAAACCCTGT CGACA
Lmo06        ACCGAACCGT GATCATTATG CGTCTGATCA TTCTCGGTCT TTTCTTCCAT TACCGAGTAA CAAACCCTGT CGACA
Lmo07        ACCGAACCGT GATCATTATG CGTCTGATCA TTCTCGGTCT TTTCTTCCAT TACCGAGTAA CAAACCCTGT CGACA
Lmo08        ACCGAACCGT GATTATTATG CGTCTGATCA TTCTCGGTCT TTTCTTCCAT TACCGAGTAA CAAACCCTGT CGACA
Lmo09        ACCGAACCGT GATTATTATG CGTCTGATCA TTCTCGGTCT TTTCTTCCAT TACCGAGTAA CAAACCCTGT CGACA
Lmo10        ACCGAACCGT GATCATTATG CGTCTGATCA TTCTCGGTCT TTTCTTCCAT tACCGAGTAA CAAACCCCGT CGACA
Lmo11        ACCGAACCGT GATCATTATG CGTCTGATCA TTCTCGGTCT TTTCTTCCAT AACCGAGTAA CAAACCCCGT CGACA
Lmo12        ACCGAACCGT GATCATTATG CGTCTGATCA TTCTCGGTCT TTTCTTCCAT TACCGAGTAA CAAACCCTGT CGACA
Lmo13        ACCGAACCGT GATCATTATG CGTCTGATCA TTCTCGGTCT TTTCTTCCAT TACCGAGTAA CAAACCCTGT CGACA
Lti01        ACCGAACTGT GATCATTATG CGTCTGATCA TTCTCGGTCT TTTCTTCCAT TACCGAGTAA CAAACCCTGT CGACA
Lti02        ACCGAACTGT GATCATTATG CGTCTGATCA TTCTCGGTCT TTTCTTCCAT TACCGAGTAA CAAACCCTGT CGACA
Lti03        ACCGAACTGT GATCATTATG CGTCTGATCA TTCTCGGTCT TTTCTTCCAT TACCGAGTAA CAAACCCTGT CGACA
Lti04        ACCGAACTGT GATCATTATG CGTCTGATCA TTCTCGGTCT TTTCTTCCAT TACCGAGTAA CAAACCCTGT CGACA
Lti05        ACCGAACTGT GATCATTATG CGTCTGATCA TTCTCGGTCT TTTCTTCCAT TACCGAGTAA CAAACCCTGT CGACA
Lti06        ACCGAACTGT GATCATTATG CGTCTGATCA TTCTCGGTCT TTTCTTCCAT TACCGAGTAA CAAACCCTGT CGACA
Lti07        ACCGAACTGT GATCATTATG CGTCTGATCA TTCTCGGTCT TTTCTTCCAT TACCGAGTAA CAAACCCTGT CGACA
Lti08        ACCGAACTGT GATCATTATG CGTCTGATCA TTCTCGGTCT TTTCTTCCAT TACCGAGTAA CAAACCCTGT CGACA
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Lti09        ACCGAACTGT GATCATTATG CGTCTGATCA TTCTCGGTCT TTTCTTCCAT TACCGAGTAA CAAACCCTGT CGACA
Mhi01        ACCGAACTGT GATCATTATG CGGCTGATCA TTCTCGGTCT TTTCTTCCAT TACCGAGTAA CAAACCCTGT GGATA
Mhi02        ACCGAACTGT GATCATTATG CGGCTGATCA TTCTCGGTCT TTTCTTCCAT TACCGAGTAA CAAACCCTGT GGATA
Mhi03        ACCGAACTGT GATCATTATG CGGCTGATCA TTCTCGGTCT TTTCTTCCAT TACCGAGTAA CAAACCCTGT GGATA
Mhi04        ACCGAACTGT GATCATTATG CGGCTGATCA TTCTCGGTCT TTTCTTCCAT TACCGAGTAA CAAACCCTGT GGATA
Mhi05        ACCGAACTGT GATCATTATG CGGCTGATCA TTCTCGGTCT TTTCTTCCAT TACCGAGTAA CAAACCCTGT GGATA
Mhi06        ACCGAACTGT GATCATTATG CGGCTGATCA TTCTCGGTCT TTTCTTCCAT TACCGAGTAA CAAACCCTGT GGATA
Mhi07        ACCGAACTGT GATCATTATG CGGCTGATCA TTCTCGGTCT TTTCTTCCAT TACCGAGTAA CAAACCCTGT GGATA
Lth01        ACCGAACTGT GATCATTATG CGTCTGATCA TTCTCGGTCT TTTCTTCCAT TACCGAGTAA CAAACCCTGT CGACA
Lth02        ACCGAACTGT GATCATTATG CGTCTGATCA TTCTCGGTCT TTTCTTCCAT TACCGAGTAA CAAACCCTGT CGACA
Lth03        ACCGAACTGT GATCATTATG CGTCTGATCA TTCTCGGTCT CTTCTTCCAT TACCGAGTAA CAAACCCTGT CGACA
Lth04        ACCGAACTGT GATCATTATG CGTCTGATCA TTCTCGGTCT TTTCTTCCAT TACCGAGTAA CAAACCCTGT CGACA
Lth05        ACCGAACTGT GATCATTATG CGTCTGATCA TTCTCGGTCT TTTCTTCCAT TACCGAGTAA CAAACCCTGT CGACA
Lth06        ACCGAACTGT GATCATTATG CGTCTGATCA TTCTCGGTCT TTTCTTCCAT TACCGAGTAA CAAACCCTGT CGACA
Lth07        ACCGAACTGT GATCATTATG CGTCTGATCA TTCTCGGTCT TTTCTTCCAT TACCGAGTAA CAAACCCTGT CGACA
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Lth10        ACCGAACTGT GATCATTATG CGTCTGATCA TTCTCGGTCT TTTCTTCCAT TACCGAGTAA CAAACCCTGT CGACA
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Mal02        ACCGAACTGT GATCATTATG CGTCTGATCA TTCTCGGTCT TTTCTTCCAT TACCGAGTAA CAAACCCTGT CGACA
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Mal07        ACCGAACTGT GATCATTATG CGTCTGATCA TTCTCGGTCT TTTCTTCCAT TACCGAGTAA CAAACCCTGT CGACA
Mal08        ACCGAACTGT GATCATTATG CGTCTGATCA TTCTCGGTCT TTTCTTCCAT TACCGAGTAA CAAACCCTGT CGAC-
Mal09        ACCGAACCGT GATCATTATG CGTCTGATCA TTCTCGGTCT TTTCTTCCAT TACCGAGTAA CGAACCCTGT TGACA
Ltr01        ACCGAACTGT GATAATTATG CGTCTGATCA TTCTCGGTCT TTTCTTTCAT TACCGAGTAA CAAACCCTGT CGACA
Ltr02        ACCGAACTGT GATAATTATG CGTCTGATCA TTCTCGGTCT TTTCTTTCAT TACCGAGTAA CAAACCCTGT CGACA
Ltr03        ACCGAACTGT GATAATTATG CGTCTGACCA TTCTCGGTCT TTTCTTTCAT TAC------- ---------- -----
Ltr04        ACCGAACTGT GATAATTATG CGTCTGATCA TTCTCGGTCT TTTCTTTCAT TACCGAGTAA CAAACCCTGT CGACA
Ltr05        ACCGAACTGT GATAATTATG CGTCTGATCA TTCTCGGTCT TTTCTTTCAT TACCGAGTAA CAAACCCTGT CGACA
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Ahi08       ACCGAACCGT GATCATTATG CGTCTGATCA TTCTCGGTCT TTTCTTCCAT TACCGAGTAA CGAACCCCGT GGACA
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Mma05       ATCGAACCGT GATCATTATG CGGCTGATCA TTCTTGGTCT TTTCTTCCAT TACCGAGTAA CAAACCCTGT GGACA
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Las02       ACCGAACTGT GATCATTATG CGGCTGATCA TTCTCGGTCT TTTCTTCCAT TACCGAGTAA CAAACCCTGT CGACA
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Las05       ACCGAACTGT GATCATTATG CGTCTGATCA TTCTCGGTCT TTTCTTCCAT TACCGAGTAA CAAACCCTGT CGACA
Las06       ACCGAACTGT GATCATTATG CGGCTGATCA TTCTCGGTCT TTTCTTCCAT TACCGAGTAA CAAACCCTGT CGACA
Las07       ACCGAACTGT GATCATTATG CGGCTGATCA TTCTCGGTCT TTTCTTCCAT TACCGAGTAA CAAACCCTGT CGACA
Las08       ACCGAACTGT GATCATTATG CGGCTGATCA TTCTCGGTCT TTTCTTCCAT TACCGAGTAA CAAACCCTGT CGACA
Lpe01       ACCGAACTGT GATCATTATG CGGCTGATCA TTCTCGGTCT TTTCTTCCAT TACCGAGTAA CAAACCCTGT CGACA
Lpe02       ACCGAACTGT GATCATTATG CGGCTGATCA TTCTCGGTCT TTTCTTCCAT TACCGAGTAA CAAACCCTGT CGACA
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Aof01       ACCGAACCGT GATCATTATG CGGCTGATCA TTCTCGGTCT TTTCTTCCAT TACCGAGTAA CGAACCCTGT CGACA
Aca01       ACCGAACCGT GATCATTATG CGGCTGATCA TTCTCGGTCT TTTCTTCCAT TACCGAGTAA CGAACCCTGT CGACA
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Ani40       ACCGAACCGT GATCATTATG CGGCTGATCA TTCTCGGTCT TTTCTTCCAT TACCGAGTAA CGAACCCTGT CGACA
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Lag201          CCCTTTGTGT CTTGTCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGT TTGTCTGCGT TGCGGTAGTC
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Lob201          CCCTTTGTGT CTTGTCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGT TTGTCTGCGT TGCGGTAGTC
Lbr201          CCCTTTGTGT CTTGTCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGT TTGTCTGCGT TGCGGTAGTC
Lol201          CCCTTTGTGT CTTGTCATGA ATGCAATTTT CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGT TTGTCTGCGT TGCGGTAGTC
Lol202          CCCTTTGTGT CTTGTCATGA ATGCAATTTT CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGT TTGTCTGCGT TGCGGTAGTC
Lol203          CCCTTTGTGT CTTGTCATGA ATGCAATTTT CCCATTTGCA AGACTTGTTT TGAGTATGAC ACCAAGGAAG GTCGAAAAAT TTGTCTGCGT TGCGGTAGTC
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Lol205          CCCTTTGTGT CTTGTCATGA ATGCAATTTT CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGT TTGTCTGCGT TGCGGTAGTC
Lol206          CCCTTTGTGT CTTGTCATGA ATGCAATTTT CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGT TTGTCTGCGT TGCGGTAGTC
Mal201          CCCTTTGTGT CTTGTCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGT TTGTCTGCGT TGCGGTAGTC
Lar201          CCCTTTGTCT CTTGTCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGT TTGTCTGCGT TGCGGTAGTC
Lar202          CCCTTTGTCT CTTGTCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGT TTGTCTGCGT TGCGGTAGTC
Lar203          CCCTTTGTCT CTTGTCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGT TTGTCTGCGT TGCGGTAGTC
Lar204          CCCTTTGTCT CTTGTCATGA ATGCAATTCC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGT TTGTCTGCGT TGCGGTAGTC
Lar205          CCCTTTGTCT CTTGTCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGT TTGTCTGCGT TGCGGTAGTC
Lar206          CCCTTTGTCT CTTGTCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGT TTGTCTGCGT TGCGGTAGTC
Lar207          CCCTTTGTCT CTTGTCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGT TTGTCTGCGT TGCGGTAGTC
Lar208          CCCTTTGTCT CTTGTCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGT TTGTCTGCGT TGCGGTAGTC
Lar209          CCCTTTGTCT CTTGTCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGT TTGTCTGCGT TGCGGTAGTC
Lmu201          CCCTTTGTCT CTTGTCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGT TTGTCTGCGT TGCGGTAGTC
Lmu202          CCCTTTGTCT CTTGTCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGT TTGTCTGCGT TGCGGTAGTC
Lmu203          CCCTTTGTCT CTTGTCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGT TTGTCTGCGT TGCGGTAGTC
Lmu204          CCCTTTGTCT CTTGTCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGT TTGTCTGCGT TGCGGTAGTC
Lmu205          CCCTTTGTGT CTTGTCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAAGAAG GTCGAAAAGT TTGTCTGCGT TGCGGTAGTC
Mne201          CCCTTTGTGT CTTGCCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGT TTGTCTGCGT TGCGGTAGTC
Mne202          CCCTTTGTGT CGTGTCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGT TTGTCTGCGT TGCGGTAGTC
Mne203          CCCTTTGTGT CGTGTCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGT TTGTCTGCGT TGCGGTAGTC
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Mne204        CCCTTTGTGT CGTGTCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGT TTGTCTGCGT TGCGGTAGTC
Mne205        CCCTTTGTGT CGTGTCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGT TTGTCTGCGT TGCGGTAGTC
Mne206        CCCTTTGTGT CGTGTCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGT TTGTCTGCGT TGCGGTAGTC
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Mni203        CCCTTTGTGT CTTGTCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAAGAAG GTCGAAAAGT TTGTCTGCGT TGCGGTAGTC
Mpa201        CCCTTTGTGT CTTGTCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAAGAAG GTCGAAAAGT TTGTCTGCGT TGCGGTAGTC
Mpa202        CCCTTTGTGT CTTGTCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAAGAAG GTCGAAAAGT TTGTCTGCGT TGCGGTAGTC
Mpa203        CCCTTTGTGT CTTGTCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAAGAAG GTCGAAAAGT TTGTCTGCGT TGCGGTAGTC
Mpa204        CCCTTTGTGT CTTGTCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAAGAAG GTCGAAAAGT TTGTCTGCGT TGCGGTAGTC
Msy201        CCCTTTGTGT CTTGTCATGA ATGCAATTTC CCTATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGT TTGTCTGCGT TGCGGTAGTC
Msy202        CCCTTTGTGT CTTGTCATGA ATGCAATTTC CCTATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGT TTGTCTGCGT TGCGGTAGTC
Msy203        CCCTTTGTGT CTTGTCATGA ATGCAATTTC CCTATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGT TTGTCTGCGT TGCGGTAGTC
Msy204        CCCTTTGTGT CTTGTCATGA ATGCAATTTC CCTATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGT TTGTCTGCGT TGCGGTAGTC
Lcr201        CCCTTTGTCT CTTGTCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAAGAAG GTCGAAAAGT TTGTCTGCGT TGCGGTAGTC
Lcr202        CCCTTTGTGT CTTGTCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAAGAAG GTCGAAAAGT TTGTCTGCGT TGCGGTAGTC
Lcr203        CCCTTTGTCT CTTGTCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGT TTGTCTGCGT TGCGGTAGTC
Lcr204        CCCTTTGTCT CTTGTCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGT TTGTCTGCGT TGCGGTAGTC
Lcr205        CTCTTCGTCT CTTGTCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGT TTGTCTGCGT TGCGGTAGTC
Lcr206        CTCTTCGTCT CTTGTCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTTGAAAAGT TTGTCTGCGT TGCGGTAGTC
Lcr207        CCCTTTGTGT CTTGTCACGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGT TTGTCTGCGT TGTGGTAGTC
Las201        CTCTTCGTCT CTTGTCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGT TTGTCTGCGT TGCGGTAGTC
Las202        CTCTTCGTCT CTTGTCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGT TTGTCTGCGT TGCGGTAGTC
Las203        CCCTTTGTGT CTTGCAATGA ATGCAATTTT CCTATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCGAGTC
Lac201        CCCTTTGTGT CTTGTCACGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATGAAGGAAG ATCGAAAAGT TTGTCTGCGT TGCGGTAGTC
Mve201        CCCTTTGTGT CTTGTCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAAGAAG GTCGAAAAGT TTGTCTGCGT TGCGGTAGTC
Mve202        CTCTTCGTCT CTTGTCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGT TTGTCTGCGT TGCGGTAGTC
Mve203        CTCTTCGTCT CTTGTCATGA ATGCAATTTC CCCATCTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGT TTGTCTGCGT TGCGGTAGTC
Lpe201        CCCTTTGTGT CTTGTCACGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGT TTGTCTGCGT TGTGGTAGTC
Lpe202        CTCTTCGTCT CTTGTCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGT TTGTCTGCGT TGCGGTAGTC
Lpe203        CTCTTCGTCT CTTGTCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGT TTGTCTGCGT TGCGGTAGTC
Lpe204        CTCTTCGTCT CTTGTCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGT TTGTCTGCGT TGCGGTAGTC
Lph201        CCC----TGT CTGGTCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGT TTGTCTGCGT TGCGGTAGTC
Lph202        CCC------- -TTGTCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GCCGAAAAGT TTGTCTGCGT TGCGGTAGTC
Lph203        CCC------- -TTGTCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGT TTGTCTGCGT TGCGGTAGTC
Aca201        CCCTTTGTGT CTTGTCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCTAAAAGT TTGTCTGCGT TGCGGTAGTC
Aca202        CCCTTTGTGT CTTGTCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCTAAAAGT TTGTCTGCGT TGCGGTAGTC
Aar201        CCCTTTGTGT CTTGTCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCTAAAAGT TTGTCTGCGT TGCGGTAGTC
Aro201        CCCTTTGTGT CTTGTCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGT TTGTCTGCGT TGCGGTAGTC
Aro202        CCCTTTGTGT CTTGTCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGT TTGTCTGCGT TGCGGTAGTC
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Kvi201          CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGGTAGTC
Kvi202          CCCTTTGTGT CTTGTCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGT TTGTCTGCGT TGCGGTAGTC
Kvi203          CCCTTTGTGT CTTGTCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGT TTGTCTGCGT TGCGGTAGTC
Mtf201          CCCTTTGTGT CTTGTCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGT TTGTCTGCGT TGCGCTAGTC
Mtf202          CCCTTTGTGT CTTGTCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGT TTGTCTGCGT TGCGCTAGTC
Mtf203          CCCTTTGTGT CTTGTCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGT TTGTCTGCGT TGCGCTAGTC
Mtf204          CCCTTTGTGT CTTGTCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGT TTGTCTGCGT TGCGCTAGTC
Mtf205          CCCTTTGTGT CTTGTCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGT TTGTCTGCGT TGCGCTAGTC
Mtf206          CCCTTTGTGT CTTGTCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGT TTGTCTGCGT TGCGCTAGTC
Mtf207          CCCTTTGTGT CTTGTCATGA ATGCAGTTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGT TTGTCTGCGT TGCGCTAGTC
 Mma201          CCCTTTGTGT CTTGTCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGT TTGTCTGCGT TGCGGTAGTC
Mma202          CCCTTTGTGT CTTGTCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGT TTGTCTTCGT TGCAGTAGTC
Aro203          CCCTTTGTGT CTTGTCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATTAAGGAAG GTCGAAAAGT TTGTCTGCGT TGCGGTAGTC
Kvi204          CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGGTAGTT
Kvi205          CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGGTAGTT
Ani201          CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGGTAGTC


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                       110        120        130        140        150        160        170        180        190        200
Ltr201          CATACGATGG TATGTATAC- ---TTTTATT TCTTGATAAA TCTTGGTGTT TTCGAAATGC TTGTTTGATT TCCCATGAAA AGAAAAAA-G ATAGAGATTT
Lag201          CATACGATGG TATGTATAC- ---TTTTAGT TCCTGATAAA TCTTTGTGTT TTCAGAATGC TTGTGTGATT TCCCATGAAA AGAAAAA-CG ATAGAGATGT
Lag202          CATACGATGG TATGTATAC- ---TTTTAGT TCCTGATAAA TCTTTGTGTT TTCAGAATGC TTGTGTGATT TCCCATGAAA AGAAAAA-CG GTAGAGATGT
Lag203          CATACGATGG TATGTATAC- ---TTTTAGT TCCTGATAAA TCTTTGTGTT TTCAGAATGC TTGTGTGATT TCCCATGAAA AGAAAAA-CG ATAGAGATGT
Lag204          CATACGATGG TATGTATAC- ---TTTTAGT TCCTGATAAA TCTTTGTGTT TTCAGAATGC TTGTGTGATT TCCCATGAAA AGAAAAA-CG ATAGAGATGT
Lag205          CATACGATGG TATGTATAC- ---TTTTAGT TCCTGATAAA TCTTTGTGTT TTCAGAATGC TTGTGTGATT TCCCATGAAA AGAAAAA-CG ATAGAGATGT
Lfl201          CATACGATGG TATGTATAC- ---TTTTAGT TCCTGATAAA TCTTTGTGTT TTCAGAATGC TTGTGTGATT TCCCATGAAA AGAAAAA-CG ATAGAGATGT
Lfl202          CATACGATGG TATGTATAC- ---TTTTAGT TCCTGATAAA TCTTTGTGTT TTCAGAATGC TTGTGTGATT TCCCATGAAA AGAAAAA-CG ATAGAGATGT
Lfl203          CATACGATGG TATGTATAC- ---TTTTAGT TCCTGATAAA TCTTTGTGTT TTCAGAATGC TTGTGTGATT TCCCATGAAA AGAAAAA-CG ATAGAGATGT
Lfl204          CATACGATGG TATGTATAC- ---TTTTAGT TCCTGATAAA TCTTTGTGTT TTCAGAATGC TTGTGTGATT TCCCATGAAA AGAAAAA-CG ATAGAGATGT
Lfl205          CATACGATGG TATGTATAC- ---TTTTAGT TCCTGATAAA TCTTTGTGTT TTCAGAATGC TTGTGTGATT TCCCATGAAA AGAAAAA-CG ATAGAGATGT
Ltp201          CATACGATGG TATGTATAC- ---TTTTAGT TCCTGATAAA TCTTTGTGTT TTCAGAATGC TTGTGTGATT TCCCATGAAA AGAAAAA-CG ATAGAGATGT
Lob201          CATACGATGG TATGTATAC- ---TTTTAGT TCCTGATAAA TCTTTGTGTT TTCAGAATGC TTGTGTGATT TCCCATGAAA AGAAAAA-CG ATAGAGATGT
Lbr201          CATACGATGG TATGTATAC- ---TTTTAGT TCCTGATAAA TCTTTGTGTT TTCGGAATGC TTGTGTGATT TCCCATGAAA AGAAAAA-CG ATAGAGATGT
Lol201          CATACGATGG TATGTATAC- ---TTTTAGT TCCTGATAAA TCTTTGTGTT TTCAGAATGC TTGTGTGATT TCCCATGAAA AGAAAAA-CG ATAGAGATGT
Lol202          CATACGATGG TATGTATAC- ---TTTTAGT TCCTGATAAA TCTTTGTGTT TTCAGAATGC TTGTGTGATT TCCCATGAAA AGAAAAA-CG ATAGAGATGT
Lol203          CATACGATGG TATGTATAC- ---TTTTAGT TCCTGATAAA TCTTTGTGTT TTCAGAATGC TTGTGTGATT TCCCATGAAA AGAAAAA-CG ATAGAGATGT
Lol204          CATACGATGG TATGTATAC- ---TTTTAGT TCCTGATAAA TCTTTGTGTT TTCAGAATGC TTGTGTGATT TCCCATGAAA AGAAAAA-CG ATAGAGATGT
Lol205          CATACGATGG TATGTATAC- ---TTTTAGT TCCTGATAAA TCTTTGTGTT TTCAGAATGC TTGTGTGATT TCCCATGAAA AGAAAAA-CG ATAGAGATGT
Lol206          CATACGATGG TATGTATAC- ---TTTTAGT TCCTGATAAA TCTTTGTGTT TTCAGAATGC TTGTGTGATT TCCCATGAAA AGAAAAA-CG ATAGAGATGT
Mal201          CATACGATGG TATGTATAC- ---TTTTAGT TCTTGATAAA TCTTTGTCTT TTAAGAATGC ATGTTTGATA TCACATGAAA AGAAAA--CG ATAGAGATGT
Lar201          CATACGATGG TATGTATAC- ---TTTTACC TCTTGATAAA TC--TGTCTT TTCAGAATGC TT-------- ---------- ---------- ----------
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Lar202         CATACGATGG TATGTATAC- ---TTTTACT TCTTGATAAA TC--TGTCTT TTCAGAATGC TT-------- ---------- ---------- ----------
Lar203         CATACGATGG TATGTATAC- ---TTTTACT TCTTGATAAA TC--TGTCTT TTCAGAATGC TT-------- ---------- ---------- ----------
Lar204         CATACGATGG TATGTATAC- ---TTTTACT TCTTGATAAA TC--TGTCTT TTCAGAATGC TT-------- ---------- ---------- ----------
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Lar206         CATACGATGG TATGTATAC- ---TTTTACT TCTTGATAAA TC--TGTCTT TTCAGAATGC TT-------- ---------- ---------- ----------
Lar207         CATACGATGG TATGTATAC- ---TTTTACT TCTTGATAAA TC--TGTCTT TTCAGAATGC TT-------- ---------- ---------- ----------
Lar208         CATACGATGG TATGTATAC- ---TTTTACT TCTTGATAAA TC--TGTCTT TTCAGAATGC TT-------- ---------- ---------- ----------
Lar209         CATACGATGG TATGTATAC- ---TTTTACT TCTTGATAAA TC--TGTCTT TTCAGAATGC TT-------- ---------- ---------- ----------
Lmu201         CATACGATGG TATGTATAC- ---TTTTACT TCTTGATAAA TC--TGTCTT TTCAGAATGC TT-------- ---------- ---------- ----------
Lmu202         CATACGATGG TATGTATAC- ---TTTTACT TCTTGATAAA TC--TGTCTT TTCAGAATGC TT-------- ---------- ---------- ----------
Lmu203         CATACGATGG TATGTATAC- ---TTTTACT TCTTGATAAA TC--TGTCTT TTCAGAATGC TT-------- ---------- ---------- ----------
Lmu204         CATACGATGG TATGTATAC- ---TTTTACT TCTTGATAAA TC--TGTCTT TTCAGAATGC TT-------- ---------- ---------- ----------
Lmu205         CATACGATGG TATGTATAC- ---TTTTACT TCTTGATACA TCTTTGTCTT TTCAGAATGC TT-------- ---------- ---------- ----------
Mne201         CATACGATGG TATGTATAC- ---TTTTACT TCTTGATAAA TCTTTGTCTT TTCAGAATGC TT-------- ---------- ---------- ----------
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Mni203         CATACGATGG TATGTATAC- ---TTTTACT TCTTGATACA TCTTTTTCTT TTCAGAATGC TT-------- ---------- ---------- ----------
Mpa201         CATACGATGG TATGTATAC- ---TTTTACT TCTTGATACA TCTTTTTCTT TTCAGAATGC TT-------- ---------- ---------- ----------
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Mpa204         CATACGATGG TATGTATAC- ---TTTTACT TCTTGATACA TCTTTGTCTT TTCAGAATGC TT-------- ---------- ---------- ----------
Msy201         CATACGATGG TATGTATAC- ---TTTTACT TCTTGATACA TCTTTGTCTT TTCAGAATGC TT-------- ---------- ---------- ----------
Msy202         CATACGATGG TATGTATAC- ---TTTTACT TCTTGATACA TCTTTGTCTT TTCAGAATGC TT-------- ---------- ---------- ----------
Msy203         CATACGATGG TATGTATAC- ---TTTTACT TCTTGATACA TCTTTGTCTT TTCAGAATGC TT-------- ---------- ---------- ----------
Msy204         CATACGATGG TATGTATAC- ---TTTTACT TCTTGATACA TCTTTGTCTT TTCAGAATGC TT-------- ---------- ---------- ----------
Lcr201         CATACGATGG TATGTATAC- ---TTTTACT TCTTGATACA TCTTTGTCTT TTCAGAATGC TT-------- ---------- ---------- ----------
Lcr202         CATACGATGG TATGTATAC- ---TTTTACT TCTTGATACA TCTTTGTCTT TTCAGAATGC TT-------- ---------- ---------- ----------
Lcr203         CATACGATGG TATGCGTAC- ---TTTTACT TCTTGATAAA TC--TGTCTT TTCAGAATGC TT-------- ---------- ---------- ----------
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Lcr205         CATACGATGG TATGCATAC- ---TTTTACT TCTTGATAAA TC--TGTCTT TTCAGAATGC TT-------- ---------- ---------- ----------
Lcr206         CATACGATGG TATGCATAC- ---TTTTACT TCTTGATATA TC--TGTCTT TTCAGAATGC TT-------- ---------- ---------- ----------
Lcr207         CATACGATGG TATGTATAC- ---TTTTAGT TATTCATAAA TCTTTGTCTT TTCAGAATGC TT-------- ---------- ---------- ----------
Las201         CATACGATGG TATGCATAC- ---TTTTACT TCTTGATAAA TC--TGTCTT TTCAGAATGC TT-------- ---------- ---------- ----------
Las202         CATACGATGG TATGCATAC- ---TTTTACT TCTTGATAAA TC--TGTCTT TTCAGAATGC TT-------- ---------- ---------- ----------
Las203         CATACGATGG TATGTATAC- ---TTTTAGT TCTTGATAAA TCTTTGTGTT TTCCAAATGT TTGTTTGATT TCCCATGAAA AGAAAAAA-A ATAGAGATGT
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Lac201          CATACGATGG TATGTATAC- ---TTTTAGT TCTTGATAAA TCTTTGTCTC TTCCGAATGC TTGTTTGATT TCCCATGAAA AGAAAAA-CG ATAGAGATGT
Mve201          CATACGATGG TATGTATAC- ---TTTTACT TCTTGATACA TCTTTGTCTT TTCAGAATGC TT-------- ---------- ---------- ----------
Mve202          CATACGATGG TATGCATAC- ---TTTTACT TCTTGATAAA TC--TGTCTT TTCAGAATGC TT-------- ---------- ---------- ----------
Mve203          CATACGATGG TATGCATAC- ---TTTTACT TCTTGATAAA TC--TGTCTT TTCAGAATGC TT-------- ---------- ---------- ----------
Lpe201          CATACGATGG TATGTATAC- ---TTTTAGT TATTCATAAA TCTTTGTCTT TTCAGAATGC TT-------- ---------- ---------- ----------
Lpe202          CATACGATGG TATGCATAC- ---TTTTACT TCTTGATAAA TC--TGTCTT TTCAGAATGC TT-------- ---------- ---------- ----------
Lpe203          CATACGATGG TATGCATAC- ---TTTTACT TCTTGATAAA TC--TGTCTT TTCAGAATGC TT-------- ---------- ---------- ----------
Lpe204          CATACGATGG TATGCATAC- ---TTTTACT TCTTGATAAA TC--TGTCTT TTCAGAATGC TT-------- ---------- ---------- ----------
Lph201          CATACGATGG TATGTATAC- ---TTTTAGT TCTTGATCAA TCTTTGTCTT TTCAGAATGC TTGTTTGATT TCCCACGAAA AGAAAAA-CG ATAGAGATGT
Lph202          CATACGATGG TATGTATAC- ---TTTTAGT TCTTGATCAA TCTTTGTCTT TTCAGAATGC TTGTTTGATT TCCCACGAAA AGAAAAA-CG ATAGAGATGT
Lph203          CATACGATGG TATGTATAC- ---TTTTAGT TCTTGATCAA TCTTTGTCTT TTCAGAATGC TTGTTTGATT TCCCACGAAA AGAAAAA-CG ATAGAGATGT
Aca201          CATACGATGG TATGTATGC- ---TTTTAGT TTTTGATAAA TCTTTGTGTA TTCAGAATGC TTGTTTGATT TCCCATGAAA AGGAAAA--A ATAGAGATGT
Aca202          CATACGATGG TATGTATGC- ---TTTTAGT TTTTGATAAA TCTTTGTGTA TTCAGAATGC TTGTTTGATT TCCCATGAAA AGGAAAA--A ATAGAGATGT
Aar201          CATACGATGG TATGTATGC- ---TTTTAGT TTTTGATAAA TCTTTGTGTA TTCAGAATGC TTGTTTGATT TCCCATGAAA AGGAAAA--A ATAGAGATGT
Aro201          CATACGATGG TATGTATGC- ---TTTTAGT TCTTGATAAA TC--TGTGTT TTCAGAACGC TTGTTTGATT TCCCATAAAA AGAAAAA--G CTAGAGATGT
Aro202          CATACGATGG TATGTATGC- ---TTTTAGT TCTTGATAAA TC--TGTGTT TTCAGAACGC TTGTTTGATT TCCCATAAAA AGAAAAA--G CTAGAGATGT
Kvi201          CATACGATGG TATGTATAC- ---TTTTAGT TCTTGATAAA TCTTTGTGTA TTCAGAATGC TTGTTTGATT TCCCATGAAA AGAAAAA--G ATAGAGATGT
Kvi202          CATACGATGG TATGTATAC- ---TTTTAGT TCTTGATAAA TCTTTGTGTA TTCAGAATGC TTGTTTGATT TCCCATGAAA AGAAAAA--G ATAGAGATGT
Kvi203          CATACGATGG TATGTATAC- ---TTTTAGT TCTTGATAAA TCTTTGTGTA TTCAGAATGC TTGTTTGATT TCCCATGAAA AGAAAAA--G ATAGAGATGT
Mtf201          CGTACGACGG TATGTGTAC- ---TTTCAGT TCTTGATAAA TC--TGTGTT TTCAGAATG- ---------- ---------- ---------- ----------
Mtf202          CGTACGACGG TATGTGTAC- ---TTTCAGT TCTTGATAAA TC--TGTGTT TTCAGAATG- ---------- ---------- ---------- ----------
Mtf203          CGTACGACGG TATGTGTAC- ---TTTCAGT TCTTGATAAA TC--TGTGTT TTCAGAATG- ---------- ---------- ---------- ----------
Mtf204          CGTACGACGG TATGTGTAC- ---TTTCAGT TCTTGATAAA TC--TGTGTT TTCAGAATG- ---------- ---------- ---------- ----------
Mtf205          CGTACGACGG TATGTGTAC- ---TTTCAGT TCTTGATAAA TC--TGTGTT TTCAGAATG- ---------- ---------- ---------- ----------
Mtf206          CGTACGACGG TATGTGTAC- ---TTTCAGT TCTTGATAAA TC--TGTGTT TTCAGAATG- ---------- ---------- ---------- ----------
Mtf207          CGTACGACGG TATGTGTAC- ---TTTCAGT TCTTGATAAA TC--TGTGTT TTCAGAATG- ---------- ---------- ---------- ----------
Mma201          CATACGATGG TATGTATAC- ---TTTCAGT TCTTGATAAA TC--TGTGTT TTCAGAATG- ---------- ---------- ---------- ----------
Mma202          CATACGATGG TATGTATGTA TACCTTCAGT TCTTGATAAA TC--TGTGTT TTCAGAATG- ---------- ---------- ---------- ----------
Aro203          CATACGATGG TATGTA---- --------GT TCTTGATAAA TCTTTGTCTT TTCAGAATGC TTGTTTGATT TCCCATGAAA AGAAAAA-CG ATAGAGATTT
Kvi204          CATACGATGG TATGTATAC- ---TTTTAGT TCTTGATAAA TCTTTGTGTT TTCCAAATGC TTGTTTGATT TCCCATGAAA AGAAAAA--G ATAGAGATGT
Kvi205          CATACGATGA TATGTATAC- ---TTTTAGT TCTTGATAAA TCTTTGTGTT TTCCAAATGC TTGTTTGATT TCCCATGAAA AGAAAAA--G ATAGAGATGT
Ani201          CATACGATGG TATGTATAC- ---TTTTAGT TCTTGATAAA TCTTTGTGTT TTCCAAATGC TTGTTTGATT TCCCATGAAA AGAAAAA--G ATAGAGATGT


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                       210        220        230        240        250        260        270        280        290        300
Ltr201          AGTGAACTGT TTAAACTGCT TAGACTGACC ACTTTGAACT CCTTCAGAGA ACCTGTTGGA CGATGTCGAA AAGGCATCTG TCGAACAATC CATGATGGCC
Lag201          AGTGAACT-- -------GCT TACACTGACC ACTTTGAAAT CCTTCAGAGA ACCTGTTGGA TGATGTCGAA AAGGCATCCG AAGAACAATC CACGATGGCT
Lag202          AGTGAACT-- -------GCT TACACTGACC ACTTTGAAAT CCTTCAGAGA ACCTGTTGGA TGATGTCGAA AAGGCATCCG AAGAACAATC CACGATGGCT
Lag203          AGTGAACT-- -------GCT TACACTGACC ACTTTGAAAT CCTTCAGAGA ACCTGTTGGA TGATGTCGAA AAGGCATCCG AAGAACAATC CACGATGGCT
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Lfl203      AGTGAACT-- -------GCT TACACTGACC ACTTTGAAAT CCTTCAGAGA ACCTGTTGGA TGATGTCGAA AAGGCATCCG AAGAACAATC CACGATGGCT
Lfl204      AGTGAACT-- -------GCT TACACTGACC ACTTTGAAAT CCTTCAGAGA ACCTGTTGGA TGATGTCGAA AAGGCATCCG AAGAACAATC CACGATGGCT
Lfl205      AGTGAACT-- -------GCT TACACTGACC ACTTTGAAAT CCTTCAGAGA ACCTGTTGGA TGATGTCGAA AAGGCATCCG AAGAACAATC CACGATGGCT
Ltp201      AGTGAACT-- -------GCT -ACACTGACC ACTTTGAAAT CCTTCAGAGA ACCTGTTGGA TGATGTCGAA AAGGCATCCG AAGAACAATC CACGATGGCT
Lob201      AGTGAACT-- -------GCT TACACTGACC ACTTTGAAAT CCTTCAGAGA ACCTGTTGGA TGATGTCGAA AAGGCATCCG AAGAACAAAC CACGATGGCT
Lbr201      AGTGAACT-- -------GCT TACACTGACC ACTTTGAAAT CCTTCAGAGA ACCTGTTGGA TGATGTCGAA AAGGCATCCG AAGAACAATC CACGATGGCT
Lol201      AGTGAACT-- -------GCT TACACTGACC ACTTTGAAAT CCTTCAGAGA ACCTGTTGGA TGATGTCGAA AAGGCATCCG AAGAACAATC CACGATGGCT
Lol202      AGTGAACT-- -------GCT TACACTGACC ACTTTGAAAT CCTTCAGAGA ACCTGTTGGA TGATGTCGAA AAGGCATCCG AAGAACAATC CACGATGGCT
Lol203      AGTGAACT-- -------GCT TACACTGACC ACTTTGAAAT CCTTCAGAGA ACCTGTTGGA TGATGTCGAA AAGGCATCCG AAGAACAATC CACGATGGCT
Lol204      AGTGAACT-- -------GCT TACACTGACC ACTTTGAAAT CCTTCAGAGA ACCTGTTGGA TGATGTCGAA AAGGCATCCG AAGAACAATC CACGATGGCT
Lol205      AGTGAACT-- -------GCT TACACTGACC ACTTTGAAAT CCTTCAGAGA ACCTGTTGGA TGATGTCGAA AAGGCATCCG AAGAACAATC CACGATGGCT
Lol206      AGTGAACT-- -------GCT TACACTGACC ACTTTGAAAT CCTTCAGAGA ACCTGTTGGA TGATGTCGAA AAGGCATCCG AAGAACAATC CACGATGGCT
Mal201      AGTGAACTGC TTAAACTGCT TAGACTGACC ATTATGAAAT CCTTCAGAGA ACCTATTGGA TGATGTCGAA AAGGCATCCG AAGAACAATC CACGATGGCT
Lar201      ---------- ---------- -AGACTGACC ACTTTGAAAT CTTTCAGAGA ACCTGTTGGA TGATGTCGAA AAGGCATCCG AAGAACAATC CACGATGGCT
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Lar209      ---------- ---------- -AGACTGACC ACTTTGAAAT CTTTCAGAGA ACCTGTTGGA TGATGTCGAA AAGGCATCCG AAGAACAATC CACGATGGCT
Lmu201      ---------- ---------- -AGACTGACC ACTTTGAAAT CTTTCAGAGA ACCTGTTGGA TGATGTCGAA AAGGCATCCG AAGAACAATC CACGATGGCT
Lmu202      ---------- ---------- -AGACTGACC ACTTTGAAAT CTTTCAGAGA ACCTGTTGGA TGATGTCGAA AAGGCATCCG AAGAACAATC CACGATGGCT
Lmu203      ---------- ---------- -AGACTGACC ACTTTGAAAT CTTTCAGAGA ACCTGTTGGA TGATGTCGAA AAGGCATCCG AAGAACAATC CACGATGGCT
Lmu204      ---------- ---------- -AGACTGACC ACTTTGAAAT CTTTCAGAGA ACCTGTTGGA TGATGTCGAA AAGGCATCCG AAGAACAATC CACGATGGCT
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Mne201      ---------- ---------- -AGACTGACC ACTTTGAAAT CTTTCAGAGA ACCTGTTGGA TGATGTCGAA AAGGCATCCG AAGAACAATC CACGATGGCT
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Mpa201      ---------- ---------- -AGACTGACC ACTTCGAAAT CTTTCAGAGA ACCTGTTGGA TGATGTCGAA AAGGCATCCG AAGAACAATC CACGATGGCT
Mpa202      ---------- ---------- -AGACTGACC ACTTTGAAAT TCTTCAGAGA ACCTGTTGGA TGATGTCGAA AAGGCATCCG AGGAACAATC CACGATGGCT
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Mpa203      ---------- ---------- -AGACTGACC ACTTTGAAAT TCTTCAGAGA ACCTGTTGGA TGATGTCGAA AAGGCATCCG AAGAACAATC CACGATGGCT
Mpa204      ---------- ---------- -AGACTGACC ACTTTGAAAT TCTTCAGAGA ACCTGTTGGA TGATGTCGAA AAGGCATCCG AAGAACAATC CACGATGGCT
Msy201      ---------- ---------- -AGACTGACC ACTTTGAAAT CCTTCAGAGA ACCTGTTGGA TGATGTCGAA AAGGCATCCG AAGAACAATC CACGTTGGCT
Msy202      ---------- ---------- -AGACTGACC ACTTTGAAAT CCTTCAGAGA ACCTGTTGGA TGATGTCGAA AAGGCATCCG AAGAACAATC CACGTTGGCT
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Msy204      ---------- ---------- -AGACTGACC ACTTTGAAAT CCTTCAGAGA ACCTGTTGGA TGATGTCGAA AAGGCATCCG AAGAACAATC CACGTTGGCT
Lcr201      ---------- ---------- -AGACTGACC ACTTTGAAAT CTTTCAGAGA ACCTGTTGGA TGATGTCGAA AAGGCATCCG AAGAACAATC CACGATGGCT
Lcr202      ---------- ---------- -AGACTGACC ACTTTGAAAT CATTCAGAGA ACCTGTTGGA TGATGTCGAA AAGGCATCCG AAGAACAATC CACGATGGCT
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Lcr206      ---------- ---------- -AGACTGACC ACTTTGAAAT CCTTCAGAGA ACCTGTTGGA TGATGTCGAA AAGGCATCCG AAGAACAATC CACGATGGCT
Lcr207      ---------- --------CT TTGATTGATC ACTTTGAAAT CCTTCAGAGA ACCTGTTGGA TGATGTCGAA AAGGCATCCG AAGAACAATC CACGATGGCT
Las201      ---------- ---------- -AGACTGACC ACTTTGAAAT CCTTCAGAGA ACCTGTTGGA TGATGTCGAA AAGGCATCCG AAGAACAATC CACGATGGCT
Las202      ---------- ---------- -AGACTGACC ACTTTGAAAT CCTTCAGAGA ACCTGTTGGA TGATGTCGAA AAGGCATCCG AAGAACAATC CACGATGGCT
Las203      AGTGAACT-- -------GCT TAGACTGACC ACTTTGAACT CCTTCAGAGA ACCTGTTGGA CGATGTCGAA AAGGCATCTG GCGAACAATC CATGATGGCT
Lac201      AGTGAACT-- -------GCT TAGACTGACC ACTTTGAAAT CCTTCAGAGA ACCTGTTGGA TGATGTCGAA AAGGCATCCG AAGAACAATC CACGATGGCT
Mve201      ---------- ---------- -AGACTGACC ACTTTGAAAT TCTTCAGAGA ACCTGTTGGA TGATGTCGAA AAGGCATCCG AAGAACAATC CACGATGGCT
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Lpe201      ---------- --------CT TTGATTGACC ACTTTGAAAT CCTTCAGAGA ACCTGTTGGA TGATGTCGAA AAGGCATCCG AAGAACAATC CACGATGGCT
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Aca201      AGTGAACTGC TTAAACTGCT TAGACTGACA ACTTTGTAAT CCTTCAGAGA ACCTGTTGGA TGATGTCGAA AAGGCATCCG AAGAACAATC CACGATGGCT
Aca202      AGTGAACTGC TTAAACTGCT TAGACTGACA ACTTTGTAAT CCTTCAGAGA ACCTGTTGGA TGATGTCGAA AAGGCATCCG AAGAACAATC CACGATGGCT
Aar201      AGTGAACTGC TTAAACTGCT TAGACTGACA ACTTTGTAAT CCTTCAGAGA ACCTGTTGGA TGATGTCGAA AAGGCATCCG AAGAACAATC CACGATGGCT
Aro201      AGTGA----- ----ACTGCT TAGACTGACC ACTTTGAAAT CCTCCAGAGA ACCTGTTGGA TGATGTCGAA AAGGCATCCG AAGAACAATC CACGATGGCT
Aro202      AGTGA----- ----ACTGCT TAGACTGACC ACTTTGAAAT CCTTCAGAGA ACCTGTTGGA TGATGTCGAA AAGGCATCCG AAGAACAATC CACGATGGCT
Kvi201      AGTGAACTGC TTAACCTGCT TAGACTGACC ACTTTGAAAT CCTTCAGAAA ACCTGTTGGA TGATGTCCAA AAGGCATCCG AAGAACAATC CACGATGGCT
Kvi202      AGTGAACTGC TTAAACTGCT TAGACTGACC ACTTTGAAAT CCTTCAGAAA ACCTGTTGGA TGATGTCCAA AAGGCATCCG AAGAACAATC CACGATGGCT
Kvi203      AGTGAACTGC TTAAACTGCT TAGACTGACC ACTTTGAAAT CCTTCAGAAA ACCTGTTGGA TGATGTTCAA AAGGCATCCG AAGAACAATC CACGATGGCT
Mtf201      -GTGAACTGC TTAGACTGCT TAGACTGACC ACTTTGAAAT CCTTCAGAGA ACCTGTTGGA TGATGTCGAA AAGGCATCCG GAGAACAATC CACGATGGCT
Mtf202      -GTGAACTGC TTAGACTGCT TAGACTGACC ACTTTGAAAT CCTTCAGAGA ACCTGTTGGA TGATGTCGAA AAGGCATCCG GAGAACAATC CACGATGGCT
Mtf203      -GTGAACTGC TTAGACTGCT TAGACTGACC ACTTTGAAAT CCTTCAGAGA ACCTGTTGGA TGATGTCGAA AAGGCATCCG GAGAACAATC CACGATGGCT
Mtf204      -GTGAACTGC TTAGACTGCT TAGACTGACC ACTTTGAAAT CCTTCAGAGA ACCTGTTGGA TGATGTCGAA AAGGCATCCG GAGAACAATC CACGATGGCT
Mtf205      -GTGAACTGC TTAGACTGCT TAGACTGACC ACTTTGAAAT CCTTCAGAGA ACCTGTTGGA TGATGTCGAA AAGGCATCCG GAGAACAATC CACGATGGCT
Mtf206      -GTGAACTGC TTAGACTGCT TAGACTGACC ACTTTGAAAT CCTTCAGAGA ACCTGTTGGA TGATGTCGAA AAGGCATCCG GAGAACAATC CACGATGGCT
Mtf207      -GTGAACTGC TTAGACTGCT TAGACTGACC ACTTTGAAAT CCTTCAGAGA ACCTGTTGGA TGATGTCGAA AAGGCATCCG GAGAACAATC CACGATGGCT
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Mma201          -GTGAG---- ----ACTGCT TAGACTGACC ACTTTGAAAT CCTTCAGAGA ACCTGTTGGA TGATGCCGAA AAGGCATCCG AAGAACAATC CACGATGGCT
Mma202          -GTGA----- ----ACTGCT TAGACTGACC ACTTTGAAAT CCTTTAGAGA ACCTGTAGGA TGATGCCGAA AAGGCATCCG AAGAACAATC CTCGATGGCT
Aro203          AGTGAA---- -----CTGCT TAGACTGACC ACTTTGAAAT CCTTCAGAGA ACCTGTTGGA TGATGAAGAA AAGGTATCCG AAGAACAATC CACGATGACT
Kvi204          AGTGAACTGA TTAAACTGCT TAGACTGACC ACTTTGAACT CCTTCAGAGA ACCTGTTGGA TGATGTCGAA AAGGCATCCG GCGAACAATC CATGATGGCT
Kvi205          AGTGAACTGA TTAAACTGCT TAGACTGACC ACTTTGAACT CCTTCAGAGA ACCTGTTGGA TGATGTCGAA AAGGCATCCG GCGAACAATC CATGATGGCT
Ani201          AGTGAGCTGC TTAAACTGCT TAGACTGACC ACTTTGAACT CCTTCAGAGA ACCTGTTGGA TGATGTCGAA AAGGCATCCG GCGAGCAATC CATGATGGCT


                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                       310        320        330        340        350        360        370        380        390        400
Ltr201          GCACATTCGA GCAAGTCCCA AGTACCGTAT TT-GCTACCT TTTAAGGGTT TT-AGCTATG ATTTGAAGGT GAATTAATGT TGGGAAACTA AGATCTCTTT
Lag201          GCATATTCGA ATAAGTCCCA AGTACTGTAT TT-GCTACCT TTTAAGGGTT TT-AGCTATG ATTTGAAGGT GAATTAATGT TGGGAAACTA AGATCTCTTT
Lag202          GCATACTCGA ATAAGTCCCA AGTACTGTAT TT-GCTACCT TTTAAGGGTT TT-AGCTATG ATTTGAAGGT GAATTAATGT TGGGAAACTA AGATCTCTTT
Lag203          GCATATTCGA ATAAGTCCCA AGTACTGTAT TT-GCTACCT TTTAAGGGTT TT-AGCTATG ATTTGAAGGT GAATTAATGT TGGGAAACTA AGATCTCTTT
Lag204          GCATATTCGA ATAAGTCCCA AGTACTGTAC TT-GCTACCT TTTAAGGGTT TT-AGCTATG ATTTGAAGGT GAATTAATGT TGGGAAACTA AGATCTCTTT
Lag205          GCATATTCGA ATAAGTCCCA AGTACTGTAT TT-GCTACCT TTTAAGGGTT TT-AGCTATG ATTTGAAGGT GAATTAATGT TGGGAAACTA AGATCTCTTT
Lfl201          GCACACTCGA ATAAGTCCCA AGTACTGTAT TT-GCTACCT TTTAAGGGTT TT-AGCTATG ATTTGAAGGT GAATTAATGT TGGGAAACTA AGATCTCTTT
Lfl202          GCATACTCGA ATAAGTCCCA AGTACTGTAT TT-GCTACCT TTTAAGGGTT TT-AGCTATG ATTTGAAGGT GAATTAATGT TGGGAAACTA AGATCTCTTT
Lfl203          GCATACTCGA ATAAGTCCCA AGTACTGTAT TT-GCTACCT TTTAAGGGTT TT-AGCTATG ATTTGAAGGT GAATTAATGT TGGGAAACTA AGATCTCTTT
Lfl204          GCATACTCGA ATAAGTCCCA AGTACTGTAT TT-GCTACCT TTTAAGGGTT TT-AGCTATG ATTTGAAGGT GAATTAATGT TGGGAAACTA AGATCTCTTT
Lfl205          GCATACTCGA ATAAGTCCCA AGTACTGTAT TT-GCTACCT TTTAAGGGTT TT-AGCTATG ATTTGAAGGT GAATTAATGT TGGGAAACTA AGATCTCTTT
Ltp201          GCATACTCGA ATAAGTCCCA AGTACTGTAT TT-GCTACCT TTTAAGGGTT TT-AGCTATG ATTTGAAGGT GAATTAATGT TGGGAAACTA AGATCTCTTT
Lob201          GCATACTCGA ATAAGTCCCA AGTATCGTAT TT-GCTACCT TTTAAGGGTT TT-AGCTATG ATTTGAAGGT GAATTAATGT TGGGAAACTA AGATCTCTTT
Lbr201          GCTTACTCGA ATAAGTCCCA AGTACCGTAT TT-GCTACCT TTTAAGGGTT TT-AGCTATG ATTTGAAGGT GAATTAATGT TGGGAAACTA AGATCTCTTT
Lol201          GCATACTCGA ATAAGTCCCA AGTATCGTAT TT-GCTACCT TTTAAGGGTT TT-AGCTATG ATTTGAAGGT GAATTAATGT TGGGAAACTA AGATCTCTTT
Lol202          GCATACTCGA ATAAGTCCCA AGTATCGTAT TT-GCTACCT TTTAAGGGTT TT-AGCTATG ATTTGAAGGT GAATTAATGT TGGGAAACTA AGATCTCTTT
Lol203          GCATACTCGA ATAAGTCCCA AGTATCGTAT TT-GCTACCT TTTAAGGGTT TT-AGCTATG ATTTGAAGGT GAATTAATGT TGGGAAACTA AGATCTCTTT
Lol204          GCATACTCGA ATAAGTCCCA AGTATCGTAT TT-GCTACCT TTTAAGGGTT TT-AGCTATG ATTTGAAGGT GAATTAATGT TGGGAAACTA AGATCTCTTT
Lol205          GCATACTCGA ATAAGTCCCA AGTATCGTAT TT-GCTACCT TTTAAGGGTT TT-AGCTATG ATTTGAAGGT GAATTAATGT TGGGAAACTA AGATCTCTTT
Lol206          GCATACTCGA ATAAGTCCCA AGTATCGTAT TT-GCTACCT TTTAAGGGTT TT-AGCTATG ATTTGAAGGT GAATTAATGT TGGGAAACTA AGATCTCTTT
Mal201          GCATACTCGA ATAAGTCCCA GGTACCGTTT TT-CCTGCCT TTTAAGGGTT TTTAGCTATG ATTTAAAGGT TAATTAATGT TGGGAAACTA AGATCTCTTT
Lar201          GCATACTCGA ATAAGTCCCA AGTACCGTAT TT-GTTGCCT TTGAAGAGTT TTTAGCTAGG ATTTAAAGGT GAATTAATGT TGGAAAACTA AGATCTCTTT
Lar202          GCACACTCGA ATAAGTCCCA AGTACCGTAT TT-GTTGCCT TTGAAGAGTT TTTAGCTAGG ATTTAAAGGT GAATTAATGT TGGAAAACTA AGATCTCTTT
Lar203          GCATACTCGA ATAAGTCCCA AGTACCGTAT TT-GTTGCCT TTGAAGAGTT TTTAGCTAGG ATTTAAAGGT GAATTAATGT TGGAAAACTA AGATCTCTTT
Lar204          GCATACTCGA ATAAGTCCCA AGTACCGTAT TT-GTTGCCT TTGAAGAGTT TTTAGCTAGG ATTTAAAGGT GAATTAATGT TGGAAAACTG AGATCTCTTT
Lar205          GCATACTCGA ATAAGTCCCA AGTACCGTAT TT-GTTGCCT TTGAAGAGTT TTTAGCTAGG ATTTAAAGGT GAATTAATGT TGGAAAACTA AGATCTCTTT
Lar206          GCATACTCGA ATAAGTCCCA AGTACCGTAT TT-GTTGCCT TTGAAGAGTT TTTAGCTAGG ATTTAAAGGT GAATTAATGT TGGAAAACTA AGATCTCTTT
Lar207          GCATACTCGA ATAAGTCCCA AGTACCGTAT TT-GTTGCCT TTGAAGAGTT TTTAGCTAGG ATTTAAAGGT GAATTAATGT TGGAAAACTA AGATCTCTTT
Lar208          GCATACTCGA ATAAGTCCCA AGTACCGTAT TT-GTTGCCT TTGAAGAGTT TTTAGCTAGG ATTTAAAGGT GAATTAATGT TGGAAAACTA AGATCTCTTT
Lar209          GCATACTCGA ATAAGTCCCA AGTACCGTAT TT-GTTGCCT TTGAAGAGTT TTTAGCTAGG ATTTAAAGGT GAATTAATGT TGGAAAACTA AGATCTCTTT
Lmu201          GCATACTCGA ATAAGTCCCA AGTACCGTAT TT-GTTGCCT TTGAAGAGTT TTTAGCTAGG ATTTAAAGGT GAATTAATGT TGGAAAACTA AGATCTCTTT
Lmu202          GCATACTCGA ATAAGTCCCA AGTACCGTAT TT-GTTGCCT TTGAAGAGTT TTTAGCTAGG ATTTAAAGGT GAATTAATGT TGGAAGACTA AGATCTCTTT
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Lmu203         GCATACTCGA ATAAGTCCCA AGTACCGTAT TT-GTTGCCT TTGAAGAGTT TTTAGCTAGG ATTTAAAGGT GAATTAATGT TGGAAGACTA AGATCTCTTT
Lmu204         GCATACTCGA ATAAGTCCCA AGTACCGTAT TT-GTTGCCT TTGAAGAGTT TTTAGCTAGG ATTTAAAGGT GAATTAATGT TGGAAAACTA AGATCTCTTT
Lmu205         GCATACTCGA ATAAGTCCCA AGTATCGTAT TT-GCTGCCT TTGAAGAGTT TTTAGCTATG ACTTAAAGGT GAATTAATGA TGGGAAACTA AGATCTCTTT
Mne201         GCATACTCGA ATAAGTCCCA AGTACCGTAT TT-GTTGCCT TTGAAGAGTT TTTAGCTAGG ATTTAAAGGT GAATTAATGT TGGAAAATTA AGATATTTTT
Mne202         GCATACTCGA ATAAGTCCCA AGTACCGTAT TT-GTTGCCT TTGAAGAGTT TTTAGCTAGG ATTTAAAGGT GAATTAATGT TGGAAAATTA AGATATTTTT
Mne203         GCATACTCGA ATAAGTCCCA AGTACCGTAT TT-GTTGCCT TTGAAGAGTT TTTAGCTAGG ATTTAAAGGT GAATTAATGT TGGAAAATTA AGATATTTTT
Mne204         GCATACTCGA ATAAGTCCCA AGTACCGTAT TT-GTTGCCT TTGAAGAGTT TTTAGCTAGG ATTTAAAGGT GAATTAATGT TGGAAAATTA AGATATTTTT
Mne205         GCATACTCGA ATAAGTCCCA AGTACCGTAT TT-GTTGCCT TTGAAGAGTT TTTAGCTAGG ATTTAAAGGT GAATTAATGT TGGAAAATTA AGATATTTTT
Mne206         GCATACTCGA ATAAGTCCCA AGTACCGTAT TT-GTTGCCT TTGAAGAGTT TTTAGCTAGG ATTTAAAGGT GAATTAATGT TGGAAAATTA AGATATTTTT
Mne207         GCATACTCGA ATAAGTCCCA AGTACCGTAT TT-GTTGCCT TTGAAGAGTT TTTAGCTAGG ATTTAAAGGT GAATTAATGT GGGAAAATTA AGATATTTTT
Mne208         GCATACTCGA ATAAGTCCCA AGTACCGTAT TT-GTTGCCT TTGAAGAGTT TTTAGCTAGG ATTTAAAGGT GAATTAATGT TGGAAAATTA AGATATTTTT
Mni201         GCATACTCGA ATAAGTCTCA AGTACCGTAT TT-GTTGCCT TTGAAGAGTT TTTAGCTATG ATTTAAAGGT GAATTGATGT TGGGAAACTA AGATATCTTT
Mni202         GCATACTCGA ATAAGTCTCA AGTACCGTAT TT-GTTGCCT TTGAAGAGTT TTTAGCTATG ATTTAAAGGT GAATTGATGT TGGGAAACTA AGATATCTTT
Mni203         GCGTACTCGA ATAAGTCTCA AGTACCGTAT TT-GTTGCCT TTGAAGAGTT TTTAGCTATG ATTTAAAGGT GAATTGATGT TGGGAAACTA AGATATCTTT
Mpa201         GCATACTCGA ATAAGTCTCA AGTACCGTAT TT-GTTGCCT TTGAAGAGTT TTTAGCTATG ATTTAAAGGT GAATTGATGT TGGGAAACTA AGATATCTTT
Mpa202         GCATACTCGA ATAAGTCCCA AGTATCGTAT TT-GCTGCCT TTGAAGAGTT TTTAGCTATG ACTTAAAGGT GAATTAATGA TGGGAAACTA AGATCTCTTT
Mpa203         GCATACTCGA ATAAGTCCCA AGTATCGTAT TT-GCTGCCT TTGAAGAGTT TTTAGCTATG ACTTAAAGGT GAATTAATGA TGGGAAACTA AGATCTCTTT
Mpa204         GCATACTCGA ATAAGTCCCA AGTATCGTAT TT-GCTGCCT TTGAAGAGTT TTTAGCTATG ACTTAAAGGT GAATTAATGA TGGGAAACTA AGATCTCTTT
Msy201         GCATACTCGA ATAAGTCTCA AGTACCGTAT TT-GTTGCCT TTGAAGAGTT TTTAGCTATG ATTTAAAGGT GAATTGATGT TGGGAAACTA AGATATCTTT
Msy202         GCATACTCGA ATAAGTCTCA AGTACCGTAT TT-GTTGCCT TTGAAGAGTT TTTAGCTATG ATTTAAAGGT GAATTGATGT TGGGAAACTA AGATATCTTT
Msy203         GCATACTCGA ATAAGTCTCA AGTACCGTAT TT-GTTGCCT TTGAAGAGTT TTTAGCTATG ATTTAAAGGT GAATTGATGT TGGGAAACTA AGATATCTTT
Msy204         GCATACTCGA ATAAGTCTCA AGTACCGTAT TT-GTTGCCT TTGAAGAGTT TTTAGCTATG ATTTAAAGGT GAATTGATGT TGGGAAACTA AGATATCTTT
Lcr201         GCATACTCGA ATAAGTCCCA AGTACCGTAT TT-CTTGCCT TTGAAGAGTT TTTAGCTATG ATTTAAAGGT GAATTGATGT TGGGAAACTA AGATATCTTT
Lcr202         GCATACTCGA ATAAGTCTCA AGTACCGTAT TT-CTTGCCT TTGAAGAGTT TTTAGCTATG ATTTAAAGGT GAATTGATGT TGGGAAACTA AGATATCTTT
Lcr203         TCATACTCGA ATAAGTCCCA AGTACCGTAT TT-GCTGCCT TTGAAGAGTT TTTAGCTATG ACTTAAAGGC GAATTAATGA TGGGAAACTA AGATCTCTTT
Lcr204         TCATACTCGA ATAAGTCCCA AGTACCGTAT TT-GCTGCCT TTGAAGAGTT TTTAGCTATG ACTTAAAGGT GAATTAATGA TGGGAAACTA AGATCTCTTT
Lcr205         TCATACTCGA ATAAGTCCCA AGTACCGTAT TT-GCTGCCT TTGAAGAGTT TTTAGCTATG ACTTAAAGGT GAATTAATGA TGGGAAACTA AGATCTCTTT
Lcr206         TCATACTCGA ATAAGTCCCA AGTACCGTAT TT-GCTGCCT TTGAAGAGTT TTTAGCTATG ACTTAAAGGT GAATTACTGA TGGGAAACTA AGATCTCTTT
Lcr207         GCATACTCGA ATAAGTCCCA AGTACCGTAT TT-GCTGCCT TTGAAGAGTT TTTAGCTATG ATTTAAAGGT GAATTGATGT TGGGAAACTA AGATATCTTT
Las201         TCATACTCGA ATAAGTCCCA AGTACCGTAT TT-GCTGCCT TTGAAGAGTT TTTAGCTATG ACTTAAAGGT GAATTAATGA TGGGAAACTA AGATCTCTTT
Las202         TCATACTCGA ATAAGTCCCA AGTACCGTAT TT-GCTGCCT TTGAAGAGTT TTTAGCTATG ACTTAAAGGT GAATTAATGA TGGGAAACTA AGATCTCTTT
Las203         GCACATTCGA ATAAGTCTCA GGTACTGTTT TC-------- --GGAAGGTT TTTAGTTATG ATC-AAAGAT C-ATTAGTGT TTAGAAATTG AGAGCTCTTT
Lac201         GCATACTCGA ATAAGTCCCA AGTACCATAT TT-GCTGCCT TTGAAGGGTT TTTAGCTATG ATTTAAAGGT GAATTAATGT TGGGAAACTA AGATCTCTTT
Mve201         GCATACTCGA ATAAGTCCCA AGTATCGTAT TT-GCTGCCT TTGAAGAGTT TTTAGCTATG TCTTAAAGGT GAATTAATGA TGGGAAACTA AGATCTCTTT
Mve202         TCATACTCGA ATAAGTCCCA AGTACCGTAT TT-GCTGCCT TTGAAGAGTT TTTAGCTATG ACTTAAAGGT GAATTAATGA TGGGAAACTA AGATCTCTTT
Mve203         TCATACTCGA ATAAGTCCCA AGTACCGTAT TT-GCTGCCT TTGAAGAGTT TTTAGCTATG ACTTAAAGGT GAATTAATGA TGGGAAACTA AGATCTCTTT
Lpe201         GCATACTCGA ATAAGTCCCA AGTACCGTAT TT-GCTGCCT TTGAAGAGTC TTTAGCTATG ATTTAAAGGT GAATTGATGT TGGGAAACTA AGATATCTTT
Lpe202         TCATACTCGA ATAAGTCCCA AGTACCGTAT TT-GCTGCCT TTGAAGAGTT TTTAGCTATG ACTTAAAGGT GAATTAATGA TGGGAAACTA AGATCTCTTT
Lpe203         TCATACTCGA ATAAGTCCCA AGTACCGTAT TT-GCTGCCT TTGAAGAGTT TTTAGCTATG ACTTAAAGGT GAATTAATGA TGGGAAACTA AGATCTCTTT
Lpe204         TCATACTCGA ATAAGTCCCA AGTACCGTAT TT-GCTGCCT TTGAAGAGTT TTTAGCTATG ACTTAAAGGT GAATTAATGA TGGGAAACTA AGATCTCTTT
Lph201         GCATACTCGA ATAAGTCCCA AGTACCGTAT TT-GCTGCCT TTGAAGGGTT TTTAGCTATG ATTTAAAGGT GAATTAATGT TGGGAAACTA AGATCTCTTT
Lph202         GCATACTCGA ATAAGTCCCA AGTACCGTAT TT-GCTGCCT TTGAAGGGTT TTTAGCTATG ATTTAAAGGT GAATTAATGT TGGGAAACTA AGATCTCTTT
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Lph203          GCATACTCGA ATAAGTCCCA AGTACCGTAT TT-GCTGCCT TTGAAGGGTT TTTAGCTATG ATTTAAAGGT GAATTAATGT TGGGAAACTA AGATCTCTTT
Aca201          GCATACTCGA ATAAGTCCCA GGTACTGTTC TT-GCTGCCT TTGAAAGG-- ---------- ---------T GAATTAATGT TGGGAAACTA AGATCTCTTT
Aca202          GCATACTCGA ATAAGTCCCA GGTACTGTTC TT-GCTGCCT TTGAAAGG-- ---------- ---------T GAATTAATGT TGGGAAACTA AGATCTCTTT
Aar201          GCATACTCGA ATAAGTCCCA GGTACTGTTC TT-GCTGCCT TTGAAAGG-- ---------- ---------T GAATTAATGT TGGGAAACTA AGATCTCTTT
Aro201          GCACACTCGA ATAAGTCCCA GGTACTGGTT TCC-TTGCCT TTGAAAGGTT GTTAGCTATG ATTTAAAGGT GAATTAATGT TGGGAACCTA AGATCTCTTT
Aro202          GCACACTCGA ATAAGTCCCA GGTACTGGTT TCC-TTGCCT TTGAAAGGTT GTTAGCTATG ATTTAAAGGT GAATTAATGT TGGGAACCTA AGATCTCTTT
Kvi201          GCATACTCGA ATAAGTCCCA GGTAATGCTT TT-GCTGCCT TTGAAAGGTT TTTAGCTATG ATTTAAAGGT GAATTAATGT TGGGAAACTA AGATCTCTTT
Kvi202          GCATACTCGA ATAAGTCCCA GGTAATGCTT TT-GCTGCCT TTGAAAGGTT TTTAGCTATG ATTTAAAGGT GAATTAATGT TGGGAAACTA AGATCTCTTT
Kvi203          GCATACTCGA ATAAGTCCCA GGTAATGCTT TT-GCTGCCT TTGAAAGGTT TTTAGCTATG ATTTAAAGGT GAATTAATGT TGGGAAACTA AGATCTCTTT
Mtf201          GCATACTCGA ATAAGTCCCA GGTACCGTCT TT-GCTGCCT TTGAAAGGTT TTTAGCTATG ATTGAAAGGT GAATTGAT-- ---------- ----------
Mtf202          GCATACTCGA ATAAGTCCCA GGTACCGTCT TT-GCTGCCT TTGAAAGGTT TTTAGCTATG ATTGAAAGGT GAATTGAT-- ---------- ----------
Mtf203          GCATACTCGA ATAAGTCCCA GGTACCGTCT TT-GCTGCCT TTGAAAGGTT TTTAGCTATG ATTGAAAGGT GAATTGAT-- ---------- ----------
Mtf204          GCATACTCGA ATAAGTCCCA GGTACCGTCT TT-GCTGCCT TTGAAAGGTT TTTAGCTATG ATTGAAAGGT GAATTGAT-- ---------- ----------
Mtf205          GCATACTCGA ATAAGTCCCA GGTACCGTCT TT-GCTGCCT TTGAAAGGTT TTTAGCTATG ATTGAAAGGT GAATTGAT-- ---------- ----------
Mtf206          GCATACTCGA ATAAGTCCCA GGTACCGTCT TT-GCTGCCT TTGAAAGGTT TTTAGCTATG ATTGAAAGGT GAATTGAT-- ---------- ----------
Mtf207          GCATACTCGA ATAAGTCCCA GGTACCGTCT TT-GCTGCCT TTGAAAGGTT TTTAGCTATG ATTGAAAGGT GAATTGAT-- ---------- ----------
Mma201          GCATACTCGA ATAAGTCCCA GGTACCGTTT TT-GCTGCCT TTGAAAGGTT TTTAGCTATG ATTGAAAGGT GAATTAATG- ---------- ----------
Mma202          GCATACTCGA ATAAGTCCCA GGTATCGTTT TT-GTTGCCT TTGAAAGGTT TTTAGCTATG ATTGAAAGGT GAATTAATG- ---------- ----------
Aro203          GCATACTCGA ATAAGTCCCA AGTACCGTAT TT-ACTGCCT TTGAAGAGTT TTAAGCTATG ATTTAAAGGT GAATTAATGT TGGGAAACTA AGATCTCTTT
Kvi204          GCACATTCGA ATAAGTCCCA GGTACTGTTT TTTGCTGTCT TTGAAAGGTT TTTAGTTATG ATT-AAAGAT C-ATTAGTGT TTAGAAATTG AGAGCTCTTT
Kvi205          GCACATTCGA ATAAGTCCCA GGTACTGTTT TTTGCTGTCT TTGAAAGGTT TTTAGTTATG ATT-AAAGAT C-ATTAGTGT TTAGAAATTG AGAGCTCTTT
Ani201          GCACATTCGA ATAAGTCCCA GGTACTGTTT TTTGCTGTCT TTGAAAGGTT TTTAATTATG ATT-AAAGAT C-ATTAGTGT TTGGAAATTG AGAGCTCTTT


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                       410        420        430        440        450        460        470        480        490        500
Ltr201          GTTATTCATA TTGGTTT-AT ACAGGATGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GTA---ATAT CAAA------
Lag201          GTTATTCATA TTGGTTT-AT ACAGGATGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GTA---ATAT CAAA------
Lag202          GTTATTCATA TTGGTTT-AT ACAGGATGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GTA---ATAT CAAA------
Lag203          GTTATTCATA TTGGTTT-AT ACAGGATGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GTA---ATAT CAAA------
Lag204          GTTATTCATA TTGGTTT-AT ACAGGATGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GTA---ATAT CAAA------
Lag205          GTTATTCATA TTGGTTT-AT ACAGGATGTT GGAGTTCATG CAAGACATAT CAGCAGTGTG TCTACATTGG ATAGTGGTAT GTAACAATAT CAA-TTATCT
Lfl201          GTTATTCATA TTGGTTT-AT ACAGGATGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GTA---ATAT CAAA------
Lfl202          GTTATTCATA TTGGTTT-AT ACAGGATGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GTA---ATAT CAAA------
Lfl203          GTTATTCATA TTGGTTT-AT ACAGGATGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GTA---ATAT CAAA------
Lfl204          GTTATTCATA TTGGTTT-AT ACAGGATGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GTA---ATAT CAAA------
Lfl205          GTTATTCATA TTGGTTT-AT ACAGGATGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GTA---ATAT CAAA------
Ltp201          GTTATTCATA TTGGTTT-AT ACAGGATGTT GGAGTTCATG CAAGACATAT CAGTAATGTG TCTACATTGG ATAGTGGTAT GTA---ATAT CAAA------
Lob201          GTTATTCATA TTGGTTT-AT ACAGGATGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GTA---ATAT CAAA------
Lbr201          GTTATTCATA TTGGTTT-AT ACAGGATGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GTA---ATAT CAAA------
Lol201          GTTATTCATA TTGGTTT-AT ACAGGATGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GTA---ATAT CAAC------
Lol202          GTTATTCATA TTGGTTT-AT ACAGGATGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GTA---ATAT CAAC------
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Lol203      GTTATTCATA TTGGTTT-AT ACAGGATGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GTA---ATAT CAAC------
Lol204      GTTATTCATA TTGGTTT-AT ACAGGATGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GTA---ATAT CAAC------
Lol205      GTTATTCATA TTGGTTT-AT ACAGGATGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GTA---ATAT CAAC------
Lol206      GTTATTCATA TTGGTTT-AT ACAGGATGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GTA---ATAT CAAC------
Mal201      GTTATTCATA TTGGTTT-AT ACAGGATGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GTA---ATAT CAAT------
Lar201      CTTATTCATA TCGGTTT-AT ACAGGACGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GCA----TAT CAAT------
Lar202      CTTATTCATA TTGGTTT-AT ACAGGACGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GCA----TAT CAAT------
Lar203      CTTATTCATA TTGGTTT-AT ACAGGACGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GCA----TAT CAAT------
Lar204      CTTATTCATA TTGGTTT-AT ACAGGACGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GCA----TAT CAAT------
Lar205      CTTATTCATA TTGGTTT-AT ACAGGACGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GCA----TAT CAAC------
Lar206      CTTATTCATA TTGGTTT-AT ACAGGACGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GCA----TAT CAAT------
Lar207      CTTATTCATA TTGGTTT-AT ACAGGACGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GCA----TAT CAAT------
Lar208      CTTATTCATA TTGGTTT-AT ACAGGACGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GCA----TAT CAAT------
Lar209      CTTATTCATA TTGGTTT-AT ACAGGACGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATCGG ATAGTGGTAT GCA----TAT CAAT------
Lmu201      CTTATTCATA TTGGTTT-AT ACAGGACGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GCA----TAT CAAT------
Lmu202      CTTATTCATA TTGGTTT-AT ACAGGACGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GCA----TAT CAAT------
Lmu203      CTTATTCATA TTGGTTT-AT ACAGGACGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GCA----TAT CAAT------
Lmu204      CTTATTCATA TTGGTTT-AT ACAGGACGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GCA----TAT CAAT------
Lmu205      ATTATTCATA TTGGTTT-AT ACAGGATGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GCA----TAT CGAT------
Mne201      CTTATTCATA TTGGTTT-AT ACAGGACGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GCA----TAT CAAT------
Mne202      CTTATTCATA TTGGTTT-AT ACAGGACGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GCA----TAT CAAT------
Mne203      CTTATTCATA TTGGTTT-AT ACAGGACGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GCA----TAT CAAT------
Mne204      CTTATTCATA TTGGTTT-AT ACAGGACGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GCA----TAT CAAT------
Mne205      CTTATTCATA TTGGTTT-AT ACAGGACGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GCA----TAT CAAT------
Mne206      CTTATTCATA TTGGTTT-AT ACAGGACGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GCA----TAT CAAT------
Mne207      CTTATTCATA TTGGTTT-AT ACAGGACGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GCA----TAT CAAT------
Mne208      CTTATTCATA TTGGTTT-GT ACAGGACGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GCA----TAT CAAT------
Mni201      GTTATTCATA TTGGTTT-AT ACAGGATGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GCA----TAT CGAT------
Mni202      GTTATTCATA TTGGTTT-AT ACAGGATGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GCA----TAT CGAT------
Mni203      GTTATTCATA TTGGTTT-AT ACAGGATGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GCA----TAT CGAT------
Mpa201      GTTATTCATA TTGGTTT-AT ACAGGATGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GCA----TAT CGAT------
Mpa202      GTTATTCATA TTGGTTT-AT ACAGGATGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GCA----TAT CGAT------
Mpa203      GTTATTCATA TTGGTTT-AT ACAGGATGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GCA----TAT CGAT------
Mpa204      GTTATTCATA TTGGTTT-AT ACAGGATGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GCA----TAT CGAT------
Msy201      GTTATTCATG TTGGTTT-AT ACAGGATGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GCA----TAT CGAT------
Msy202      GTTATTCATA TTGGTTT-AT ACAGGATGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GCA----TAT CGAT------
Msy203      GTTATTCATA TTGGTTT-AT ACAGGATGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GCA----TAT CGAT------
Msy204      GTTATTCATA TTGGTTT-AT ACAGGATGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GCA----TAT CGAT------
Lcr201      GTTATTCATA TTGGTTT-AT ACAGGATGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GCA----TAT CGAT------
Lcr202      GTTATTCATA TTGGTTT-AT ACAGGATGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GCA----TAT CGAT------
Lcr203      GTTATTCATA TTGGTTT-AT ACAGGATGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GCA----TAT CAAT------
Lcr204      GTTATTCATA TTGGTTT-AT ACAGGATGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GCA----TAT CAAT------
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Lcr205       GTTATTCATA TTGGTTT-AT ACAGGATGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GCA----TAT CAAT------
Lcr206       GTTATTCATA TTGGTTT-AT ACAGGATGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GCA----TAT CAAT------
Lcr207       GTTATTCATA TTGGTTT-AT ACAGGATGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GCA----TAT CGAT------
Las201       GTTATTCATA TTGGTTT-AT ACAGGATGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCAACATTGG ATAGTGGTAT GCA----TAT CAAT------
Las202       GTTATTCATA TTGGTTT-AT ACAGGATGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCAACATTGG ATAGTGGTAT GCA----TAT CAAT------
Las203       GTTATTCATG TTGGTTTTAT ACAGGATGTT GGAGTTCATG CAAGACATAT CAGCAGTGTG TCTACATTGG ATAGTGGTAT GTAATACTAT CAATTTATCT
Lac201       GTTATTCATA TTGGTTT-AT ACAGGATGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GCA----TAT CAAT------
Mve201       GTTATTCATA TTGGTTT-AT ACAGGATGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GCA----TAT CGAT------
Mve202       GTTATTCATA TTGGTTC-AT AGAGGATGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GCA----TAT CAAT------
Mve203       GTTATTCATA TTGGTTT-AT AGAGGATGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GCA----TAT CAAT------
Lpe201       GTTATTCATA TTGGTTT-AT ACAGGATGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GCA----TAT CGAT------
Lpe202       GTTATTCATA TTGGTTT-AT ACAGGATGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GCA----TAT CAAT------
Lpe203       GTTATTCATA TTGGTTT-AT ACAGGATGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GCA----TAT CAAT------
Lpe204       GTTATTCATA TTGGTTT-AT ACAGGATGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GCA----TAT CAAT------
Lph201       GTTATTCATA TTGGTTT-AT ACAGGATGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GTA----CAT CAAT------
Lph202       GTTATTCATA TTGGTTT-AT ACAGGATGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GTA----CAT CAAT------
Lph203       GTTATTCATA TTGGTTT-AT ACAGGATGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GTA----CAT CAAT------
Aca201       GTTATTTATG TTGGTTT-AT ACAGGATGTT GGAGTTCATG CAAGACATAT CAGTACTGTG TCTACATTGG ATAGTGGTAT GTA---ATAT CAAT------
Aca202       GTTATTTATG TTGGTTT-AT ACAGGATGTT GGAGTTCATG CAAGACATAT CAGTACTGTG TCTACATTGG ATAGTGGTAT GTA---ATAT CAAT------
Aar201       GTTATTCATG TTGGTTT-AT ACAGGATGTT GGAGTTCATG CAAGACATAT CAGTACTGTG TCTACATAGG ATAGTGGTAT GTA---ATAT CAAT------
Aro201       GTTATTCATG TTGGTTT-AT ACAGGATGTT GGCGTTCATG CAAGACATAT CAGTACTGTG TCTACATTGG ATAGTGGTAT GTA---ATAT CAAT------
Aro202       GTTATTCATG TTGGTTT-AT ACAGGATGTT GGCGTTCGTG CAAGACATAT CAGTACTGTG TCTACATTGG ATAGTGGTAT GTA---ATAT CAAT------
Kvi201       GTTATTCATG TTGGTTT-AT ACAGGATGCT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GTA---ATAT CAAT------
Kvi202       GTTATTCATG TTGGTTT-AT ACAGGATGCT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GTA---ATAT CAAT------
Kvi203       GTTATTCATG TTGGTTT-AT ACAGGATGCT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GTA---ATAT CAAT------
Mtf201       ----TTCATG TTGGTTT-AT ACAGGATGCT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GTA---ATAT CAAC------
Mtf202       ----TTCATG TTGGTTT-AT ACAGGATGCT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GTA---ATAT CAAC------
Mtf203       ----TTCATG TTGGTTT-AT ACAGGATGCT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GTA---ATAT CAAC------
Mtf204       ----TTCATG TTGGTTT-AT ACAGGATGCT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GTA---ATAT CAAC------
Mtf205       ----TTCATG TTGGTTT-AT ACAGGATGCT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GTA---ATAT CAAC------
Mtf206       ----TTCATG TTGGTTT-AT ACAGGATGCT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTAGTAT GTA---ATAT CAAC------
Mtf207       ----TTCATG TTGGTTT-AT ACAGGATGCT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GTA---ATAT CAAC------
Mma201       ---------- TTGGTTT-AT ACAGGATGCT GGAGTTCATG CTAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GTA---AGAT CAAC------
Mma202       ---------- TTGGTTT-AT ACAGGATGCT GGAGTTCATG CTAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GTA---AGAT CAAC------
Aro203       GTTATTCATA TTGGTTT-AT ACAGGATGTT GGAGTTCATG CAAGACATAT CAGTAGTGTG TCTACATTGG ATAGTGGTAT GCA----TAT CAAT------
Kvi204       GTTATTCATG TTGGTTTTAT ACAGGATGTT GGAGTTCATG CAAGACATAT CAGCAGTGTG CCTACATTGG ATAGTGGTGT GTA---ATAT CAAT------
Kvi205       GTTATTCATG TTGGTTTTAT ACAGGATGTT GGAGTTCATG CAAGACATAT CAGCAGTGTG TCTACATTGG ATAGTGGTGT GTA---ATAT CAATTTATCT
Ani201       GTTATTCATG TTGGTTTTAT ACAGGATGTT GGAGTTCATG CAAGACATAT CAGCAGTGTG TCTACATTGG ATAGTGGTAT GTA---ATAT CAATTTATCT


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                    510        520        530        540        550        560        570        580        590        600
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Ltr201      TTCTTCCATA CTATTT-AAG AGAAGA---T TCAATTATAA ATATCTAACT GCCTCGTTCG ATGTTTTTGT GAAGAAATGA CTGAAGACAA TGGAAACCCG
Lag201      TTCTTCCATA CTATTT-AAG AGAAGA---T TCAATTATAA ATATCTGACT GCCTCGTTCG ATGTTTTTGT GAAGAAATGA CTGAAGACAA TGGAAACCCG
Lag202      TTCTTCCATA CTATTT-AAG AGAAGA---T TCAATTATAA ATATCTGACT GCCTCGTTCG ATGTTTTTGT GAAGAAATGA CTGAAGACAA TGGAAACCCG
Lag203      TTCTTCCATA CTATTT-AAG AGAAGA---T TCAATTATAA ATATCTGACT GCCTCGTTCG ATGTTTTTGT GAAGAAATGA CTGAAGACAA TGGAAACCCG
Lag204      TTCTTCCATA CTATTT-AAG AGAAGA---T TCAATTATAA ATATCTGACT GCCTCGTTCG ATGTTTTTGT GAAGAAATGA CTGAAGACAA TGGAAACCCG
Lag205      TTCTTCAATG ACCCTTCAAG AAAAAAATA- TCAATTCTAG AGATCTAATT GTCTGGTTCG ATGTTTTCGT GAAGAAATGA CCGAAGACAA TGGGAACCCG
Lfl201      TTCTTCCATA CTATTT-AAG AGAAGA---T TCAATTATAA ATATCTGACT GCCTCGTTCG ATGTTTTTGT GAAGAAATGA CTGAAGACAA TGGAACCCCG
Lfl202      TTCTTCCATA CTATCT-AAG AGAAGA---T TCAATTATAA ATATCTGACT GCCTCGTTCG ATGTTTTTGT GAAGAAATGA CTGAAGACAA TGGAACCCCG
Lfl203      TTCTTCCATA CTATTT-AAG AGAAGA---T TCAATTATAA ATATCTGACT GCCTCGTTCG ATGTTTTTGT GAAGAAATGA CTGAAGACAA TGGAACCCCG
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Lfl205      TTCTTCCATA CTATTT-AAG AGAAGA---T TCAATTATAA ATATCTGACT GCCTCGTTCG ATGTTTTTGT GAAGAAATGA CTGAAGACAA TGGAACCCCG
Ltp201      TTCTTCCATA CTATTT-AAG AGAAGA---T TCAATTATAA ATATCTGACT GCCTCGTTCG ATGTTTTTGT GAAGAAATGA CTGAAGACAA TGGAAACCCG
Lob201      TTCTTCCATA ATATTT-AAG AGAAGA---T TCAATTATAA ATATCTAACT GCCTCGTTCG ATGTTTTTGT GAAGAAATGA CTGAAGACAA TGGAAACCCG
Lbr201      TTCTTCCATA CTATTT-AAG AGAAGA---T TCAATTATAA ATATCTAACT GCCTCGTTCG ATATTTTTGT GCAGAAATGA CTGAAGACAA TGGAAACCCG
Lol201      TTCTTACATA CTATTT-AAG AAA-GA---C TCGATTATAA ATATCTAACT GCCTCGTTCG ATGTTTTTCT GAAGAAATGA CCGAAGACAA TGGAAACCCG
Lol202      TTCTTACATA CTATTT-AAG AAA-GA---C TCGATTATAA ATATCTAACT GCCTCGTTCG ATGTTTTTCT GAAGAAATGA CCGAAGACAA TGGAAACCCG
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Lol205      TTCTTACATA CTATTT-AAG AAA-GA---C TCGATTATAA ATATCTAACT GCCTCGTTCG ATGTTTTTCT GAAGAAATGA CCGAAGACAA CGGAAACCCG
Lol206      TTCTTACATA CTATTT-AAG AAA-GA---C TCGATTATAA ATATCTAACT GCCTCGTTCG ATGTTTTTCT GAAGAAATGA CCGAAGACAA TGGAAACCCG
Mal201      TTCTTCCATA CTATTT-AAG AGAAGA---T TCGATTATAA ATATCTAACT GCCTCGTTCG ATGTTTTTGT GAAGAAATGA CCGAAGACAA TAGAAATCCG
Lar201      TTCTTCCATA CTATTT-AAG AGAAGA---T TCGATTATAA ATATCTAACC GCCTCGTTCG ATGTTTTTGT GAAGAAATGA CAGAAGACAA TGGAAACCCG
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Lar206      TTCTTCCATA CTATTT-AAG AGAAGA---T TCGATTATAA ATATCTAACC GCCTCGTTCG ATGTTTTTGT GAAGAAATGA CAGAAGACAA TGGAAACCCG
Lar207      TTCTTCCATA CTATTT-AAG AGAAGA---T TCGATTATAA ATATCTAACC GCCTCGTTCG ATGTTTTTGT GAAGAAATGA CAGAAGACAA TGGAAACCCG
Lar208      TTCTTCCATA CTATTT-AAG AGAAGA---T TCGATTATAA ATATCTAACC GCCTCGTTCG ATGTTTTTGT GAAGAAATGA CAGAAGACAA TGGAAACCCG
Lar209      TTCTTCCATA CTATTT-AAG AGAAGA---T TCGATTATAA ATATCTAACC GCCTCGTTCG ATGTTTTTGT GAAGAAATGA CAGAAGACAA TGGAAACCCG
Lmu201      TTCTTCCATA CTATTT-AAG AGAAGA---T TCGATTATAA ATATCTAACC GCCTCGTTCG ATGTTTTTGT GAAGAAATGA CAGAAGACAA TGGAAACCCG
Lmu202      TTCTTCCATA CTATTT-AAG AGAAGA---T TCGATTATAA ATATCTAACC GCCTCGTTCG ATGTTTTTGT GAAGAAATGA CAGAAGACAA TGGAAACCCG
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Mne201      TTCTTCCATA CTATTT-AAG AGAAGA---T TCGATTATAA ATATCTAACC GCCTCGTTCG ATGTTTTTGT GAAGAAATGA CAGAAGACAA TGGAAACCCG
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Mne206      TTCTTCCATA CTATTT-AAG AGAAGA---T TCGATTATAA ATATCTAACC GCCTCGTTCG ATGTTTTTGT GAAGAAATGA CAGAAGACAA TGGAAACCCG
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Mni201        TTCTTCCATA CTATTT-AAG AGAAGA---T TCGATTATAA ATATCTAACC GCATCGTTCC ATGTTTTTGT GAAGAAATGA CTGAAGAAAA TGGAAACCCG
Mni202        TTCTTCCATA CTATTT-AAG AGAAGA---T TCGATTATAA ATATCTAACC GCATCGTTCC ATGTTTTTGT GAAGAAATGA CTGAAGAAAA TGGAAACCCG
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Mpa204        TTCTTCCATA CTATTT-AAG AGAAGA---T TCGATTATAA CTATCTAACC GCATCGTTCG ATGTTTTTGT GAAGAAATGA CCGAAGACAA TGGAAACCCG
Msy201        TTCTTCCATA CTATTT-AAG AGAAGA---T TCGATTATAA ATATCTAACC GCATCGTTCC ATGTTTTTGT GAAGAAATGA CTGAAGAAAA TGGAAACCCG
Msy202        TTCTTCCATA CTATTT-AAG AGAAGA---T TCGATTATAA ATATCTAACC GCATCGTTCC ATGTTTTTGT GAAGAAATGA CTGAAGAAAA TGGAAACCCG
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Lcr201        TTCTTCCATA CTATTT-AAG AGAAGA---T TCGATTATAA ATATCTAACC GCATCGTTCC ATGTTTTTGT GAAGAAATGA CTGAAGAAAA TGGAAACCCG
Lcr202        TTCTTCCATA CTATTT-AAG AGAAGA---T TCGATTATAA ATATCTAACC GCATCGTTCC ATGTTTTTGT GAAGAAATGA CTGAAGAAAA TGGAAACCCG
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Lcr207        TTCTTCCATA CAATTT-AAG AGTAGA---T TCGATTATAA ATATCTAACC GCATCGTTCG ATGTTTTTGT GAAGAAATGA CCGAAGAAAA TGGAAACCCG
Las201        TTCTTCCATA CTT----AAG AGAAGA---T TCGATTATAA ATATCTAACC ACATCGTTCG ATGTTTTTGT GAAGAAATGA CCGAAGAAAA TGGAAACCCG
Las202        TTCTTCCATA CTT----AAG AGAAGA---T TCGATTATAA ATATCTAACC ACATCGTTCG ATGTTTTTGT GAAGAAATGA CCGAAGAAAA TGGAAACCCG
Las203        TTCTTCAATG TTCCTTCAAG AAACAGAAA- TCAATTCTAG AGATCTAATT GTCTGGTTCG ATGTTTTCGT GAAGAAATGA CCGAAGACAA TGGGAACCCG
Lac201        TTCTTCCATA CTATTT-AAG AGAAGA---T TCGATTATAA ATATCTAACG GCCTCGTTCG ATGTTTTTGT GAAGAGATGA CCGAAGACAA TGGAAACCCG
Mve201        TTCTTCCATA CTATTT-AAG AGAAGA---T TCGATTATAA CTATCTAACC GCATCGTTCG ATGTTTTTGT GAAGAAATGA CCGAAGACAA TGGAAACCCG
Mve202        TTCTTCCATA CTT----GAG AGAAGA---T TCGATTATAA ATATCTAACC ACATCGTTCG ATGTTTTTGT GAAGAAATGA CCGAAGAAAA TGGAAACCCG
Mve203        TTCTTCCATA CTT----GAG AGAAGA---T TCGATTATAA ATATCTAACC ACATCGTTCG ATGTTTTTGT GAAGAAATGA CCGAAGAAAA TGGAAACCCG
Lpe201        TTCTTCCATA CTATTT-AAG AGTAGA---T TCGATTATAA ATATCTAACC GCATCGTTCG ATGTTTTTGT GAAGAAATGA CCGAAGAAAG TGGAAACCCG
Lpe202        TTCTTCCATA CTT----AAG AGAAGA---T TCGATTATAA ATATCTAACC ACATCGTTCG ATGTTTTTGT GAAGAAATGA CCGAAGAAAA TGGAAACCCG
Lpe203        TTCTTCCATA CTT----AAG AGAAGA---T TCGATTATAA ATATCTAACC ACATCGTTCG ATGTTTTTGT GAAGAAATGA CCGAAGAAAA TGGAAACCCG
Lpe204        TTCTTCCATA CTT----AAG AGAAGA---T TCGATTATAA ATATCTAACC ACATCGTTCG ATGTTTTTGT GAAGAAATGA CCGAAGAAAA TGGAAACCCG
Lph201        TTCTTCCATA CTATTT-AAG AGAAGA---T TCGATTATAA ATATCTAACC GCCTCG---- ATGTTTTTGT GAAGAAATGA CCGAAGACAA TGGAAACCCG
Lph202        TTCTTCCATA CTATTT-AAG AGAAGA---T TCGATTATAA ATATCTAACC GCCTCG---- ATGTTTTTGT GAAGAAATGA CCGAAGACAA TGGAAACCCG
Lph203        TTCTTCCATA CTATTT-AAG AGAAGA---T TCGATTATAA ATATCTAACC GCCTCG---- ATGTTTTTGT GAAGAAATGA CCGAAGACAA TGGAAACCCG
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Aca202        TTCTTCCATA CAATTT-AGG AGAAGA---T TCGATCATAA ATCTCTAACT GCTTCGTTCG ATGTTCTCGT GAAGAAATGA CCGAAGACAA TGGAAACCCT
Aar201        TTCTTCCATA CTATTT-AGG AGAAGA---T TCGATCATAA ATCTCTAACT GCTTCGTTCG ATGTTCTCGT CAAGAAATGA CCGAAGACAA TGGAAACCCT
Aro201        TTCTTCCATA CTATTT-AAG AGAAGA---T TCAATTATAA ATCTCGAACT GCTTCGTTCG ATGTTTTTGT GAAGAAATGA CCGAAGACAA TGGAAACCCG
Aro202        TTCTTCCATA CTATTT-AAG AGAAGA---T TCAATTATAA ATCTCGAACT GCTTCGTTCG ATGTTTTTGT GAAGAAATGA CCGAAGACAA TGGAAACCCG
Kvi201        TTATTCCATA CTATTT-AAG AGAAGA---T TAGATTATAA ATCTCTAACT GCCTCGCTCG ATGTTTTTGT GAAGAAATGA CTGAAGACAA TGGAAACCCG
Kvi202        TTATTCCATA CTATTT-AAG AGAAGA---T TAGATTATAA ATCTCTAACT GCCTCGCTCG ATGTTTTTGT GAAGAAATGA CTGAAGACAA TGGAAACCCG
Kvi203        TTATTCCATA CTATTT-AAG AGAAGA---T TAGATTATAA ATCTCTAACT GCCTCGCTCG ATGTTTTTGT GAAGAAATGA CTGAAGACAA TGGAAACCCG
Mtf201        TTCTTCCATA CTATTT-AAG GGGAGA---T TCGATTATAA ATCTGT---- -CTCGTTTCG ATGTTTTTGT GAAGAAATGA CCGAAGACAA TGGAAACCCG
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Mtf202          TTCTTCCATA CTATTT-AAG GGAAGA---T TCGATTATAA ATCTGT---- -CTCGTTTCG ATGTTTTTGT GAAGAAATGA CCGAAGACAA TGGAAACCCG
Mtf203          TTCTTCCATA CTATTT-AAG GGAAGA---T TCGATTATAA ATCCGT---- -CTCGTTTCG ATGTTTTTGT GAAGAAATGA CCGAAGACAA TGGAAACCCG
Mtf204          TTCTTCCATA CTATTT-AAG GGAAGA---T TCGATTATAA ATCTGT---- -CTCGTTTCG ATGTTTTTGT GAAGAAATGA CCGAAGACAA TGGAAACCCG
Mtf205          TTCTTCCATA CTATTT-AAG GGAAGA---T TCGATTATAA ATCTGT---- -CTCGTTTCG ATGTTTTTGT GAAGAAATGA CCGAAGACAA TGGAAACCCG
Mtf206          TTCTTCCATA CTATTT-AAG GGAAGA---T TCGATTATAA ATCTGT---- -CTCGTTTCG ATGTTTTTGT GAAGAAATGA CCGAAGACAA TGGAAACCCG
Mtf207          TTCTTCCATA CTATTT-AAG GGAAGA---T TCGATTATAA ATCTGT---- -CTCGTTTCG ATGTTTTTGT GAAGAAATGA CCGAAGACAA TGGAAACCCG
Mma201          CTCTTCCATA CTATTT-AAG GGAAGA---T TCGATTATAA ATCTGT---- -CTCGTT-CG ATGTTTTTGT GAAGAAATGA CCGAAGACAA CGGAAACCCG
Mma202          CTCTTCCATA CTATTT-AAG GGAAGA---T TCGATTATAA ATCTGT---- -CTCGTT-CG ATATTTTTGT GAAGAAATGA CCGAAGACAA TGGAAACCCG
Aro203          TTCTTCCATA CTATTT-AAG AGAAGA---T TCGATTATAT ATATCTAACC GCCTCGTTCG ATGTTTTTGT GAAGAAATGA CCGAAGACAA TGGAAACCCG
Kvi204          TTATTCCATA CTATTT-AAG AGAAGA---T TAGATTATAA ATCTCTAACT GCCTCGCTCG ATGTTTTTGT GAAGAAATGA CTGAAGACAA TGGAAACCCG
Kvi205          TTCTTCAATG TTCCTTCAAG AAAAAA---A TCAATTCTAG AGATCTAATT GTCTGGTTTG ATGTTTTCGT GAAGAAATGA CTGAAGACAA TGGGAACCCA
Ani201          TTCTTCAATG TTCCTTCAAG AAAAAA---A TCAATTTTAG AGATCTAATT GTCTGGTTTG ATGTTTTCGT GAAGAAATGA CTGAAGACAA TGGGAACCCG


                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                       610        620        630        640        650        660        670        680        690        700
Ltr201          ATATGGAAGA ACAGGGTGGA AAGTTGGAAG GAAAAGAAGA ACAAGAAGAA AAAGGCT--- GCAACAACTA AGGCTGACAG AGAGGCTGAA GTCCCACCTG
Lag201          ATATGGAAGA ACAGGGTGGA AAGTTGGAAG GAAAAGAAGA ACAAGAAGAA AAAGGCT--- GCAACAACTA AGGCTGACAG AGAGGCTGAA GTCCCACCTG
Lag202          ATATGGAAGA ACAGGGTGGA AAGTTGGAAG GAAAAGAAGA ACAAGAAGAA AAAGGCT--- GCAACAACTA AGGCTGACAG AGAGGCTGAA GTCCCACCTG
Lag203          ATATGGAAGA ACAGGGTGGA AAGTTGGAAG GAAAAGAAGA ACAAGAAGAA AAAGCCTACT GCAACAACTA AGGCTGACAT AGAGGCTGAA GTCCCACCTG
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Lag205          ATTTGGAAGA ACAGGGTGGA AAGTTGGAAG GAAAAGAAGA ACAAGAAGAA AAAGCCTACT GCAACAACTA AGGCTGACAT AGAGGCTGAA GTCCCACCTG
Lfl201          ATATGGATGA ACAGGGTGGA AAGTTGGAAG GAAAAGAAGA ACAAGAAGAA AAAGGCT--- GCAACAACTA AGGCTGACAG AGAGGCTGAA GTCCCACCTG
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Ltp201          ATATGGAAGA ACAGGGTGGA AAGTTGGAAG GAAAAGAAGA ACAAGAAGAA AAAGGCT--- GCAACAACTA AGGCTGACAG AGAGGCTGAA GTCCCACCTG
Lob201          ATATGGAAGA ACAGGGTGGA AAGTTGGAAG GAAAAGAAGA ACAAGAAGAA AAAGGCT--- GCAACAACTA AGGCTGACAG AGAGGCTGAA GTCCCACCTG
Lbr201          ATATGGAAGA ACAGGGTGGA AAGTTGGAAG GAAAAGAAGA ACAAGAAGAA AAAGGCT--- GCAACAACTA AGGCTGACAG AGAGGCTGAA GTCCCACCTG
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Mpa204        ATATGGAAGA ACAGGGTGGA AAGTTGGAAG GAAAAGAAGA ACAAGAAGAA AAAGGCT--- GCAACAACTA AGGCTGA--- ---------A GTCCCACCTG
Msy201        ACATGGAAGA ACAGGGTGGA AAGTTGGAAG GAAAAGAAGA ACAAGAAGAA AAAGGCT--- GCAACAACTA AGGCTGACAG AGAGGCTGAA GTCCCACCTG
Msy202        ATATGGAAGA ACAGGGTGGA AAGTTGGAAG GAAAAGAAGA ACAAGAAGAA AAAGGCT--- GCAACAACTA AGGCTGACAG AGAGGCTGAA GTCCCACCTG
Msy203        ATATGGAAGA ACAGGGTGGA AAGTTGGAAG GAAAAGAAGA ACAAGAAGAA AAAGGCT--- GCAACAACTA AGGCTGACAG AGAGGCTGAA GTCCCACCTG
Msy204        ATATGGAAGA ACAGGGTGGA AAGTTGGAAG GAAAAGAAGA ACAAGAAGAA AAAGGCT--- GCAACAACTA AGGCTGACAG AGAGGCTGAA GTCCCACCTG
Lcr201        ATATGGAAGA ACAGGGTGGA AAGTTGGAAG GAAAAGAAGA ACAAGAAGAA AAAGGCT--- GCAACAACTA AGGCTGACAG AGAGGCTGAA GTCCCACCTG
Lcr202        ATATGGAAGA ACAGGGTGGA AAGTTGGAAG GAAAAGAAGA ACAAGAAGAA AAAGGCT--- GCAACAACTA AGGCTGACAG AGAGGCTGAA GTCCCAGCTG
Lcr203        ATATGGAAGA ACAGGGTGGA AAGTTGGAAG GAAAAGAAGA ACAAGAAGAA AAAGGGT--- GCAACAACTA AGGCTGACAG AGAGGCTGAA GTCCCACCTG
Lcr204        ATATGGAAGA ACAGGGTGGA AAGTTGGAAG GAAAAGAAGA ACAAGAAGAA AAAGGCT--- GCAACAACTA AGGCTGACAG AGAGGCTGAA GTCCCACCTG
Lcr205        ATATGGAAGA ACAGGGTGGA AAGTTGGAAG GAAAAGAAGA ACAAGAAGAA AAAGGGT--- GCAACAACTA AGGCTGACAG AGAGGCTGAA GTCCCACCTG
Lcr206        ATATGGAAGA ACAGGGTGGA AAGTTGGAAG GAAAAGAAGA ACAAGAAGAA AAAGGGT--- GCAACAACTA AGGCTGACAG AGAGGCTGAA GTCCCACCTG
Lcr207        ATATGGAAGA ACAGGGTGGA AAGTTGGAAG GAAAAGAAGA ACAAGAAGAA AAAGGCT--- GCAACAACTA AGGCTGACAG AGAGGCTGAA GTCCCACCTG
Las201        ATATGGAAGA ACAGGGTGGA AAGTTGGAAG GAAAAGAAGA ACAAGAAGAA AAAGGGT--- GCAACAACTA AGGCTGACAG AGAGGCTGAA GTCCCACCTG
Las202        ATATGGAAGA ACAGGGTGGA AAGTTGGAAG GAAAAGAAGA ACAAGAAGAA AAAGGGT--- GCAACAACTA AGGCTGACAG AGAGGCTGAA GTCCCACCTG
Las203        ATTTGGAAGA ACAGGGTGGA AAGTTGGAAG GAAAAGAAGA ACAAAAAGAA AAAGCCTACT GCAACAACAA AGGCTGACAT AGAGGCTGAA GTCCCACCTG
Lac201        ATATGGAAGA ACAGGGTGGA AAGTTGGAAG GAAAAGAAGA ACAAGAAGAA AAAGGCT--- GCAACAACTA AGGCTGACAG AGAGGCTGAA GTCCCACCTG
Mve201        ATATGGAAGA ACAGGGTGGA AAGTTGGAAG GAAAAGAAGA ACAAGAAGAA AAAGGCT--- GCAACAACTA AG-------- ----GCTGAA GTCCCACCTG
Mve202        ATATGGAAGA ACAGGGTGGA AAGTTGGAAG GAAAAGAAGA ACAAGAAGAA AAAGGGT--- GCAACAACTA AGGCTGACAG AGAGGCTGAA GTCCCACCTG
Mve203        ATATGGAAGA ACAGGGTGGA AAGTTGGAAG GAAAAGAAGA ACAAGAAGAA AAAGGGT--- GCAACAACTA AGGCTGACAG TGAGGCTGAA GTCCCACCTG
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Lpe201          ATATGGAAGA ACAGGGTGGA AAGTTGGAAG GAAAAGAAGA ACAAGAAGAA AAAGGCT--- GCAACAACTA AGGCTGACAG AGACGCTGAA GTCCCACCTG
Lpe202          ATATGGAAGA ATAGGGTGGA AAGTTGGAAG GAAAAGAAGA ACAAGAAGAA AAAGGGT--- GCAACAACTA AGGCTGACAG AGAGGCTGAA GTCCCACCTG
Lpe203          ATATGGAAGA ATAGGGTGGA AAGTTGGAAG GAAAAGAAGA ACAAGAAGAA AAAGGGT--- GCAACAACTA AGGCTGACAG AGAGGCTGAA GTCCCACCTG
Lpe204          ATATGGAAGA ATAGGGTGGA AAGTTGGAAG GAAAAGAAGA ACAAGAAGAA AAAGGGT--- GCAACAACTA AGGCTGACAG AGAGGCTGAA GTCCCACCTG
Lph201          ATATGGAAGA ACAGGGTGGA AAGTTGGAAG GAAAAGAAGA ACAAGAAGAA AAAGGCT--- GCAACAACTA AGGCTGACAG AGAGGCTGAA GTCCCACCTG
Lph202          ATATGGAAGA ACAGGGTGGA AAGTTGGAAG GAAAAGAAGA ACAAGAAGAA AAAGGCT--- GCAACAACTA AGGCTGACAG AGAGGCTGAA GTCCCACCTG
Lph203          ATATGGAAGA ACAGGGTGGA AAGTTGGAAG GAAAAGAAGA ACAAGAAGAA AAAGGCT--- GCAACAACTA AGGCTGACAG AGAGGCTGAA GTCCCACCTG
Aca201          GTATGGAAGA ACAGGGTGGA AAGTTGGAAG GAAAAGAAGA ACAAGAAGAA GAAGCCT--- GCAACAACTA AGGCTGACAG AGAGGCTGAA GTCCCACCTG
Aca202          GTATGGAAGA ACAGGGTGGA AAGTTGGAAG GAAAAGAAGA ACAAGAAGAA GAAGCCT--- GCAACAACTA AGGCTGACAG AGAGGCTGAA GTCCCACCTG
Aar201          GTAAGGAAGA ACAGGGTGGA AAGTTGGAAG GAAAAGAAGA ACAAGAAGAA GAAGCCT--- GCAACAAATA AGGCTGACAG AGAGGCTGAA GTCCCACCTG
Aro201          GTATGGAAGA ACAGGGTGGA AAGTTGGAAG GAAAAGAAGA ACAAGAAGAA AAAGCCT--- GCAACAACTA AAGCTGACAG AGAGCCTGAA GACCCACCTG
Aro202          GTATGGAAGA ACAGGGTGGA AAGTTGGAAG GAAAAGAAGA ACAAGAAGAA AAAGCCT--- GCAACAACTA AAGCTGACAG AGAGCCTGAA GTCCCACCTG
Kvi201          GTATGGAAGA ACAGGGTGGA AAGTTGGAAG GAAAAGAAGA ACAAGAAGAA GAAGGCT--- GCAACAACTA AGGCTGACAG AGAGGCTGAA GTCCCACCTG
Kvi202          GTATGGAAGA ACAGGGTGGA AAGTTGGAAG GAAAAGAAGA ACAAGAAGAA AAAGGCT--- GCAACAACTA AGGCTGACAG AGAGGCTGAA GTCCCACCTG
Kvi203          GTATGGAAGA ACAGGGTGGA AAGTTGGAAG GAAAAGAAGA ACAAGAAGAA AAAGGCT--- GCAACAACTA AGGCTGACAG AGAGGCTGAA GTCCCACCTG
Mtf201          ATATGGAAGA ACAGGGTGGA AAGTTGGAAG GAAAAGAAGA ACAAGAAGAA AAAGCCT--- GCAACAACTA AGCCTGACAT AGAGGCTGAA GTCCCACCTC
Mtf202          ATATGGAAGA ACAGGGTGGA AAGTTGGAAG GAAAAGAAGA ACAAGAAGAA AAAGCCT--- GCAACAACTA AGCCTGACAT AGAGGCTGAA GTCCCACCTC
Mtf203          ATATGGAAGA ACAGGGTGGA AAGTTGGAAG GAAAAGAAGA ACAAGAAGAA AAAGCCT--- GCAACAACTA AGCCTGACAT AGAGGCTGAA GTCCCACCTC
Mtf204          ATATGGAAGA ACAGGGTGGA AAGTTGGAAG GAAAAGAAGA ACAAGAAGAA AAAGCCT--- GCAACAACTA AGCCTGACAT AGAGGCTGAA GTCCCACCTC
Mtf205          ATATGGAAGA ACAGGGTGGA AAGTTGGAAG GAAAAGAAGA ACAAGAAGAA AAAGCCT--- GCAACAACTA AGCCTGACAT AGAGGCTGAA GTCCCACCTC
Mtf206          ATATGGAAGA ACAGGGTGGA AAGTTGGAAG GAAAAGAAGA ACAAGAAGAA AAAGCCT--- GCAACAACTA AGGCCGACAA AGAGGCTGAA GTCCCACCTG
Mtf207          ATATGGAAGA ACAGGGTGGA AAGTTGGAAG GAAAAGAAGA ACAAGAAGAA AAAGCCT--- GCAACAACTA AGCCTGACAT AGAGGCTGAA GTCCCACCTC
Mma201          ATATGGAAGA ACAGGGTGGA AAGTTGGAAG GAAAAGAAGA ACAAAAAGAA AAAGCCT--- GCAACAACTA AGCCTAACAT AGAGGCTGAA GTCCCACCTG
Mma202          ATATGGAAGA ACAGGGTGGA AAGTTGGAAG GAAAAGAAGA ACAAGAAGAA AAAGCCT--- GCAACAACTA AGCCTGACAT AGAGGCTGAA GTCCCACCTG
Aro203          ATATGGAAGA ACAGGGTGGA AAGTTGGAAG GAAAAGAAGA ACAAGAAGAA AAAGGCT--- GCAACAACTA AGGCTGACAG AGAGGCTGAA GTCTCACCTG
Kvi204          GTATGGAAGA ACAGGGTGGA AAGTTGGAAG GAAAAGAAGA ACAAGAAGAA AAAGGCT--- GCAACAACTA AGGCTGACAG AGAGGCTGAA GTCCCACCTG
Kvi205          ATTTGGAAGA ACAGGGTGGA AAGTTGGAAA GAAAAGAAGA ACAAGAAGAA AAAGCCT--- GCAACAACTA AGGCTGACAG AGAGGCTGAA GTCCCACCTG
Ani201          ATTTGGAAGA ACAGGGTGGA AAGTTGGAAG GAAAAGAAGA ACAAGAAGAA AAAGCCT--- GCAACAACTA AGGCTGACAG AGAGGCTGAA GTCCCACCTG


                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                       710        720        730        740        750        760        770        780        790        800
Ltr201          AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATATATATAC ACACAC---- ---------- ----GAAGCA GATCAATGAT AAGATTCTAC TTAGTGCAAT
Lag201          AGCAACAAAT GGAAGATAAA CCGTAAGTAT GTATATATAT ATATATATAT ATATATACAC ACACGTAGCA GATCAATGAT AAGATTCTAC TCAGTGCAAG
Lag202          AGCAACAAAT GGAAGATAAA CCGTAAGTAT GTATATATAT ATATATATAT ATATATACAC ACACGTAGCA GATCAATGAT AAGATTCTAC TCAGTGCAAG
Lag203          AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATATATACAC ACAC------ ---------- ----GAAGCA GATCAATGAT AAGATTCTAC TTAGTGCAAT
Lag204          AGCAACAAAT GGAAGGTAAA CCGTAAGTAT ATATATACAC ACAC------ ---------- ----GAAGCA GATCAATGAT AAGATTCTAC TTAGTGCAAT
Lag205          AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATATATACAC ACAC------ ---------- ----GAAGCA GATCAATGAT AAGATTCTAC TTAGTGCAAT
Lfl201          AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATATATACAC ACACAC---- ---------- ----GAAGCA GATCAATGAT AAGATTCTAC TTAGTGCAAT
Lfl202          AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATATATACAC ACACGC---- ---------- ----GAAGCA GATCAATGAT AAGATTCTAC TTAGTGCAAT
Lfl203          AGCAACAAAT GGAAGATAAA CCGTAAGTAT AGAGATATAT ACAC------ ---------- ----GTAGCA GATCAATGAT AAGATTCTAC TCAGTGCAAG
Lfl204          AGCAACAAAT GGAAGATAAA CCGTAAGTAT AGAGATATAT ACAC------ ---------- ----GTAGCA GATCAATGAT AAGATTCTAC TCAGTGCAAG
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Lfl205        AGCAACAAAT GGAAGATAAA CCGTAAGTAT AGAGATATAT ACAC------ ---------- ----GTAGCA GATCAATGAT AAGATTCTAC TCAGTGCAAG
Ltp201        AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATATATATAC ACAC------ ---------- ----GTAGCA GATCAATGAT AAGATTCTAC TCAGTGCAAG
Lob201        AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATATATATAT ATATATATAC AC-------- ----GTAGCA GATCAATGAT AAGATTCTAC TCAGTGCAAG
Lbr201        AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATATATATAT ATATAAACAC ACACAC---- ----GTAGCA GATCAATGAT AAGATTCTAC TCAGTGCAAG
Lol201        AGCAACAAAT GGAAGATAAA CCGTAAGTGT GTATATATAC ---------- ---------- ----GTAGCA GATCAAT--- AAGATTCTAC TTGGTGCAAG
Lol202        AGCAACAAAT GGAAGATAAA CCGTAAGTGT GTATATATAC ---------- ---------- ----GTAGCA GATCAAT--- AAGATTCTAC TTGGTGCAAG
Lol203        AGCAACAAAT GGAAGACAAA CCGTAAGTGT GTATATATAC ---------- ---------- ----GTAGCA GATCAAT--- AAGATTCTAC TTGGTGCAAG
Lol204        AGCAACAAAT GGAAGATAAA CCGTAAGTGT GTATATATAC ---------- ---------- ----GTAGCA GATCAAT--- AAGATTCTAC TTGGTGCAAG
Lol205        AGCAACAGAT GGAAGATAAA CCGTAAGTGT GTATATATAC ---------- ---------- ----GTAGCA GATCAAT--- AAGATTCTAC TTGGTGCAAG
Lol206        AGCAACAAAT GGAAGATAAA CCGTAAGTGT GTATATATAC ---------- ---------- ----GTAGCA GATCAAT--- AAGATTCTAC TTGGTGCAAG
Mal201        AGCAACAAAT GGAAGATAAA CCGTAAGTGT GTATATATAT ATATAT---- ---------- ----GTAGCA GATCAAT--- ACGATTCTAC TTGGTGCAAG
Lar201        AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATATGTATCT ATATATAC-- ---------- ----GTAGCA GATCAATGCT AAGATTCTAC TTAGTGCAAG
Lar202        AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATATGTATAT ATATATAC-- ---------- ----GTAGCA GATCAATGCT AAGATTCTAC TTAGTGCAAG
Lar203        AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATATGTATAT ATATATAC-- ---------- ----GTAGCA GATCAATGCT AAGATTCTAC TTAGTGCAAG
Lar204        AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATATGTATAT ATATATAC-- ---------- ----GTAGCA GATCAATGCT AAGATTCTAC TTAGTGCAAG
Lar205        AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATATGTATAT ATATATAC-- ---------- ----GTAGCA GATCAATGCT AAGATTCTAC TTAGTGCAAG
Lar206        AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATATGTATAT ATATATAC-- ---------- ----GTAGCA GATCAATGCT AAGATTCTAC TTAGTGCAAG
Lar207        AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATATGTATAT ATATATAC-- ---------- ----GTAGCA GATCAATGCT AAGATTCTAC TTAGTGCAAG
Lar208        AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATATGTATAT ATATATAC-- ---------- ----GTAGCA GATCAATGCT AAGATTCTAC TTAGTGCAAG
Lar209        AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATATGTATAT ATATATAC-- ---------- ----GTAGCA GATCAATGCT AAGATTCTAC TTAGTGCAAG
Lmu201        AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATATGTATAT ATATATAC-- ---------- ----GTAGCA GATCAATGCT AAGATTCTAC TTAGTGCAAG
Lmu202        AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATATGTATAT ATATATAC-- ---------- ----GTAGCA GATCAATGCT AAGATTCTAC TTAGTGCAAG
Lmu203        AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATATGTATAT ATATATAC-- ---------- ----GTAGCA GATCAATGCT AAGATTCTAC TTAGTGCAAG
Lmu204        AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATATGTATAT ATATATAC-- ---------- ----GTAGCA GATCAATGCT AAGATTCTAC TTAGTGCAAG
Lmu205        AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATATATATAT GTATATAC-- ---------- ----GTAGCA GATCGATGTT AAGATTCTAC TTAGTGCAAG
Mne201        AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATATGTATAT ATATAC---- ---------- ----GTAGCA GATCAATGAT AAGATTCTAC TTAGTGCAAG
Mne202        AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATATGTATAT ATATATAC-- ---------- ----GTAGCA GATCAATGAT AAGATTCTAC TTAGTGCAAG
Mne203        AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATATGTATAT ATATATAC-- ---------- ----GTAGCA GATCAATGAT AAGATTCTAC TTAGTGCAAG
Mne204        AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATATGTATAT ATATAC---- ---------- ----GTAGCA GATCAATGAT AAGATTCTAC TTAGTGCAAG
Mne205        AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATATGTATAT ATATAC---- ---------- ----GTAGCA GATCAATGAT AAGATTCTAC TTAGTGCAAG
Mne206        AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATATGTATAT ATATAC---- ---------- ----GTAGCA GATCAATGAT AAGATTCTAC TTAGTGCAAG
Mne207        AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATATGTATAT ATATAC---- ---------- ----GTAGCA GATCAATGAT AAGATTCTAC TTAGTGCAAG
Mne208        AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATATGTATAT ATATAC---- ---------- ----GTAGCA GATCAATGAT AAGATTCTAC TTAGTGCAAG
Mni201        AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATATGTATAT ATATATATAC ---------- ----GTAGCA GATCAATGAT AAGATTCTAC TTAGTGCAAG
Mni202        AGCAACAAAT GGAAGATAAA CCGTAAGTAT ACATATATAT ATATATATAT ACAC------ ----GAAGCA TATCAATTAT AAGATTCTAC TTAGTGCAAT
Mni203        AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATATGTATAT ATATATATAC ---------- ----GTAGCA GATCAATGAT AAGATTCTAC TTAGTGCAAG
Mpa201        AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATATGTATAT ATATATATAC ---------- ----GTAGCA GATCAATGAT AAGATTCTAC TTAGTGCAAG
Mpa202        AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATATATATAT GTATATAC-- ---------- ----GTAGCA GATCGATGTT AAGATTCTAC TTAGTGCAAG
Mpa203        AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATATATATAT GTATATAC-- ---------- ----GTAGCA GATCGATGTT AAGATTCTAC TTAGTGCAAG
Mpa204        AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATATATATAT GTATATAC-- ---------- ----GTAGCA GATCGATGTT AAGATTCTAC TTAGTGCAAG
Msy201        AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATATGTATAT ATATATATAT AC-------- ----GTAGCA GATCAATGAT AAGATTCTAC TTAGTGCAAG
Msy202        AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATATGTATAT ATATATATAT AC-------- ----GTAGCA GATCAATGAT AAGATTCTAC TTAGTGCAAG
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Msy203        AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATATGTATAT ATATATATAC AC-------- ----GTAGCA GATCAATGAT AAGATTCTAC TTAGTGCAAG
Msy204        AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATATGTATAT ATATATATAT AC-------- ----GTAGCA GATCAATGAT AAGATTCTAC TTAGTGCAAG
Lcr201        AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATATGTATAT ATATATATAT ACAC------ ----GTAGCA GATCAATGAT AAGATTCTAC TTAGTGCAAG
Lcr202        AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATATGTATAT ATATAC---- ---------- ----GTAGCA GATCAATGAT AAGATTCTAC TTAGTGCAAG
Lcr203        AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATATGTATAT ATATATATAT ACAC------ ----GTAGCA GATCAATGAT AAGATTCTAC TTAGTGCAAG
Lcr204        AGCAACAAAT GGAAGATAAA CCGTATGTAT ATATATATGT ATATAC---- ---------- ----GTAGCA AGCAAATGTT AAGATTCTAC TTAGTGCAAG
Lcr205        AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATATGTATAT ATATATATAT ACAC------ ----GTAGCA GATCAATGAT AAGATTCTAC TTAGTGCAAG
Lcr206        AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATATGTATAT ATATATATAT ACAC------ ----GTAGCA GATCAATGAT AAGATTCTAC TTAGTGCAAG
Lcr207        AGCAACAAAT GGAAGATAAA CCGTATGTAT ATATATATGT ATATAC---- ---------- ----GTAGCA AGCAAATGTT AAGATTCTAC TTAGTGCAAG
Las201        AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATATATCACA CAC------- ---------- ----GTAGCA GATCAATGAT AAGATTCTAC TTAGTGCAAG
Las202        AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATATATCACA CAC------- ---------- ----GTAGCA GATCAATGAT AAGATTCTAC TTAGTGCAAG
Las203        AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATATATATAT ATATA----- ---------- ---------- ---------- ---------- TTAGTGCAAT
Lac201        AGCAACAAAT GGAAGATAAA CCGTATGTGT ATATATATAT ACAC------ ---------- ----GTAGCA GATCAATGAT AAGACTCTAC TTAGTGCAAG
Mve201        AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATATATATAT GTATATAC-- ---------- ----GTAGCA GATCGATGTT AAGATTCTAC TTAGTGCAAG
Mve202        AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATATGTGTAT ATATATATAT ATATA----- ---------- ---------- ---------- ---GTGCAAG
Mve203        AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATATGTATAT ATATATATAT ATATA----- ---------- ---------- ---------- ---GTGCAAG
Lpe201        AGCAACAAAT GGAAGATAAA CCGTATGTGT ATATATATAT ATATATATAT GTATATAC-- ----GTAGCA AGCAAATGTT AAGATTCTAC TTAGTGCAAG
Lpe202        AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATATGTATAT ATATATATAC AC-------- ----GTAGCA GATCAATGAT AAGATTCTAC TTAGTGCAAG
Lpe203        AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATATGTATAT ATATATATAC AC-------- ----GTAGCA GATCAATGAT AAGATTCTAC TTAGTGCAAG
Lpe204        AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATATGTATAT ATATATATAC AC-------- ----GTAGCA GATCAATGAT AAGATTCTAC TTAGTGCAAG
Lph201        AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATATATAC-- ---------- ---------- ----GTAGCA GATCAATGAT AAGATTCTAC TTAGTGCAAG
Lph202        AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATATATAC-- ---------- ---------- ----GTAGCA GATCAATGAT AAGATTCTAC TTAGTGCAAG
Lph203        AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATATATAC-- ---------- ---------- ----GTAGCA GATCAATGAT AAGATTCTAC TTAGTGCAAG
Aca201        AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATAAAC---- ---------- ---------- ----GAAGCA GATCAATGAT GAGATTCTAC TTAGTGCAAT
Aca202        AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATAAAC---- ---------- ---------- ----GAAGCA GATCAATGAT GAGATTCTAC TTAGTGCAAT
Aar201        AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATAAAC---- ---------- ---------- ----GAAGCA GATCAATGAT GAGATTCTAC TTAGTGCAAT
Aro201        AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATACAT---- ---------- ---------- ----GAAGCA GATCAATGAT GAGATTCTAC TTAGTGAAAG
Aro202        AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATACAT---- ---------- ---------- ----GAAGCA GATCAATGAT GAGATTCTAC TTAGTGAAAG
Kvi201        AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATATAC---- ---------- ---------- ----GAAGCA GATCAATGAT AAGATTCTAC TTAGTGCAGG
Kvi202        AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATATAC---- ---------- ---------- ----GAAGCA GATCAATGAT AAGATTCTAC TTTGTGCAGG
Kvi203        AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATATAC---- ---------- ---------- ----GAAGCA GATCAATGAT AAGATTCTAC TTAGTGCAGG
Mtf201        AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATACATATAT ATATATACAT ACGATAATAC ----GAAGCA GATCAATGAT AAGATTCTAC TTAGTGCAAG
Mtf202        AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATACATATAT ATATATACAT ACGATAATAC ----GAAGCA GATCAATGAT AAGATTCTAC TTAGTGCAAG
Mtf203        AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATACATATAT ATATATACAT ACGATAATAC ----GAAGCA GATCAATGAT AAGATTCTAC TTAGTGCAAG
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Mtf205        AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATACATATAT ATATATACAT ACGATAATAC ----GAAGCA GATCAATGAT AAGATTCTAC TTAGTGCAAG
Mtf206        AGCAACAAAT GGAAGATAAA CCGTACGTGT ATATATATAT ATATATATAC ---------- ----GAAGCA GATCGATGAT ACGATTCGAC TTAGTGCAAT
Mtf207        AGCAACAAAT GGAAGATAAA CCGTACGTGT GTGTGTATAT ATATATATAT ATATATATAT ATATGAAGCA GATCGATGAT ACGATTCGAC TTAGTGCAAT
Mma201        AGCAACAAAT GGAAGATAAG CCGTAAGTAT ATATATACAC GATAATAC-- ---------- ----GAAGCA GATCAATGAT AAGATTCTAC TTAGTGCAAG
Mma202        AGCAACAAAT GGAAGATAAG CCGTAAGTGT ATATATATAC ACGATAATAC ---------- ----GAAGCA GATCAATGAT AAGATTCTAC TTAGTGCAAG
Aro203        AGCAACAAAT GGAAGATAAA CCGTAAGTGT ATATATATAT ATAC------ ---------- ----GTAGCA GATAAATGAT AAGATTCTAC TTAGGGCAAG
Kvi204        AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATATAC---- ---------- ---------- ----GAAGCA GATCAATGAT AAGATTCTAC TTAGTGCAGG
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Kvi205       AGCAACAAAT GGAAGATAAA CCGTAAGTAT AAAAAC---- ---------- ---------- ----GAAGCA GATCAATGAT AAGATTCTAC TTAGTGCAAT
Ani201       AGCAACAAAT GGAAGATAAA CCGTAAGTAT ATATAC---- ---------- ---------- ----AAAGCA TATCAATGAT AAGATTCTAC TTAGTGCAAT


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                    810        820        830        840        850        860        870        880        890        900
Ltr201       GTTTTTGTTT ATGTTAAGTC TCAC--TGAT ATGTAAAA-T TTGGTTTTGC ----AGGACA CGA---GATG CTTCTCAGCC CCTCTCCACT ATAATTCCAA
Lag201       GTTTTTATTT ACC-AAAGTC TTAC--TGAT ATGTAAAA-C TTGCATTTGT ----AGGGCA CCA---GATG CTTCCCAGCC CCTCTCCACT ATAATTCCAA
Lag202       GTTTTTATTT ACC-AAAGTC TTAC--TGAT ATGTAAAA-C TTGCATTTGT ----AGGGCA CCA---GATG CTTCCCAGCC CCTCTCCACT ATAATTCCAA
Lag203       GTTTTTGTTT ATGTTAAGTC TCAC--TGAT ATGTAAAA-T TTGGTTTTGC ----AGGACA CCA---GATG CTTCTCAGCC CCTCTCCACT ATAATTCCAA
Lag204       GTTTTTGTTT ATGTTAAGTC TCAC--TGAT ATGTAAAA-T TTGGTTTTGC ----AGGACA CCA---GATG CTTCTCAGCC CCTCTCCACT ATAATTCCAA
Lag205       GTTTTTGTTT ATGTTAAGTC TCAC--TGAT ATGTAAAA-T TTGGTTTTGC ----AGGACA CCA---GATG CTTCTCAGCC CCTCTCCACT ATAATTCCAA
Lfl201       GTTTTTGTTT ATGTTAAGTC TCAC--TGAT ATGTAAAA-T TTGGTTTTGC ----AGGACA CCA---GATG CTTCTCAGCC CCTCTCCACT ATAATTCCAA
Lfl202       GTTTTTGTTT ATGTTAAGTC TCAC--TGAT ATGTAAAA-T TTGGTTTTGC ----AGGACA CCA---GATG CTTCTCAGCC CCTCTCCACT ATAATTCCAA
Lfl203       GTTTTTATTT ACC-AAAGTC TTAC--TGAT ATGTAAAA-C TTGCATTTGT ----AGGGCA CCA---GATG CTTCCCAGCC CCTCTCCACT ATAATTCCAA
Lfl204       GTTTTTATTT ACC-AAAGTC TTAC--TGAT ATGTAAAA-C TTGCATTTGT ----AGGGCA CCA---GATG CTTCCCAGCC CCTCTCCACT ATAATTCCAA
Lfl205       GTTTTTATTT ACC-AAAGTC TTAC--TGAT ATGTAAAA-C TTGCATTTGT ----AGGGCA CCA---GATG CTTCCCAGCC CCTCTCCACT ATAATTCCAA
Ltp201       GTTTTTATTT ACC-AAAGTC TTAC--TGAT ATGTAAAA-C TTGCATTTGT ----AGGGCA CCA---GATG CTTCCCAACC CCTCTCCACT ATAATTCCAA
Lob201       GTTTTTATTT ACC---AGTC TTAC--TGAT ATGTAAAA-C TTGCATTTGT ----AGGGCA CCA---GATG CTTCCCAGCC CCTCTCCACT ATAATTCCAA
Lbr201       GTTTTTACTT ACC-AAAGTC TTAC--TGAT ATGTAAAA-C TTGCATTTGT ----AGGGCA CCA---GATG CTTCTCAGCC CCTCTCCACT ATAATTCCAA
Lol201       GTTTTTATTT ACC-AAAGTC TTAC--TGAT ATGTAAAA-C TTGCATTTGC ----AGGGCA CCA---GATG CTTCCCAGCC CCTCTCCACT ATAATTCCAA
Lol202       GTTTTTATTT ACC-AAAGTC TTAC--TGAT ATGTAAAA-C TTGCATTTGC ----AGGGCA CCA---GATG CTTCCCAGCC CCTCTCCACT ATAATTCCAA
Lol203       GTTTTTATTT ACC-AAAGTC TTAC--TGAT ATGTAAAA-C TTGCATTTGC ----AGGGCA CCA---GATG CTTCCCAGCC CCTCTCCACT ATAATTCCAA
Lol204       GTTTTTATTT ACC-AAAGTC TTAC--TGAT ATGTAAAA-C TTGCATTTGC ----AGGGCA CCA---GATG CTTCCCAGCC CCTCTCCACT ATAATTCCAA
Lol205       GTTTTTATTT ACC-AAAGTC TTAC--TGAT ATGTAAAA-C TTGCATTTGC ----AGGGCA CCA---GAKG CTTCCCAGCC CCTCTCCACT ATAATTCCAA
Lol206       GTTTTTATTT ACC-AAAGTC TTAC--TGAT ATGTAAAA-C TTGCATTTGC ----AGGGCA CCA---GATG CTTCCCAGCC CCTCTCCACT ATAATTCCAA
Mal201       GTTTTTATTT ACC-AAAGTC TTAC--TGAT ATGTAAAA-C TTGCATTTGC ----AGGGCA CCA---GATG CTTCCCAGCC CCTCTCCACT ATAATTCCAA
Lar201       GTTTTTATTT ACC-AAAGTC TTAC--TGAT ATGTAAAAAC TTGCATTTGC TTGCAGGGCA GCA---GATG CTTCCCAGCC CCTCTCCACT ATAATTCCAA
Lar202       GTTTTTATTT ACC-AAAGTC TTAC--TGAT ATGTAAAAAC TTGCATTTGC TTGCAGGGCA GCA---GATG CTTCCCAGCC CCTCTCCACT ATAATTCCAA
Lar203       GTTTTTATTT ACC-AAAGTC TTAC--TGAT ATGTAAAAAC TTGCATTTGC TTGCAGGGCA GCA---GATG CTTCCCAGCC CCTCTCCACT ATAATTCCAA
Lar204       GTTTTTATTC ACC-AAAGTC TTAC--TGAT ATGTAAAAAC TTGCATTTGC TTGCAGGGCA GCA---GATG CTTCCCAGCC CCTCTCCACT ATAATTCCAA
Lar205       GTTTTTATTT ACC-AAAGTC TTAC--TGAT ATGTAAAAAC TTGCATTTGC TTGCAGGGCA GCA---GATG CTTCCCAGCC CCTCTCCACT ATAATTCCAA
Lar206       GTTTTTATTT ACC-AAAGTC TTAC--TGAT ATGTAAAAAC TTGCATTTGC TTGCAGGGCA GCA---GATG CTTCCCAGCC CCTCTCCACT ATAATTCCAA
Lar207       GTTTTTATTT ACC-AAAGTC TTAC--TGAT ATGTAAAAAC TTGCATTTGC TTGCAGGGCA GCA---GATG CTTCCCAGCC CCTCTCCACT ATAATTCCAA
Lar208       GTTTTTATTT ACC-AAAGTC TTAC--TGAT ATGTAAAAAC TTGCATTTGC TTGCAGGGCA GCT---GATG CTTCCCAGCC CCTCTCCACT ATAATTCCAA
Lar209       GTTTTTATTT ACC-AAAGTC TTAC--TGAT ATGTAAAAAC TTGCATTTGC TTGCAGGGCA GCA---GATG CTTCCCAGCC CCTCTCCACT ATAATTCCAA
Lmu201       GTTTTTATTT ACC-AAAGTC TTAC--TGAT ATGTAAAAAC TTGCATTTGC TTGCAGGGCA GCA---GATG CTTCCCAGCC CCTCTCCACT ATAATTCCAA
Lmu202       GTTTTTATTT ACC-AAAGTC TTAC--TGAT ATGTAAAAAC TTGCATTTGC TTGCAGGGCA GCA---GATG CTTCCCAGCC CCTCTCCACT ATAATTCCAA
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Lmu204       GTTTTTATTT ACC-AAAGTC TTAC--TGAT ATGTAAAAAC TTGCATTTGC TTGCAGGGCA GCA---GATG CTTCCCAGCC CCTCTCCACT ATAATTCCAA
Lmu205       GTTTTTATTT ACC-AAAGTC TTAC--TGAT ATGTAAAA-C TTGCATTTGC TTGCAGGGCA GCA---GATG CTTCCCAGCC CCTCTCCACT ATAATTCCAA
Mne201       GTTTTTATTT ACC-AAAGTC TTAC--TGAT ATGTAAAAAC TTGCATTTGC TTGCAGGGCA GCA---GATG CTTCCCAGCC CCTCTCCACT ATAATTCCAA
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Mne202          GTTTTTATTT ACC-AAAGTC TTAC--TGAT ATGTAAAAAC TTGCATTTGC TTGCAGGGCA GCA---GATG CTTCCCAGCC CCTCTCCACT ATAATTCCAA
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Mne206          GTTTTTATTT ACC-AAAGTC TTAC--TGAT ATGTAAAAAC TTGCATTTGC TTGCAGGGCA GCA---GATG CTTCCCAGCC CCTCTCCACT ATAATTCCAA
Mne207          GTTTTTATTT ACC-AAAGTC TTAC--TGAT ATGTAAAAAC TTGCATTTGC TTGCAGGGCA GCA---GATG CTTCCCAGCC CCTCTCCACT ATAATTCCAA
Mne208          GTTTTTATTT ACC-AAAGTC TTAC--TGAT ATGTAAAAAC TTGCATTTGC TTGCAGGGCA GCA---GATG CTTCCCAGCC CCTCTCCACT ATAATTCCAA
Mni201          GTTCTTATTT ACC---AATC TTAC--TGAT AT-------C TTGCATTTGC TTGCAGGGCA GCA---GATG CTTCCCAGCC CCTCTCCACT ATAATTCCAA
Mni202          GTTTTTGTTT ACG-TAAGTC TCAC--TGAT ATCTAAAA-T TTGCTTTTGC ----AGGGCA CCA---GATG CTTCTCAGCC CCTCTCCACT ATAATTCCAA
Mni203          GTTTTTATTT ACC---AATC TTAC--TGAT AT-------C TTGCATTTGC TTGCAGGGCA GCA---GATG CTTCCCAGCC CCTCTCCACT ATAATTCCAA
Mpa201          GTTTTTATTT ACC---AATC TTAC--TGAT AT-------C TTGCATTTGC TTGCAGGGCA GCA---GATG CTTCCCAGCC CCTCTCCACT ATAATTCCAA
Mpa202          GTTTTTATTT ACC-AAAGTC TTAC--TGAT ATGTAAAA-C CTGCATTTGC TTGCAGGGCA GCA---GATG CTTCCCAGCC CCTCTCCACT ATAATTCCAA
Mpa203          GTTTTTATTT ACC-AAAGTC TTAC--TGAT ATGTAAAA-C TTGCATTTGC TTGCAGGGCA GCA---GATG CTTCCCAGCC CCTCTCCACT ATAATTCCAA
Mpa204          GTTTTTATTT ACC-AAAGTC TTAC--TGAT ATGTAAAA-C TTGCATTTGC TTGCAGGGCA GCA---GATG CTTCCCAGCC CCTCTCCACT ATAATTCCAA
Msy201          GTTTTTATTT ACC---AATC TTAC--TGAT AT-------C TTGCATTTGC TTGCAGGGCA GCA---GATG CTTCCCAGCC CCTCTCCACT ATAATTCCAA
Msy202          GTTTTTATTT ACC---AATC TTAC--TGAT AT-------C TTGCATTTGC TTGCAGGGCA GCA---GATG CTTCCCAGCC CCTCTCCACT ATAATTCCAA
Msy203          GTTTTTATTT ACC---AATC TTAC--TGAT AT-------C TTGCATTTGC TTGCAGGGCA GCA---GATG CTTCCCAGCC CCTCTCCACT ATAATTCCAA
Msy204          GTTTTTATTT ACC---AATC TTAC--TGAT AT-------C TTGCATTTGC TTGCAGGGCA GCA---GATG CTTCCCAGCC CCTCTCCACT ATAATTCCAA
Lcr201          GTTTTTATTT ACC-CAAGTC TTAC--TGAT ATGTAAAAAC TTGCATTTGC TTGCAGGGCA GCA---GATG CTTCCCAGCC CCTCTCCACT ATAATTCCAA
Lcr202          GTTTTTATTT ACC---AATC TTAC--TGAT AT-------C TTGCATTTGC TTGCAGGGCA GCA---GATG CTTCCCAGCC CCTCTCCACT ATAATTCCAA
Lcr203          GTTTTTATTT ACC-CAAGTC TTAC--TGAT ATGTAAAAAC TTGCATT-GC TTGCAGGGCA GCA---GATG CTTCCCAGCC CCTCTCCACT ATAATTCCAA
Lcr204          GTTTTTATTT ACC-AAAGTC TTAC--TGAT ATGTAAAA-C TTGCATTTGC TTGCAGGGCA GCA---GATG CTTCCCAGCC CCTCTCCACT ATAATTCCAA
Lcr205          GTTTTTATTT ACC-CAAGTC TTAC--TGAT ATGTAAAAAC TTGCATTTGC TTGCAGGGCA GCA---GATG CTTCCCAGCC CCTCTCCACT ATAATTCCAA
Lcr206          GTTTTTATTT ACC-CAAGTC TTAC--TGAT ATGTAAAAAC TTGCATTTGC TTGCAGGGCA GCA---GATG CTTCCCAGCC CCTCTCCACT ATAATTCCAA
Lcr207          GTTTTTATTT ACC-AAAGTC TTAC--TGAT ATGTAAAA-C TTGCATTTGC TTGCAGGGCA GCA---GATG CTTCCCAGCC CCTCTCCACT ATAATTCCAA
Las201          GTTTTTATTT ACC-CAAGTC TTAC--TGAT ATGTAAAAAC TTGCATTTGC TTGCAGGGCA GCA---GATG CTTCCCAgCC CCTCTCCACT ATAATTCCAA
Las202          GTTTTTATTT ACC-CAAGTC TTAC--TGAT ATGTAAAAAC TTGCATTTGC TTGCAGGGCA GCA---GATG CTTCCCAGCC CCTCTCCACT ATAATTCCAA
Las203          GTTTTTGTTT ACGTTAAGTC TCACACTGAT ATGTAAAT-T TTGCTTTTGC ----AGGGCA CCA---GATG CTTCTCAGCC CCTCTCCACT ATAATTCCAA
Lac201          GTTTTTATTT ACC-AGTGTC TTAC--TGAT ATGTAAAA-C TTGCATTTGC ----AGGGCA GCA---GATG CTTCCCAGCC TCTCTCCACT ATAATTCCAA
Mve201          GTTTTTATTT ACC-AAAGTC TTAC--TGAT ATGTAAAC-- TTGCATTTGC TTGCAGGGCA GCA---GATG CTTCCCAGCC CCTCTCCACT ATAATTCCAA
Mve202          GTTTTTATTT ACC-CAAGTC TTAC--TGAT ATGTAAAAAT TTGCATTTGC TTGCAGGGCA GCA---GATG CTTCCCAGCC CCTCTCCACT ATAATTCCAA
Mve203          GTTTTTATTT ACC-CAAGTC TTAC--TGAT ATGTAAAAAT TTGCATTTGC TTGCAGGGCA GCA---GATG CTTCCCAGCC CCTCTCCACT ATAATTCCAA
Lpe201          GTTTTTATTT ACC-AAAGTC TTAC--TGAT ATGTAAAA-C TTGCATTTGC TTGCAGGGCA GCA---GATG CTTCCCAGCC CCTCTCCACT ATAATTCCAA
Lpe202          GTTCTTATTT ACC-CAAGTC TTAC--TGAT ATGTAAAAAC TTGCATTTGC TTGCAGGGCA GCA---GATG CTTCCCAGCC CCTCTCCACT ATAATTCCAA
Lpe203          GTTTTTATTT ACC-CAAGTC TTAC--TGAT ATGTAAAAAC TTGCATTTGC TTGCAGGGCA GCA---GATG CTTCCCAGCC CCTCTCCACT ATAATTCCAA
Lpe204          GTTTTTATTT ACC-CAAGTC TTAC--TGAT ATGTAAAAAC TTGCATTTGC TTGCAGGGCA GCA---GATG CTTCCCAGCC CCTCTCCACT ATAATTCCAA
Lph201          GTTTTTATTT ACC-AAAGTC TTAC--TGAT ATGTAAAA-C TTGCATTTGC ----AGGGCA CCG---GATG CTTCCCAGCC CCTCTCCACT ATAATTCCAA
Lph202          GTTTTTATTT ACC-AAAGTC TTAC--TGAT ATGTAAAA-C TTGCATTTGC ----AGGGCA CCG---GATG CTTCCCAGCC CCTCTCCACT ATAATTCCAA
Lph203          GTTTTTATTT ACC-AAAGTC TTAC--TGAT ATGTAAAA-C TTGCATTTGC ----AGGGCA CCG---GATG CTTCCCAGCC CCTCTCCACT ATAATTCCAA
Aca201          GTTTTTGTTT ATCTTAAGTC TTAC--TTGT ATGTAAAA-T TTGCATTTGC ----AGGGCA CCA---GATG CTTCCCAGCC CCTCTCTACT ATAATTCCAA
Aca202          GTTTTTGTAT ATGTTAAGTC TTAC--TGAT ATGTAAAA-T TTGCATTTGC ----AGAGCA CCA---GATG CTTCCCAGCC CCTCTCCACT ATAATTCCAA
Aar201          GTTTTTGTTT ATCTTAAGTC TTAC--TGGT ATGTAAAA-T TTGCATTTGC ----AGGGCA CCA---GATG CTTCCCAGCC CCTCTCTACT ATAATTCCAA
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Aro201          GTTTGTGTTT ATGTTAAGTC TTAC--TGAT ATGTAAAA-C TTGCATTTGC ----AGGGCA CCA---GATG CTTCTCAGCC CCTCTCCACT ATAATTCCAA
Aro202          GTTTGTGTTT ATGTTAAGTC TTAC--TGAT ATGTAAAA-C TTGCATTTGC ----AGGGCA CCA---GATG CTTCTCAGCC CCTCTCCACT ATAATTCCAA
Kvi201          GTTTTTGTTT ATGTTAAGTC TTAC--TGAT ATGTAAAA-C TTGCATTTGC ----AGGGCA CCA---GATG CTTCCCAGCC CCTCTCCACT ATAATTCCAA
Kvi202          GTTTTTGTTT ATGTTAAGTC TTAC--TGAT ATGTAAAA-C TTGCATTTGC ----AGGGCA CCA---GATG CTTCCCAGCC CCTCTCCACT ATAATTCCAA
Kvi203          GTTTTTGTTT ATGTTAAGTC TTAC--TGAT ATGTAAAA-C TTGCATTTGC ----AGGGCA CCA---GGTG CTTCCCAGCC CCTCTCCACT ATAATTCCAA
Mtf201          GTTTTTGTTT ATGTCAAGTG TTAC--TGAT ATGTAAAA-C TTGCATTTGC ----AGGGCA CCACCAGATG CTTCCCAGCC CCTCTCCGCT ATAATTCCAA
Mtf202          GTTTTTGTTT ATGTCAAGTG TTAC--TGAT ATGTAAAA-C TTGCATTTGC ----AGGGCA CCACCAGATG CTTCCCAGCC CCTCTCCGCT ATAATTCCAA
Mtf203          GTTTTTGTTT ATGTCAAGTG TTAC--TGAT ATGTAAAA-C TTGCATTTGC ----AGGGCA CCACCAGATG CTTCCCAGCC CCTCTCCGCT ATAATTCCAA
Mtf204          GTTTTTGTTT ATGTCAAGTG TTAC--TGAT ATGTAAAA-C TTGCATTTGC ----AGGGCA CCACCAGATG CTTCCCAGCC CCTCTCCGCT ATAATTCCAA
Mtf205          GTTTTTGTTT ATGTCAAGTG TTAC--TGAT ATGTAAAA-C TTGCATTTGC ----AGGGCA CCACCAGATG CTTCCCAGCC CCTCTCCGCT ATAATTCCAA
Mtf206          GCTTATGTTT ATGTTAAGTC TAAA--TTAT ATGTAAAA-C TTGGTTTTGC ----AGGGCA CCA---GATG CTTCTCAGCC CCTGTCCGCT ATAATTCCAA
Mtf207          GCTTATGTTT ATGTTAAGTC TAAA--TTAT ATGTAAAA-C TTGGTTTTGC ----AGGGCA CCA---GATG CTTCTCAGCC CCTGTCCACT ATAATTCCAA
Mma201          GTTTTTGTTT ATGTCAAGTC TTAC--TGAT ATGTAAAA-C TTGCATTTGC ----AGGGCA CCACCAGATG CTTCCCAGCC CCTCTCCGCT ATAATTCCAA
Mma202          GTTTTTGTTT ATGTCAAGTC TTAC--TGAT ATGTAAAA-C TTGCATTTGC ----AGGGCA CCACCAGATG CTTCCCAGCC CCTCTCCGCT ATAATTCCAA
Aro203          GTTTTTATTT ACC-AAAGTC TTAC--TGAT ATGTAAAA-C TTGCATTTGC ----AGGGCA GCA---GATG CTTCCCAGCC CCTCTCCACT ATAATTCCAA
Kvi204          GTTTTTGTTT ATGTTAAGTC TTAC--TGAT ATGTAAAA-C TTGCATTTGC ----AGGGCA CCA---GATG CTTCCCAGCC CCTCTCCACT ATAATTCCAA
Kvi205          GTTTTTGTTT ATGTTAAGTC TTAC--TGAT AGGTAAAA-T TTGCATTTGC ----AGAGCA CCA---GATG CTTCCCAGCC CCTCTCCACT ATAATTCCAA
Ani201          GTTTTTGTTT ATGTTAAGTC TTAC--TGAT ATGTAAAA-T TTGCTTTTGC ----AGGGCA CCA---GATG CTTCCCAGCC CCTCTCCACT ATAATTCCAA


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                       910        920        930        940        950        960        970        980        990
Ltr201          TTCCGAAAAG CAAACTTGCA CCATACCGAA CTGTGATAAT TATGCGTCTG ATCATTCTCG GTCTTTTCTT TCATTACCGA GTAACAAACC CTGTCGACA
Lag201          TTCCGAAAAG CAAACTTGCA CCGTACCGAA CTGTGATCAT CATGCGATTG ATCATTCTCG GTCTTTTTTT CCATTACCGA GTAACGAACC CTGTTGACA
Lag202          TTCCGAAAAG CAAACTTGCA CCGTACCGAA CTGTGATCAT CATGCGATTG ATCATTCTCG GTCTTTTTTT CCATTACCGA GTAACGAACC CTGTTGACA
Lag203          TTCCGAAAAG CAAACTTGCA CCATACCGAA CTGTGATAAT TATGCGTCTG ATCATTCTCG GTCTCTTCTT TCATTACCGA GTAACAAACC CTGTCGACA
Lag204          TTCCGAAAAG CAAACTTGCA CCATACCGAA CTGTGATAAT TATGCGTCTG ATCATTCTCG GTCTTTTCTT TCATTACCGA GTAACAAACC CTGTCGACA
Lag205          TTCCGAAAAG CAAACTTGCA CCATACCGAA CTGTGATAAT TATGCGTCTG ATCATTCTCG GTCTTTTCTT TCATTACCGA GTAACAAACC CTGTCGACA
Lfl201          TTCCGAAAAG CAAACTTGCA CCATACCGAA CTGTGATAAT TATGCGTCTG ATCATTCTCG GTCTTTTCTT TCATTACCGA GTAACAAACC CTGTCGACA
Lfl202          TTCCGAAAAG CAAACTTGCA CCATACCGAA CTGTGATAAT TATGCGTCTG ATCATTCTCG GTCTTTTCTT TCATTACCGA GTAACAAACC CTGTCGACA
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Ltp201          TTCCGAAAAG CAAACTTGCA CCGTACCGAA CTGTGATCAT CATGCGATTG ATCATTCTCG GTCTTTTTTT CCATTACCGA GTAACGAACC CTGTTGACA
Lob201          TTCCGAAAAG CAAACTTGCA CCGTACCGAA CTGTGATCAT CATGCGATTG ATCATTCTCG GTCTTTTTTT CCATTACCGA GTAACGAACC CTGTTGACA
Lbr201          TTCCGAAAAG CAAACTTGCA CCGTACCGAA CTGTGATCAT CATGCGATTG ATCATTCTCG GTCTTTTTTT CCATTACCGA GTAACGAACC CTGTTGACA
Lol201          TTCCGAAAAG CAAACTTGCA CCGTACCGAA CTGTGATCAT CATGCGATTG ATCATTCTCG GTCTTTTTTT CCATTACCGA GTAACGAACC CTGTTGACA
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Lol205          TTCCGAAAAG CAAACTTGCA CCGTACCGAA CTGTGATCAT CATGCGATTG ATCATTCTCG GTCTTTTTTT CCATTACCGA GTAACGAACC CTGTTGACA
Lol206          TTCCGAAAAG CAAACTTGCA CCGTACCGAA CTGTGATCAT CATGCGATTG ATCATTCTCG GTCTTTTTTT CCATTACCGA GTAACGAACC CTGTTGACA
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Mal201      TTCCGAAAAG CAAACTTGCA CCGTACCGAA CTGTGATCAT CATGCGATTG ATCATTCTCG GTCTTTTTTT CCATTACCGA GTAACGAACC CTGTTGGCA
Lar201      TTCCGAAAAG CAAACTTGCA CCGTATCGAA CTGTGATCAT CATGCGATTG ATCATTCTCG GTCTTTTTTT CCATTACCGA GTAACCAACC CTGTTGATA
Lar202      TTCCGAAAAG CAAACTTGCA CCGTATCGAA CTGTGATCAT CATGCGATTG ATCATTCTCG GTCTTTTTTT CCATTACCGA GTAACCAACC CTGTTGATA
Lar203      TTCCGAAAAG CAAACTTGCA CCGTATCGAA CTGTGATCAT CATGCGATTG ATCATTCTCG GTCTTTTTTT CCATTACCGA GTAACCAACC CTGTTGATA
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Lar207      TTCCGAAAAG CAAACTTGCA CCGTATCGAA CTGTGATCAT CATGCGATTG ATCATTCTCG GTCTTTTTTT CCATTACCGA GTAACCAACC CTGTTGATA
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Lar209      TTCCGAAAAG CAAACTTGCA CCGTATCGAA CTGTGATCAT CATGCGATTG ATCATTCTCG GTCTTTTTTT CCATTACCGA GTAACCAACC CTGTTGATA
Lmu201      TTCCGAAAAG CAAACTTGCA CCGTATCGAA CTGTGATCAT CATGCGATTG ATCATTCTCG GTCTTTTTTT CCATTACCGA GTAACCAACC CTGTTGATA
Lmu202      TTCCGAAAAG CAAACTTGCA CCGTATCGAA CTGTGATCAT CATGCGATTG ATCATTCTCG GTCTTTTTTT CCATTACCGA GTAACCAACC CTGTTGATA
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Lcr201      TTCCGAAAAG CAAACTTGCA CCGTACCGAA CTGTGATCAT CATGCGATTG ATCATTCTCG GTCTTTTTTT CCATTACCGA GTAACCAACC CTGTTGATA
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Lcr204      TTCCGAAAAG CAAACTTGCA CCTTACCGAA CTGTGATCAT CATGCGATTG ATCATTCTCG GTCTTTTTTT CCATTACCGA GTAACCCACC CTGTTGATA
Lcr205      TTCCGAAAAG CAAACTTGCA CCGTACCGAA CTGTGATCAT CATGCGATTG ATCATTCTCG GTCTTTTTTT CCATTACCGA GTAACCAACC CTGTTGATA
Lcr206      TTCCGAAAAG CAAACTTGCA CCGTACCGAA CTGTGATCAT CATGCGATTG ATCATTCTCG GTCTTTTTTT CCATTACCGA GTAACCAACC CTGTTGATA
Lcr207      TTCCGAAAAG CAAACTTGCA CCTTACCGAA CTGTGATCAT CATGCGACTG ATCATTCTCG GTCTTTTTTT CCATTACCGA GTAACCCACC CTGTTGATA
Las201      TTCCGAAAAG CAAACTTGCA CCGTACCGAA CTGTGATCAT CATGCGATTG ATCATTCTCG GTCTTTTTTT CCATTACCGA GTAACCAACC CTGTTGATA
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Las202        TTCCGAAAAG CAAACTTGCA CCGTACCGAA CTGTGATCAT CATGCGATTG ATCATTCTCG GTCTTTTTTT CCATTACCGA GTAACCAACC CTGTTGATA
Las203        TTCCGAAAAG CAAACTTGCA CCATACCGAA CTGTGATCAT TATGCGTCTG ATCATTCTCG GTCTTTTCTT CCATTACCGA GTAACAGACC CTGTCGACA
Lac201        TTCCGAAAAG CAAACTTGCA CCGTGCCGAA CTGTGATCAT CATGCGATTG ATCATTCTCG GTCTTTTTTT CCATTACCGA GTAACCAACC CTGTTGACA
Mve201        TTCCGAAAAG CAAACTTGCA CCGTACCGAA CTGTGATCAT CATGCGATTG ATCATTCTCG GTCTTTTTTT CCATTACCGA GTAACCAACC CTGTTGATA
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Mve203        TTCCGAAAAG CAAACTTGCA CCGTACCGAA CTGTGATCAT CATGCGATTG ATCATTCTCG GTCTTTTTTT CCATTACCGA GTGACCAACC CTGTTGATA
Lpe201        TTCCGAAAAG CAAACTTGCA CCTTACCGAA CTGTGATCAT CATGCGATTG ATCATTCTCG GTCTTTTTTT CCATTACCGA GTAACCCACC CTGTTGATA
Lpe202        TTCCGAAAAG CAAACTTGCA CCGTACCGAA CTGTGATCAT CATGCGATTG ATCATTCTCG GTCTTTTTTT CCATTACCGA GTAACCAACC CTGTTGATA
Lpe203        TTCCGAAAAG CAAACTTGCA CCGTACCGAA CTGTGATCAT CATGCGATTG ATCATTCTCG GTCTTTTTTT CCATTACCGA GTAACCAACC CTGTTGATA
Lpe204        TTCCGAAAAG CAAACTTGCA CCGTACCGAA CTGTGATCAT CATGCGATTG ATCATTCTCG GTCTTTTTTT CCATTACCGA GTAACCAACC CTGTTGATA
Lph201        TTCCGAAAAG CAAACTTGCA CCGTACCGAA CTGTGATCAT CATGCGATTG ATCATTCTCG GTCTTTTTTT CCATTACCGA GTTACCAACC CTGTtGACA
Lph202        TTCCGAAAAG CAAACTTGCA CCGTACCGAA CTGTGATCAT CATGCGATTG ATCATTCTCG GTCTTTTTTT CCATTACCGA GTTACCAGCC CTGTtGACA
Lph203        TTCCGAAAAG CAAACTTGCA CCGTACCGAA CTGTGATCAT CATGCGATTG ATCATTCTCG GTCTTTTTTT CCATTACCGA GTTACCAACC CTGTtGACA
Aca201        TTCCGAAAAG CAAACTTGCA CCGTACCGAA CTGTGATTAT CATGCGATTG ATCATTCTCG GTCTTTTCCT CCATTACCTA GTAACGAACC CTGTTGACA
Aca202        TTCCGAAAAG CAAACTTGCA CCGTACCGAA CTGTGATTAT CATGCGATTG ATCATTCTTG GTCTTTTCTT CCATTACCGA GTAACGAACC CTGTCGATA
Aar201        TTCCGAAAAG CAAACTTGCA CCGTACCGAA CTGTGATTAT CATGCGATTG ATCATTCTCG GTCTTTTCTT CCATTACCTA GTAACGAACC CTGTTGACA
Aro201        TTCCGAAAAG CAAACTTGCA CCGTACCGAA CTGTGATTAT CATGCGATTG ATCATTCTCG GTCTTTTCTT CCATTACCGA GTAACGAACC CTGTTGACA
Aro202        TTCCGAAAAG CAAACTTGCA CCGTACCGAA CTGTGATTAT CATGCGATTG ATCATTCTCG GTCTTTTCTT CCATTACCGA GTAACGAACC CTGTTGACA
Kvi201        TTCCGAAAAG CAAACTTGCA CCGTACCGAA CTGTGATTAT CATGCGATTG ATCATTCTCG GTCTTTTCTT CCATTACCGA GTAACGAACC CTGTTGACA
Kvi202        TTCCGAAAAG CAAACTTGCA CCGTACCGAA CTGTGATTAT CATGCGATTG ATCATTCTCG GTCTTTTCTT CCATTACCGA GTAACGAACC CTGTTGACA
Kvi203        TTCCGAAAAG CAAACTTGCA CCGTACCGAA CTGTGATTAT CATGCGATTG ATCATTCTCG GTCTTTTCTT CCATTACCGA GTAACGAACC CTGTTGACA
Mtf201        TTCCGAAAAG CAAACTTGCA CCGTACCGAA CTGTGATCAT CATGAGATTG ATCATTCTCG GTCTCTTCTT CCATTACCGA GTAACGAACC CTGTTGACA
Mtf202        TTCCGAAAAG CAAACTTGCA CCGTACCGAA CTGTGATCAT CATGAGATTG ATCATTCTCG GTCTCTTCTT CCATTACCGA GTAACGAACC CTGTTGACA
Mtf203        TTCCGAAAAG CAAACTTGCA CCGTACCGAA CTGTGATCAT CATGAGATTG ATCATTCTCG GTCTCTTCTT CCATTACCGA GTAACGAACC CTGTTGACA
Mtf204        TTCCGAAAAG CAAACTTGCA CCGTACCGAA CTGTGATCAT CATGAGATTG ATCATTCTCG GTCTCTTCTT CCATTACCGA GTAACGAACC CTGTTGACA
Mtf205        TTCCGAAAAG CAAACTTGCA CCGTACCGAA CTGTGATCAT CATGAGATTG ATCATTCTCG GTCTCTTCTT CCATTACCGA GTAACGAACC CTGTTGACA
Mtf206        TTCCGAAAAG CAAGCTTGCA CCATATCGAA CCGTGATCAT TATGCGGCTG ATCATTCTCG GACTTTTCTT CCATTACCGA GTAACAAACC CTGTCGACA
Mtf207        TTCCGAAAAG CAAGCTTGCA CCATATCGAA CCGTGATCAT TATGCGGCTG ATCATTCTCG GACTTTTCCT CCATTACCGA GTAAACAACC CTGTCGACA
Mma201        TTCCGAAAAG CAAACTTGCA CCGTACCGAA CTGTGATCAT CATGCGACTG ATCATTCTCG GTCTCTTCTT CCATTACCGA GTAACGAACC CTGTTGACA
Mma202        TTCCGAAAAG CAAACTTGCA CCGTACCGAA CTGTGATCAT CATGCGACTG ATCATTCTCG GTCTCTTCTT CCATTACCGA GTAACGAACC CTGTTGACA
Aro203        TTCCGAAAAG CAAACTTGCA CCGTACCGAA CTGTGATCAT CATGCGATTG ATCATTCTCG GTCTTTTTTT CCATTACCGA GTAACCAACC CTGTTGACA
Kvi204        TTCCGAAAAG CAAACTTGCA CCGTACCGAA CTGTGATTAT CATGCGATTG ATCATTCTCG GTCTTTTCTT CCATTACCGA GTAACGAACC CTGTTGACA
Kvi205        TTCCGAAAAG CAAACTTGCA CCGTACCGAA CTGTGATTAT TATGCGATTG ATCATTCTTG GTCTTTTCTT CCATTACTGA GTAACGAACC CTGTCGATA
Ani201        TTCCGAAAAG CAAACTTGCA CCATACCGAA CCGTGATCAT TATGCGGCTG ATCATTCTCG GTCTTTTCTT CCATTACCGA GTAACGAACC CTGTCGACA
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*ces*A1b P3

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                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                        10         20         30         40         50         60         70         80         90        100
Ltr301          CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTAGTC
Ltp301          CCCTTTGTGT CTTGTCATGA ATGCAATTTC CCCATTTGCA AGACTTATTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGT TTGTCTGCGT TGCGGTAGTC
Ltp302          CCCTTTGTGT CTTGTCATGA ATGCAATTTC CCCATTTGCA AGACTTATTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGGTACTC
Lob301          CCCTTTGTGT CTTGCCATGA ATGCAATTTC CCCATTTGCA AGACTTGCTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGGTACTC
Lcr301          CCCTTTGTTT CTTGCCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGGTAGTC
Lcr302          CCCTTTGTGT CTTGCCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGGTAGTC
Lcr303          CCCTTTGTGT CTTGCCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGGTAGTC
Lcr304          CCCTTTGTGT CTTGCCACGA ATGCAATTTC CCCATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGGTAGTC
Mve301          CCCTTTGTTT CTTGCCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGGTAGTC
Mve302          CCCTTTGTGT CGTGCCATGA ATGCAATTCC CCCTTTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGGTAGTC
Mve303          CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCTATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCGAGTC
Mne301          CCCTTTGTGT CTTGCCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC ATGTCTGCGT TGCGGTAGTC
Mne302          CCCTTTGTGT CTTGCCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC ATGTCTGCGT TGCGGTAGTC
Mne303          CCCTTTGTGT CTTGCCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC ATGTCTGCGT TGCGGTAGTC
Mne304          CCCTTTGTGT CGTGTCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGT TTGTCTGCGT TGCGGTAGTC
Lac301          CCCTTTGTGT CTTGCCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCAAAAAGC TTGTCTGCGT TGCGGTAGTC
Lma301          CCCTTTGTGT CTTGCCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGGTAGTC
Lma302          CCCTTTGTGT CTTGCCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGGTAGTC
Lma303          CCCTTTGTGT CTTGCCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGGTAGTC
Lma304          CCCTTTGTGT CCTGCCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGGTAGTC
Lma305          CCCTTTGTGT CTTGCCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGGTAGTC
Lph301          CCC------- --TGCCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGGTAGTC
Lph302          CCC------- --TGCCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGGTAGTC
Mca301          CCCTTTGTGT CTTGCCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT CGAGTATGAC GTCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTACTC
Mca302          CCCTTTGTGT CTTGCCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT CGAGTATGAC GTCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTACTC
Mca303          CCCTTTGTGT CTTGCCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT CGACTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTACTC
Mca304          CCCTTTGTGT CTTGCCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT CGACTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTACTC
Mca305          CCCTTTGTGT CTTGCCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT CGAGTATGAC GTCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTACTC
Mca306          CCCTTTGTGT CTTGCCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT CGAGTATGAC GTCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTACTC
Mca307          CCCTTTGTGT CTTGCCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT CGAGTATGAC GTCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTACTC
Mca308          CCCTTTGTGT CTTGCCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT CGAGTATGAC GTCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTACTC
Mca309          CCCTTTGTGT CTTGCCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT CGACTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGCTACTC
Mtr301          CCCTTTGTGT CTTGCCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTTCGT TGCGCTACTC
Mtr302          CCCTTTGTGT CTTGCCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTTCGT TGCGCTACTC
Mtr303          CCCTTTGTGT CTTGCCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTTCGT TGCGCTACTC
Mtr304          CCCTTTGTGT CTTGCCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTTCGT TGCGCTACTC
Mtr305          CCCTTTGTGT CTTGCCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTTCGT TGCGCTACTC
Mtr306          CCCTTTGTGT CTTGCCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTTCGT TGCGCTACTC
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Mae301          CCCTTTGTGT CTTGCCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT CGAGTATGAC ATTAAGGAAG GTCGAAAAGC TTGTCTTCGT TGCGCTACAC
Mae302          CCCTTTGTGT CTTGCCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT CGAGTATGAC ATTAAGGAAG GTCGAAAAGC TTGTCTTCGT TGCGCTACAC
Mae303          CCCTTTGTGT CTTGCCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT CGAGTATGAC ATTAAGGAAG GTCGAAAAGC TTGTCTTCGT TGCGCTACAC
Mae304          CCCTTTGTGT CTTGCCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT CGAGTATGAC ATTAAGGAAG GTCGAAAAGC TTGTCTTCGT TGCGCTACAC
Aro301          CCCTTTGTGT CTTGCCGTGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAGG GTCGAAAAGC TTGTCTGCGT TGCGGTAGTC
 Aro302          CCCTTTGTGT CTTGCCATGA ATGCAATTTC TCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAGG GTCGAAAAGC TTGTCTGCGT TGCGGTAGTC
Aro303          CCCTTTGTGT CTTGCCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAGG GTCGAAAAGC TTGTCTGCGT TGCGGTAGTC
Aro304          CCCTTTGTGT CTTGCCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAGG GTCGAAAAGC TTGTCTGCGT TGCGGTAGTC
Aro305          CCCTTTGTGT CTTGCCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAGG GTCGAAAAGC TTGTCTGCGT TGCGGTAGTC
Aro306          CCCTTTGTGT CTTGCCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAGG GTCGAAAAGC TTGTCTGCGT TGCGGTAGTC
Aro307          CCCTTTGCGT CTTGCCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAGG GTCGAAAAGC TTGTCTGCGT TGCGGTAGTC
Aca301          CCGTTTGTGG CTTGCCATGA ATGCAATTTC CCCATTTGCC AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGGTAGTC
Aca302          CCGTTTGTGG CTTGCCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGGTAGTC
Aca303          CCCTTTGTGT CTTGCCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGGTAGTC
Kvi301          CCCTTTGTGT CTTGCCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGGTAGTC
Kvi302          CCCTTTGTGT CTTGCCATGA ATGCAATTTC CCCATTTGCA AGACTTGTTT TGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGGTAGTC
Kvi303          CCCTTTGTGT CTTGCCATGA ATGCAATTTT CCAATTTGCA AGACTTGTTT CGAGTATGAC ATCAAGGAAG GTCGAAAAGC TTGTCTGCGT TGCGGTAGTT


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                       110        120        130        140        150        160        170        180        190        200
Ltr301          CATACGATGG TATGTATACT TTTATTTCTT GATAAATCTT TGTGTCTTCC AAATGCTTGT TTGATTTCCC A--------- ---------- --TGTAGTGA
Ltp301          CATACGATGG TATGTATACT TTTAGTTCCT GATAAATCTT TGTGTTTTCA GAATGCTTGT GTGATTTCCC ATGAAAAGAA AAACGATAGA GATGTAGTGA
Ltp302          CATACGATGG TATGTGTACT TTTAGTTCTT GATAAATCTT TGTGTCTTCC AAATGCTTGT TTGATTTCCC A--------- ---------- --TGTAGTGA
Lob301          CATACAATGG TATGTGTACT TTTAGTTCTT GATAAATCTT TGTGTCTTCC AAATGCTTGT TTGATTTCCC A--------- ---------- --TGTAGTGA
Lcr301          CATACGATGG TATGCATGCT TTTAGTTCTT GATAAGTCTT TGTTTCTTCC CA-------- ---------- ---------- ---------- --TGTAGTGA
Lcr302          CATACGATGG TATGTATGCT TTTAGTTCTT GATAAGTCTT TGTGTCTTCC CG-------- ---------- ---------- ---------- --TGTAGTGA
Lcr303          CATACGATGG TATGTATGCT TTTAGTTCTT GATAAGTCTT TGTGTCTTCC CG-------- ---------- ---------- ---------- --TGTAGTGA
Lcr304          CATACGATGG TATGTATGCT TTCAGTTCTT GATAAGTCTT TGTGTCTTCC CG-------- ---------- ---------- ---------- --TGTAGTGA
Mve301          CATACGATGG TATGCATGCT TTTAGTTCTT GATAAGTCTT TGTTTCTTCC CA-------- ---------- ---------- ---------- --TGTAGTGA
Mve302          CATACGATGG TATGTATGCT TTTAGTTCTT GATAAGTCTT TGTGTCTTCC CG-------- ---------- ---------- ---------- --TGTAGTGA
Mve303          CATACGATGG TATGTATACT TTTAGTTCTT GATAAATCTT TGTGTTTTCC AAATGCTTGT TTGATTTCCC ATGAAAAGAA AAAAAATAGA GATGTAGTGA
Mne301          CATACGATGG TATGTATGCT TTTAGTTCTT GATAAGTCTT TGTGTCTTC- ---------- ---------- ---------- ---------- ----------
Mne302          CATACGATGG TATGTATGCT TTTAGTTCTT GATAAGTCTT TGTGTCTTC- ---------- ---------- ---------- ---------- ----------
Mne303          CATACGATGG TATGTATGCT TTTAGTTCTT GATAAGTCTT TGTGTCTTC- ---------- ---------- ---------- ---------- ----------
Mne304          CATACGATGG TATGTATACT TTTAGTTCTT GATAAGTCTT TGTGTCTTC- ---------- ---------- ---------- ---------- ----------
Lac301          CATACGATGG TATGTATGCT TTTAGTTCTT GATAAGTCTT TGTGTCTTCC AAATGCTTGT TTGATTTCCC A--------- ---------- --TGTAGTGA
Lma301          CATACGATGG TATGTATGCT TTTAGTTCTT GATAAGTCTT TGTGTCTTCC AAATGCTTGT TTGATTTCCC A--------- ---------- --TGTAGTGA
Lma302          CATACGATGG TATGTATGCT TTTAGTTCTT GATAAGTCTT TGTGTCTTCC AAATGCTTGT TTGATTTCCC A--------- ---------- --TGTAGTGA
Lma303          CATACGATGG TATGTATGC- TTTAGTTCTT GATAAGTCTT TGTGTCTTCC AAATGCTTGT TTGATTTCCC A--------- ---------- --TGTAGTGA
Lma304          CATACGATGG TATGTATGCT TTTAGTTCTT GGTAAGTCTT TGTGTCTTCC AAATGCTTGT TTGATTTCCC A--------- ---------- --TGTAGTGA
Lma305          CATACGATGG TATGTATGCT TTTAGTTCTT GATAAGTCTT TGTGTCTTCC AAATGCTTGT TTGATTTCCC A--------- ---------- --TGTAGTGA
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Lph301          CATACGATGG TATGCATGCT TTTAGTTCTT GACAAGTCTT TGTGTCTTCC AAATGCTTGT TTGATTTCCC A--------- ---------- --TGTAGTGA
Lph302          CATACGATGG TATGCATGCT TTTAGTTCTT GACAAGTCTT TGTGTCTTCC AAATGCTTGT TTGATTTCCC A--------- ---------- --TGTAGTGA
Mca301          CATTCGATGG TATGTCTACT TTTACTTCTT CATAAGCCTT TGTGCCT--- ---------- ---------- ---------- ---------- ----------
Mca302          CATTCGATGG TATGTCTACT TTTACTTCTT CATAAGCCTT TGTGCCT--- ---------- ---------- ---------- ---------- ----------
Mca303          CATTCCATGG TATGTCTACT TTTACTTCTT CATAAGCCTT TGTGCCT--- ---------- ---------- ---------- ---------- ----------
Mca304          CACTCCATGG TATGTCTACT TTTACTTCTT CATAAGCCTT TGTGCCT--- ---------- ---------- ---------- ---------- ----------
Mca305          CATTCGATGG TATGTCTACT TTTACTTCTT CATAAGCCTT TGTGCCT--- ---------- ---------- ---------- ---------- ----------
Mca306          CATTCGATGG TATGTCTACT TTTACTTCTT CATAAGCCTT TGTGCCT--- ---------- ---------- ---------- ---------- ----------
Mca307          CATTCGATGG TATGTCTACT TTTACTTCTT CATAAGCCTT TGTGCCT--- ---------- ---------- ---------- ---------- ----------
Mca308          CATTCGATGG TATGTCTACT TTTACTTCTT CATAAGCCTT TGTGCCT--- ---------- ---------- ---------- ---------- ----------
Mca309          CACTCCATGG TATGTCTACT TTTACTTCTT CATAAGCCTT TGTGCCT--- ---------- ---------- ---------- ---------- ----------
Mtr301          CATACGATGG TATGTATGCT TTTACTTCTT GATGAATCTT TGTGTCTTCC AAATGCTTG- ---------- ---------- ---------- ----------
Mtr302          CATACGATGG TATGTATGCT TTTACTTCTT GATGAATCTT TGTGTCTTCC AAATGCTTG- ---------- ---------- ---------- ----------
Mtr303          CATACGATGG TATGTATGCT TTTACTTCTT GATGAATCTT TGTGTCTTCC AAATGCTTG- ---------- ---------- ---------- ----------
Mtr304          CATACGATGG TATGTATGCT TTTACTTCTT GATGAATCTT TGTGTCTTCC AAATGCTTG- ---------- ---------- ---------- ----------
Mtr305          CATACGATGG TATGTATGCT TTTACTTCTT GATGAATCTT TGTGTCTTCC AAATGCTTG- ---------- ---------- ---------- ----------
Mtr306          CATACGATGG TATGTATGCT TTTACTTCTT GATGAATCTT TGTGTCTTCC AAATGCTTG- ---------- ---------- ---------- ----------
Mae301          CATACGATGG TATGCATACT TTTATTTCTT GATAAATC-- TGT------- ---------- ---------- ---------- ---------- -----AGTGA
Mae302          CATACGATGG TATGCATACT TTTATTTCTT GATAAATC-- TGT------- ---------- ---------- ---------- ---------- -----AGTGA
Mae303          CATACGATGG TATGCATACT TTTATTTCTT GATAAATC-- TGT------- ---------- ---------- ---------- ---------- -----AGTGA
Mae304          CATACGATGG TATGCATACT TTTATTTCTT GATAAATC-- TGT------- ---------- ---------- ---------- ---------- -----AGTGA
Aro301          CATACGATGG TATGTATACT TTTATTTCTT GATAAGTCTT TGTGTTCTCC AAATGTTTGT TTGATTTCCC ATGAAAAGAA AAA-TATGGA GATGTAGTGA
Aro302          CATACGATGG TATGTATACT TTTATTTCTT GATAAGTCTT TGTGTTCTCC AAATGTTTGT TTGATTTCCC ATGAAAAGAA AAA-TATGGA GATGTAGTGA
Aro303          CATACGATGG TATGTATACT TTTATTTCTT GATAAGTCTT TGTGTTCTCC AAATGTTTGT TTGATTTCCC ATGAAAAGAA AAA-TATGGA GATGTAGTGA
Aro304          CATACGATGG TATGTATACT TTTATTTCTT GATAAGTCTT TGTGTTCTCC AAATGTTTGT TTGATTTCCC ATGAAAAGAA AAA-TATGGA GATGTAGTGA
Aro305          CATACGATGG TATGTATACT TTTATTTCTT GATAAGTCTT TGTGTTCTCC AAATGTTTGT TTGATTTCCC ATGAAAAGAA AAA-TATGGA GATGTAGTGA
Aro306          CATACGATGG TATGTATACT TTTATTTCTT GATAAGTCTT TGTGTTCTCC AAATGTTTGT TTGATTTCCC ATGAAAAGAA AAA-TATGGA GATGTAGTGA
Aro307          CATACGATGG TATGTATACT TTTATTTCTT GATAAGTCTT TGTGTTCTCC AAATGTTTGT TTGATTTCCC ATGAAAAGAA AAA-TATGGA GATGTAGTGA
Aca301          CATACGATGG TACGTATACT TTTAGTTCTT GATAAATCTT TGTGTTCTCC AAATGCTTGT TTGATTTCCC ATGAGAAGAA AAA-TATGGT GATGCATTGA
Aca302          CATACGATGG TACGTATACT TTTAGTTCTT GATAAATCTT TGTGTTCTCC AAATGCTTGT TTGATTTCCC ATGAGAAGAA AAA-TATGGT GATGCAGTGA
Aca303          CATACGATGG TACGTATACT TTTAGTTCTT GATAAATCTT TGTGTTCTCC AAATGCTTGT TTGATTTCCC ATGAGAAGAA AAA-TATGGT GATGCAGTGA
Kvi301          CATACGACGG TATATATACT TTTAGTTCTT GATAAATCTT TGTGTTTTCC AAATGCTTGT TTGATTTCCC ATGGAAAGAA AAA-TATAGA GATGTAGTGA
Kvi302          CATACGACGG TATATATACT TTTAGTTCTT GATAAATCTT TGTGTTTTCC AAATGCTTGT TTGATTTCCC ATGAAAAGAA AAA-TATAGA GATGTAGTGA
Kvi303          CATACGATGA TATGTATACT TTTAGTTCTT GATAAATCTT TGTGTTTTCC AAATGCTTGT TTGATTTCCC ATGAAAAGAA AAA-GATAGA GATGTAGTGA


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                       210        220        230        240        250        260        270        280        290        300
Ltr301          ACTGTTTAAA CTTCTTAGAC TGACCACTTT GAACTCCTTC AGAGAACGTG TTGGATGGTG TCGAAAAGGC GTCCGGCGAA CAATCCATGA TGGCTGCACA
Ltp301          ---------A CTGCTTACAC TGACCACTTT GAAATCCTTC AGAGAACGTG TTGGATGGTG TCGAAAAGGC GTCCGGCGAA CAATCCATGA TGGCTGCACA
Ltp302          ACTGTTTAAA CTTCTTAGAC TGACCACTTT GAACTCCTTC AGAGAACGTG TTGGATGGTG TCGAAAAGGC GTCCGGCGAA CAATCCATGA TGGCTGCACA
Lob301          ACTGTTTAGA CTTCTTAGAC TGACCACTTT GAACTCCTTC AGAGAACGTG TTGGATGATG TCGAAAAGGC GTCCGGCGAA CAATCCACGA TGGCTGCACA
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Lcr301       ACTGTTTAAA CTGCTTGTAC TGACCACTTT GAACTCCTTC AGAGAACGTG TTGGATGATG TCGAAAAGGG GTCTGGCGAA CAATCCATGA TGGCTGCACA
Lcr302       ACTGTTTAAA CTGCTTGTAC TGACCACTTT GAACTCCTGC AGAGAACGTG TTGGATGATG TCGAAAAGGC GTCTGGTGAA CAATCCATGA TGGCTGCACA
Lcr303       ACTGTTTAAA CTGCTTGTAC TGACCACTTT GAACTCCTGC AGAGAACGTG TTGGATGATG TCGAAAAGGC GTCTGGTGAA CAATCCATGA TGGCTGCACA
Lcr304       ACTGTTTAAA CTGCTTGTAC TGACCACTTT GAACTCCTTC AGAGAACGTG TTGGATGATG TCGAAAAGGG GTCTGGCGAA CAATCCATGA TGGCTGCACA
Mve301       ACTGTTTAAA CTGCTTGTAC TGACCACTTT GAACTCCTTC AGAGAACGTG TTGGATGATG TCGAAAAGGG GTCTGGCGAA CAATCCATGA TGGCTGCACA
Mve302       ACTGTTTAAA CTGCTTGTAC TGACCACTTT GAACTCCTGC AGAGAACGTG TTGGATGATG TCGAAAAGGC GTCTGGTGAA CAATCCATGA TGGCTGCACA
Mve303       ---------A CTGCTTAGAC TGACCACTTT GAACTCCTGC AGAGAACGTG TTGGATGATG TCGAAAAGGC GTCTGGTGAA CAATCCATGA TGGCTGCACA
Mne301       ---------A CTGCTTGTAC TGACCACTTT GAACTCCTTC AGAGAACGTG TTGGATGATG TCGAAAAGGC GTCTGGCGAA CAATCCATGA TGGCTGCACA
Mne302       ---------A CTGCTTGTAC TGACCACTTT GAACTCCTTC AGAGAACGTG TTGGATGATG TCGAAAAGGC GTCTGGCGAA CAATCCATGA TGGCTGCACA
Mne303       ---------A CTGCTTGTAC TGACCACTTT GAACTCCTTC AGAGAACGTG TTGGATGATG TCGAAAAGGC GTCTGGCGAA CAATCCATGA TGGCTGCACA
Mne304       ---------A CTGCTTGTAC TGACCACTTT GGACTCCTTC AGAGAACGTG TTGGATGATG TCGAAAAGGC GTCTGGCGAA CAATCCATGA TGGCTGCACA
Lac301       ACTGTTTAAA CTGCTTGTAC TGACCACTTT GAACTCCTTC AGAGAACGTG TTGGATGATG TCGAAAAGGC GTCTGGCGAA CAATCCATGA TGGCTGCACA
Lma301       ACTTTTTAAA CTGCTTGCAT TGACCACTTT AAACTCCT-C AGAGAACGTG TTGGATGATG TCAAAAAGGC GTCTGGCGAA CAATCCATGA TGGCTGCACA
Lma302       ACTCTTTAAA CTGCTTGCAT TGACCACTTT GAACTCCT-C AGAGAACGTG TTGGATGATG TCAAAAAGGC GTCTGGCGAA CAATCCATGA TGGCTGCGCA
Lma303       ACTTTTTAAA CTGCTTGCAT TGACCACTTT GAACTCCT-C AGAGAACGTG TTGGATGATG TCAAAAAGGC GTCTGGCGAA CAATCCATGA TGGCTGCACA
Lma304       ACTTTTTAAA CTGCTTGCAT TGACCACTTT GAACTCCT-C AGAGAACGTG TTGGATGATG TCAAAAAGGC GTCTGGCGAA CAATCCATGA TGGCTGCACA
Lma305       ACTTTTTAAA CTGCTTGCAT TGACCACTTT AAACTCCT-C AGAGAACGTG TTGGATGATG TCAAAAAGGC GTCTGGCGAA CAATCCATGA TGGCTGCACA
Lph301       AGTGTTTAAA CTGCTTGTAC TGACCACTTT GAACTCCTTC AGAGAACGTG TTGGATGATG TCGAAAAGGC GTCTGGCGAA CAATCCATGA TGGCTGCACA
Lph302       AGTGTTTAAA CTGCTTGTAC TGACCACTTT GAACTCCTTC AGAGAACGTG TTGGATGATG TCGAAAAGGC GTCTGGCGAA CAATCCATGA TGGCTGCACA
Mca301       ---------- ------AGAC TGACCACTTT GAACTCCTTC AGAGAACCTG CTTGATGATG TCGAAAAGGC ATCCGGCGAA CAATCC---- ----------
Mca302       ---------- ------AGAC TGACCACTTT GAACTCCTTC AGAGAACCTG CTTGATGATG TCGAAAAGGC ATCCGGCGAA CAATCC---- ----------
Mca303       ---------- ------AGAC TGACCACTTT GAACTCCTTC AGAGAACCTG CTTGATGATG TCGAAAAGGC ATCCGGCGAA CAATCC---- ----------
Mca304       ---------- ------AGAC TGACCACTTT GAACTCCTTC AGAGAACCTG CTTGATGATG TCGAAAAGGC ATCCGGCGAA CAATCC---- ----------
Mca305       ---------- ------AGAC TGACCACTTT GAACTCCTTC AGAGAACCTG CTTGATGATG TCGAAAAGGC ATCCGGCGAA CAATCC---- ----------
Mca306       ---------- ------AGAC TGACCACTTT GAACTCCTTC AGAGAACCTG CTTGATGATG TCGAAAAGGC ATCCGGCGAA CAATCC---- ----------
Mca307       ---------- ------AGAC TGACCACTTT GAACTCCTTC AGAGAACCTG CTTGATGATG TCGAAAAGGC ATCCGGCGAA CAATCC---- ----------
Mca308       ---------- ------AGAC TGACCACTTT GAACTCCTTC AGAGAACCTG CTTGATGATG TCGAAAAGGC ATCCGGCGAA CAATCC---- ----------
Mca309       ---------- ------AGAC TGACCACTTT GAACTCCTTC AGAGAACCTG CTTGATGATG TCGAAAAGGC ATCCGGCGAA CAATCC---- ----------
Mtr301       ---------- -----TACTG AGACCACTTT GAACTCCTTC AGAGAACGCG TTGGATGATG TCGAAAAGGC GTCCATCGAA CAATCCACGA TGGCTGCACA
Mtr302       ---------- -----TACTG AGACCACTTT GAACTCCTTC AGAGAACGCG TTGGATGATG TCGAAAAGGC GTCCATCGAA CAATCCACGA TGGCTGCACA
Mtr303       ---------- -----TACTG AGACCACTTT GAACTCCTTC AGAGAACGCG TTGGATGATG TCGAAAAGGC GTCCATCGAA CAATCCACGA TGGCTGCACA
Mtr304       ---------- -----TACTG AGACCACTTT GAACTCCTTC AGAGAACGCG TTGGATGATG TCGAAAAGGC GTCCATCGAA CAATCCACGA TGGCTGCACA
Mtr305       ---------- -----TACTG AGACCACTTT GAACTCCTTC AGAGAACGCG TTGGATGATG TCGAAAAGGC GTCCATCGAA CAATCCACGA TGGCTGCACA
Mtr306       ---------- -----TACTG AGACCACTTT GAACTCCTTC AGAGAACGCG TTGGATGATG TCGAAAAGGC GTCCATCGAA CAATCCACGA TGGCTGCACA
Mae301       ACTGTTTAAA CTGCTTAGAC TGATCACTTT GAACTCGTTC AGAGAACCTG CTAGACGATG TCGAAAAGGC GTCCATCGAA CAATCCACAA TGGCTGCACA
Mae302       ACTGTTTAAA CTGCTTAGAC TGATCACTTT GAACTCGTTC AGAGAACCTG CTAGACGATG TCGAAAAGGC GTCCATCGAA CAATCCACAA TGGCTGCACA
Mae303       ACTGTTTAAA CTGCTTAGAC TGATCACTTT GAACTCGTTC AGAGAACCTG CTAGACGATG TCGAAAAGGC GTCCATCGAA CAATCCACAA TGGCTGCACA
Mae304       ACTGTTTAAA CTGCTTAGAC TGATCACTTT GAACTCGTTC AGAGAACCTG CTAGACGATG TCGAAAAGGC GTCCATCGAA CAATCCACAA TGGCTGCACA
Aro301       ACTGTTTAAA CTGCTTAGAC TGACCACTTT GAACTCCTTC AGAGAACCTG TTGGATGATG TCGAAAAGGC ATCCGGCGAA CAATCCACGA TGGCTGCACA
Aro302       ACTGTTTGAA CTGCTTAGAC TGACCACTTT GAACTCCTTC AGAGAACCTG TTGGATGATG TCGAAAAGGC ATCCGGCGAA CAATCCACGA TGGCTGCACA
Aro303       ACTGTTTAAA CTGCTTAGAC TGACCACTTT GAACTCCTCC AGAGAACCTG TTGGATGATG TCGAAAAGGC ATCCGGCGAA CAATCCACGA TGGCTGCACA
Aro304       ACTGTTTAAA CTGCTTAGAC TGACCACTTT GAACTCCTTC AGAGAACCTG TTGGATGATG TCGAAAAGGC ATCCGGCGAA CAATCCACGA TGGCTGCACA
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Aro305       ACTGTTTAAA CTGCTTAGAC TGACCACTTT GAACTCCTTC AGAGAACCTG TTGGATGATG TCGAAAAGGC ATCCGGCGAA CAATCCACGA TGGCTGCACA
Aro306       ACTGTTTAAA CTGCTTAGAC TGACCACTTT GAACTCCTTC AGAGAACCTG TTGGATGATG TCGAAAAGGC ATCCGGCGAA CAATCCACGA TGGCTGCACA
Aro307       ACTGTTTAAA CTGCTTAGAC TGACCACTTT GAACTCCTTC AGAGAACCTG TTGGATGATG TCGAAAAGGC ATCCGGCGAA CAATCCACGA TGGCTGCACA
Aca301       ACTTTTTAAA CTGCTTAGAC TGACCACTTT GAACTCCTTC AGAGAACCTG TTCGATGATG TCGAAAAGGC ATCCGGGGAA CAATCCACGA TGGCTGCACA
Aca302       ACTGTTTAAA CTGCTTATAC TGACCACTTT GAACTCCTTC AGAGAACCTG TTGGATGATG TCGAAAAGGC ATCCGGCGAA CAATCCACGA TGGCTGCACA
Aca303       ACTGTTTAAA CTGCTTATAC TGACCACTTT GAACTCCTTC AGAGAACCTG TTCGATGATG TCGAAAAGGC ATCCGGGGAA CAATCCACGA TGGCTGCACA
Kvi301       ACTGTTTAAA CTGCTTAGAC TGACCACTTT GAACTCCTTC AGAGAACCTG TTGGATGATG TCGAAAAGGC ATCCGGCGAA CAATCCACGA TGGCTGCACA
Kvi302       ACTGTTTAAA CTGCTTAGAC TGACCACTTT GAACTCCTTC AGAGAACCTG TTGGATGATG TCGAAAAGGC ATCCGGCGAA CAATCCACGA TGGCTGCACA
Kvi303       ACTGATTAAA CTGCTTAGAC TGACCACTTT GAACTCCTTC AGAGAACCTG TTGGATGATG TCGAAAAGGC ATCCGGCGAA CAATCCATGA TGGCTGCACA


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                    310        320        330        340        350        360        370        380        390        400
Ltr301       CTCGAATAAG TCCCAGGTA- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Ltp301       CTCGAATAAG TCCCAGGTA- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Ltp302       CTCGAATAAG TCCCAGGTA- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Lob301       CTCGAATAAG TCCCAGGTA- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Lcr301       CTCGAA---- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Lcr302       CTCGAA---- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Lcr303       CTCGAA---- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Lcr304       CTCGAA---- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Mve301       CTCGAA---- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Mve302       CTCGAA---- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Mve303       CTCGAA---- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Mne301       CTCGAA---- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Mne302       CTCGAA---- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Mne303       CTCGAA---- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Mne304       CTCGAA---- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Lac301       CTCGAATAAG CCCCAGGTA- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Lma301       CGCGAA---- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Lma302       CGCGAA---- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Lma303       CGCGAA---- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Lma304       CGCGAA---- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Lma305       CGCGAA---- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Lph301       CTCGAATAAG CCCCAGGTA- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Lph302       CTCGAATAAG CCCCAGGTA- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Mca301       -TCGAATAAG TCCCAGGTA- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Mca302       -TCGAATAAG TCCCAGGTA- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Mca303       -TCGAATAAG TCCCAGGTA- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Mca304       -TCGAATAAG TCCCAGGTA- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Mca305       -TCGAATAAG TCCCAGGTA- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Mca306       -TCGAATAAG TCCCAGGTA- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
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Mca307          -TCGAATAAG TCCCAGGTA- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Mca308          -TCGAATAAG TCCCAGGTA- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Mca309          -TCGAATAAG TCCCAGGTA- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Mtr301          CTCGAATAAG TCCCAGGTA- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Mtr302          CTCGAATAAG TCCCAGGTA- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Mtr303          CTCGAATAAG TCCCAGGTA- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Mtr304          CTCGAATAAG TCCCAGGTA- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Mtr305          CTCGAATAAG TCCCAGGTA- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Mtr306          CTCGAATAAG TCCCAGGTA- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Mae301          CTCGAATAAG TCCCAGGTA- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Mae302          CTCGAATAAG TCCCAGGTA- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Mae303          CTCGAATAAG TCCCAGGTA- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Mae304          CTCGAATAAG TCCCAGGTA- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Aro301          CTCGAATAAG TCCCAGGTAC TGGTTTTTGT TGCCTTTGAA AGGTTTTAAG TTATGATTAA AGGTAATTTA GTTTTAGGAA ACTGAGAGCT CTTTGTAATT
Aro302          CTCGAATAAG TCCCAGGTAC TGGTTTTTGT TGCCTTTGAA AGGTTTTAAG TTATGATTAA AGGTAATTTA GTTTCAGGAA ACTGAGAGCT CTTTGTAATT
Aro303          CTCGAATAAG TCCCAGGTAC TGGTTTTTGT TGCCTTTGAA AGGTTTTAAG TTATGATTAA AGGTAATTTA GTTTTAGGAA ACTGAGAGCT CTTTGTAATT
Aro304          CTCGAATAAG TCCCAGGTAC TGGTTTTTGT TGCCTTTGAA AGGTTTTAAG TTATGATTAA AGGTAATTTA GTTTTAGGAA ACTGAGAGCT CTTTGTAATT
Aro305          CTCGAATAAG TCCCAGGTAC TGGTTTTTGT TGCCTTTGAA AGGTTTTAAG TTATGATTAA AGGTAATTTA GTTTTAGGAA ACTGAGAGCT CTTTGTAATT
Aro306          CTCGAATAAG TCCCAGGTAC TGGTTTTTGT TGCCTTTGAA AGGTTTTAAG TTATGATTAA AGGTAATTTA GTTTTAGGAA ACTGAGAGCT CTTTGTAATT
Aro307          CTCGAATAAG TCCCAGGTAC TGGTTTTTGT TGCCTTTGAA AGGTTTTAAG TTATGATTAA AGGTAATTTA GTTTTAGGAA ACTGAGAGCT CTTTGTAATT
Aca301          CTCGAATAAG TCCCAAGTAC ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Aca302          CTCGAATAAG TCCCAAGTAC ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Aca303          CTCGAATAAG TCCCAAGTAC ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
Kvi301          CTCGAATAAG TCCCAGGTAC TGGTTTTTGT TGCCTTTGAA GGGTTTTTAG TTGTGATTAA AGGTAATTTA GTTTTAGGAA ACTGAGAGCT CTTTGTTATT
Kvi302          CTCGAATAAG TCCCAGGTAC TGGTTTTTGT TGCCTTTGAA GGGTTTTTAG TTGTGATTAA AGGTAATTTA GTTTTAGGAA ACTGAGAGCT CTTTGTTATT
Kvi303          TTCGAATAAG TCCCAGGTAC TGTTTTTTGC TGTCTTTGAA AGGTTTTTAG TTATGATTAA AGATCATT-A GTGTTTAGAA ATTGAGAGCT CTTTGTTATT


                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                       410        420        430        440        450        460        470        480        490        500
Ltr301          ---------- -----CAGGA TGTTGGAGTT CATGCAAGAC ATATCAGCAG TGTGTCTACA TTGGATAGTG GTATGTA--- ATATCAAT-- ----TTCTTC
Ltp301          ---------- -----CAGGA TGTTGGAGTT CATGCAAGAC ATATCAGCAG TGTGTCTACA TTGGATAGTG GTATGTA--- ATATCAAT-- ----TTCTTC
Ltp302          ---------- -----CAGGA TGTTGGGGTT CATGCAAGAC ATATCAGCAG TGTGTCTACA TTGGATAGTG GTATATA--- ATATCAAT-- ----TTCTTC
Lob301          ---------- -----CAGGA TGTTGGAGTT CATGCAAGAC ATATCAGCAG TGTGTCTACA TTGGATAGTG GTATGTA--- ATATCAAT-- ----TTCTTC
Lcr301          ---------- -------GGA TGTTGGAGTT CATGCAAGAT ATATCAGCAG TGTGTCTACA TTGGATAGTG GTATGTA--- ATATCAAT-- ----TTCTTG
Lcr302          ---------- -------GGA AGTTGGAGTT CATGCACGAC ATATCAGCAG TGTGTCTACA TTGGATAGTG GTATGTA--- ATATCAAT-- ----TTCTTC
Lcr303          ---------- -------GGA TGTTGGAGTT CATGCACGAC ATATCAGCAG TGTGTCTACA TTGGATAGTG GTATGTA--- ATATCAAT-- ----TTCTTC
Lcr304          ---------- -------GGA TGTTGGAGTT CATGCAAGAT ATATCAGCAG TGTGTCTACA TTGGATAGTG GTATGTA--- ATATCAAT-- ----TTCTTG
Mve301          ---------- -------GGA TGTTGGAGTT CATGCAAGAC ATATCAGCAG TGTGTCTACA TTGGATAGTG GTATATA--- ATATCAAT-- ----TTCTTG
Mve302          ---------- -------GGA TGTTGGAGTT CATGCACGAC ATATCAGCAG TGTGTCTACA TTGGATAGTG GTATGTA--- ATATCAAT-- ----TTCTTC
Mve303          ---------- -------GGA TGTTGGAGTT CATGCACGAC ATATCAGCAG TGTGTCTACA TTGGATAGTG GTATGTA--- ATATCAAT-- ----TTCTTC
Mne301          ---------- -------GGA TGTTGGAGTT CATGCACGAC ATATCAGCAG CGTGTCTACA TTGGATAGTG GTACGTA--- ATATCAAA-- ----TTCTTC
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Mne302       ---------- -------GGA TGTTGGAGTT CATGCACGAC ATATCAGCAG CGTGTCTACA TTGGATAGTG GTATGTA--- ATATCAAA-- ----TTCTTC
Mne303       ---------- -------GGA TGTTGGAGTT CATGCACGAC ATATCAGCAG CGTGTCTACA TTGGATAGTG GTATGTA--- ATATCAAA-- ----TTCTTC
Mne304       ---------- -------GGA TGTTGGAGTT CATGCACGAC ATATCAGCAG CGTGTCTACA TTGGATAGTG GTATGTA--- ATATCAAA-- ----TTCTTC
Lac301       ---------- -----CAGGA TGTTGGAGTT CATGCAAGAC ATATCAGCAG TGTGTCTACA TTGGATAGTG GTATGTA--- ATATCAAT-- ----TTCTTC
Lma301       ---------- -------GGA TGTTGGAGTT CATGCAAGAC ATATCAGCAG TGTGTCTACA TTGGATAGTG GTATGTA--- ATATCAAT-- ----TTCTTC
Lma302       ---------- -------GGA TGTTGGAGTT CATGCAAGAC ATATCAGCAG TGTGTCTACA TTGGATAGTG GTATGTA--- ATATCAAT-- ----TTCTTC
Lma303       ---------- -------GGA TGTTGGAGTT CATGCAAGAC ATATCAGCAG TGTGTCTACA TTGGATAGTG GTATGTA--- ATATCAAT-- ----TTCTTC
Lma304       ---------- -------GGA TGTTGGAGTT CATGCAAGAC ATATCAGCAG TGTGTCTACA TTGGATAGTG GTATGTA--- ATATCAAT-- ----TTCTTC
Lma305       ---------- -------GGA TGTTGGAGTT CATGCAAGAC ATATCAGCAG TGTGTCTACA TTGGATAGTG GTATGTA--- ATATCAAT-- ----TTCTTC
Lph301       ---------- -----CAGGA TGTTGGAGTT CATGCAAGAC ATATCAGCAG TGTGTCAACA TTGGATAGTG GTATGTA--- ATATCAAT-- ----TTCTTC
Lph302       ---------- -----CAGGA TGTTGGAGTT CATGCAAGAC ATATCAGCAG TGTGTCAACA TTGGATAGTG GTATGTA--- ATATCAAT-- ----TTCTTC
Mca301       ---------- -----CAGGA TGTTGGAGTT CATGCAAGAC ATATCAGCAG TGTGTCTACA TTGGATAGTG GTATGTAATA CTATCAAT-- ----TTCTTC
Mca302       ---------- -----CAGGA TGTTGGAGTT CATGCAAGAC ATATCAGCAG TGTGTCTACA TTGGATAGTG GTATGTAATA CTATCAAT-- ----TTCTTC
Mca303       ---------- -----CAGGA TGTTGGAGTT CATGCAAGAC ATATCAGCAG TGTGTCTACA TTGGATAGTG GTATGTAATA CTATCAAT-- ----TTCTTC
Mca304       ---------- -----CAGGA TGTTGGAGTT CATGCAAGAC ATATCAGCAG TGTGTCTACA TTGGATAGTG GTATGTA--- ATATCAAT-- ----TTCTTC
Mca305       ---------- -----CAGGA TGTTGGAGTT CATGCAAGAC ATATCAGCAG TGTGTCTACA TTGGATAGTG GTATGTA--- ATATCAAT-- ----TTCTTC
Mca306       ---------- -----CAGGA TGTTGGAGTT CATGCAAGAC ATATCAGCAG TGTGTCTACA TTGGATAGTG GTATGTA--- ATATCAAT-- ----TTCTTC
Mca307       ---------- -----CAGGA TGTTGGAGTT CATGCAAGAC ATATCAGCAG TGTGTCTACA TTGGATAGTG GTATGTA--- ATATCAAT-- ----TTCTTC
Mca308       ---------- -----CAGGA TGTTGGAGTT CATGCAAGAC ATATCAGCAG TGTGTCTACA TTGGATAGTG GTATGTAATA CTATCAAT-- ----TTCTTC
Mca309       ---------- -----CAGGA TGTTGGAGTT CATGCAAGAC ATATCAGCAG TGTGTCTACA TTGGATAGTG GTATGTA--- ATATCAAT-- ----TTCTTC
Mtr301       ---------- -----CAGGA TGTTGGAGTT CATGCAAGAC ATATCAGCAG TGTGTCTACA TTGGATAGTG GTATGTA--- ATATCAAT-- ----TTCT--
Mtr302       ---------- -----CAGGA TGTTGGAGTT CATGCAAGAC ATATCAGCAG TGTGTCTACA TTGGATAGTG GTATGTA--- ATATCAAT-- ----TTCT--
Mtr303       ---------- -----CAGGA TGTTGGAGTT CATGCAAGAC ATATCAGCAG TGTGTCTACA TTGGATAGTG GTATGTA--- ATATCAAT-- ----TTCT--
Mtr304       ---------- -----CAGGA TGTTGGAGTT CATGCAAGAC ATATCAGCAG TGTGTCTACA TTGGATAGTG GTATGTA--- ATATCAAT-- ----TTCT--
Mtr305       ---------- -----CAGGA TGTTGGAGTT CATGCAAGAC ATATCAGCAG TGTGTCTACA TTGGATAGTG GTATGTA--- ATATCAAT-- ----TTCT--
Mtr306       ---------- -----CAGGA TGTTGGAGTT CATGCAAGAC ATATCAGCAG TGTGTCTACA TTGGATAGTG GTATGTA--- ATATCAAT-- ----TTCT--
Mae301       ---------- -----CAGGA TGTTGGTGTT CATGCAAGAC ATATCAGCAG TGTGTCTACA TTGGATAGTG GTATGTA--- ATATCAAT-- ----TTCT--
Mae302       ---------- -----CAGGA TGTTGGTGTT CATGCAAGAC ATATCAGCAG TGTGTCTACA TTGGATAGTG GTATGTA--- ATATCAAT-- ----TTCT--
Mae303       ---------- -----CAGGA TGTTGGTGTT CATGCAAGAC ATATCAGCAG TGTGTCTACA TTGGATAGTG GTATGTA--- ATATCAAT-- ----TTCT--
Mae304       ---------- -----CAGGA TGTTGGTGTT CATGCAAGAC ATATCAGCAG TGTGTCTACA TTGGATAGTG GTATGTA--- ATATCAAT-- ----TTCT--
Aro301       CATGTTGGTT T-ATACAGGA TGTTGGAGTT CATGCAAGAC ATATCAGCAG TGTGTCTACA TTAGATAGTG GTATGTA--- ATATCAAT-- ----TTCTTC
Aro302       CATGTTGGTT T-ATACAGGA TGTTGGAGTT CATGCAAGAC ATATCAGCAG TGTGTCTACA TTAGATAGTG GTATGTA--- ATATCAAT-- ----TTCTTC
Aro303       CATGTTGGTT T-ATACAGGA TGTTGGAGTT CATGCAAGAC ATATCAGCAG TGTGTCTACA TTAGATAGTG GTATGTA--- ATATCAAT-- ----TTCTTC
Aro304       CATGTTGGTT T-ATACAGGA TGTTGGAGTT CATGCAAGAC ATATCAGCAG TGTGTCTACA TTAGATAGTG GTATGTA--- ATATCAAT-- ----TTCTTC
Aro305       CATGTTGGTT T-ATACAGGA TGTTGGAGTT CATGCAAGAC ATATCAGCAG TGTGTCTACA TTAGATAGTG GTATGTA--- ATATCAAT-- ----TTCTTC
Aro306       CATGTTGGTT T-ATACAGGA TGTTGGAGTT CATGCAAGAC ATATCAGCAG TGTGTCTACA TTAGATAGTG GTATGTA--- ATATCAAT-- ----TTCTTC
Aro307       CATGTTGGTT T-ATACAGGA TGTTGGAGTT CATGCAAGAC ATATCAGCAG TGTGTCTACA TTAGATAGTG GTATGTA--- ATATCAAT-- ----TTCTTC
Aca301       ---------- ------AGGA TGTTGGAGTT CATGCAAGAC ATATCAGCAG TGTGTCTACA TTGGATAGTG GTATGTA--- ATTTCAAT-- ----TTCTTC
Aca302       ---------- ------AGGA TGTTGGAGTT CATGCAAGAC ATATCAGCAG TGTGTCTACA TTGGATAGTG GTATGTA--- ATATCAAT-- ----TTCTTC
Aca303       ---------- ------AGGA TGTTGGAGTT CATGCAAGAC ATATCAGCAG TGTGTCTACA TTGGATAGTG GTATGTA--- ATTTCAAT-- ----TTCTTC
Kvi301       CATGTTGGTT T-ATACAGGA TGTTGGAGTT CATGCAAGAC ATATCAGCAG TGTGTCTACA TTGGATAGTG GTATGTA--- ATATCAAT-- ----TTCTTC
Kvi302       CATGTTGGTT T-ATACAGGA TGTTGGAGTT CATGCAAGAC ATATCAGCAG TGTGTCTACA TTGGATAGTG GTATGTA--- ATATCAAT-- ----TTCTTC
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Kvi303          CATGTTGGTT TTATACAGGA TGTTGGAGTT CATGCAAGAC ATATCAGCAG TGTGTCTACA TTGGATAGTG GTGTGTA--- ATATCAATTT ATCTTTCTTC


                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                       510        520        530        540        550        560        570        580        590        600
Ltr301          AA-TACTATT G-AACAAAAG AG--TGGATC ATAAAGCTCT AACTG-CCTC CTTCGATGTT TTCGTGTAGA AATGACAGAA GAAAACGGGA ACCCGATTTG
Ltp301          AA-TACTATT G-AACAAAAG AG--TGGATC ATAAAGCTCT AACTG-CCTC CTTCGATGTT TTCGTGTAGA AATGACAGAA GAAAACGGGA ACCCGATTTG
Ltp302          AA-TACTATT G-AACAAAAG AG--TGGATC ATAAAGCTCT AACTG-CCTC CTTCGATGTT TTCGTGTAGA AATGACAGAA GAAAACGGGA ACCCGATTTG
Lob301          AA-TACTATT G-AACAAAAG AG--TGGATC ATAAAGCTCT AACTG-CCTC CTTCGATGTT TTCGTGTAGA AATGACAGAA GACAACGGGA ACCCGATTTG
Lcr301          AA-TACTATT G-AACAAAAG AG--TGGATC ATA------T AAG---CCTC CTTCGATGTT TTCGTGTAGA AATGACTGAA GACAACGGGA ACCCGATTTG
Lcr302          AA-TACTATT G-AACAAAAG AG--TGGATC ATA------T AAG---CCTC CTTCGATGTT TTCGTGTAGA AATGACTGAA GACAACAGGA ACCCGATTTG
Lcr303          AA-TACTATT G-AACAAAAG AG--TGGATC ATA------T AAG---CCTC CTTCGATGTT TTCGTGTAGA AATGACTGAA GACAACAGGA ACCCGATTTG
Lcr304          AA-TACTATT G-AACAAAAG AG--TGGATC ATA------T AAG---CCTC CTTCGATGTT TTCGTGTAGA AATGACTGAA GACAACGGGA ACCCGATTTG
Mve301          AA-TACTATT G-AACAAAAG AG--TGGATC ATA------T AAG---CCTC CTTCGATGTT TTCGTGTAGA AATGACTGAA GACAACGGGA ACCCAATTTG
Mve302          AA-TACTATT G-AACAAAAG AG--TGGATC ATA------T AAG---CCTC CTTCGATGTT TTCGTGTAGA AATGACTGAA GACAACAGGA ACCCGATTTG
Mve303          AA-TACTATT G-AACAAAAG AG--TGGATC ATA------T AAG---CCTC CTTCGATGTT TTCGTGTAGA AATGACTGAA GACAACAGGA ACCCGATTTG
Mne301          AA-TACTATT G-AACAAAAG AG--TGGATC ATA------T AAG---CCTC CTTCGATGTT TTCGTGTAGA AATGACTGAA GACAACGGGA ACCCGATTTG
Mne302          AA-TACTATT G-AACAAAAG AG--TGGATC ATA------T AAG---CCTC CTTCGATGTT TTCGTGTAGA AATGACTGAA GACAACGGGA ACCCGATTTG
Mne303          AA-TACTATT G-AACAAAAG AG--TGGATC ATA------T AAG---CCTC CTTCGATGTT TTCGTGTAGA AATGACTGAG GACAACGGGA ACCCGATTTG
Mne304          AA-TACTATT G-AACAAAAG AG--TGGATC ATA------T AAG---CCTC CTTCGATGTT TTCGTGTAGA AATGACTGAA GACAACGGGA ACCCGATTTG
Lac301          GA-TCCTATT G-AACAAAGG AG--TGGATC ATAAAGCTCT AACTG-CCTC CTTCGATGTT TTCGTGTAGA AATGACTGAA GACAACGGGA ACCCGATTTG
Lma301          AA-TACTATT G-AACAAAAG AG--TGGATC ATAAAGCACT AACTG-CCTC CTTCGATGTT TTCGTGTAGA AATGACTGAA GACAACGGGA ACCCGATTTG
Lma302          AA-TACTATT G-AACAAAAG AG--TGGATC ATAAAGCACT AACTG-CCTC CTTCGATGTT TTCGTGTAGA AATGACTGAA GACAACGGGA ACCCGATTTG
Lma303          AA-TACTATT G-AACAAAAG AG--TGGATC ATAAAGCACT AACTG-CCTC CTTCGATGTT TTCGTGTAGG AATGACTGAA GACAACGGGA ACCCGATTTG
Lma304          AA-TACTATT G-AACAAAAG AG--TGGATC ATAAAGCACT AACTG-CCTC CTTCGATGTT TTCGTGTAGA AATGACTGAA GACAACGGGA ACCCGATTTG
Lma305          AA-TACTATT G-AACAAAAG AG--TGGATC ATAAAGCACT AACTG-CCTC CTTCGATGTT TTCGTGTAGA AATGACTGAA GACAACGGGA ACCCGATTTG
Lph301          AA-TACTATT G-AACAAAAG AG--TGGATC ATAAAGCTCT AACTG-CCTC CTTCGATGTT TTCGTGTAGA AATGACTGAA GACAACGGGA ACCCAATTTG
Lph302          AA-TACTATT G-AACAAAAG AG--TGGATC ATAAAGCTCT AACTG-CCTC CTTCGATGTT TTCGTGTAGA AATGACTGAA GACAACGGGA ACCCAATTTG
Mca301          AA-TACTATT C-AAGACAAA AGAGTCGACT ATTAAGCTCT AACTGCCCTC CTTTGATGTT TTTGTGTAGA AATGACCGGA GACAACGGGA ACCCGATTTG
Mca302          AA-TACTATT C-AAGACAAA AGAGTCGACT ATTAAGCTCT AACTGCCCTC CTTTGATGTT TTTGTGTAGA AATGACCGAA GACAACGGGA ACCCGATTTG
Mca303          AA-TACTATT C-AAGACAAA AGAGTCGACT ATTAAGCTCT AACTGCCCTC CTTTGATGTT TTTGTGTAGA AATGACCGAA GACAACGGGA ACCCGATTTG
Mca304          AA-TACTATT C-AAGAAAAA GAG-TTGATT ATTAAGCTCT AACTGCCCTC CTTCAATTTT TTCGTGTAGA AATGACCGAA GACAACGGGA ACCCGATTTG
Mca305          AA-TACTATT C-AAGAAAAA GAG-TTGATT ATTAAGCTCT AACTGCCCTC CTTCAATTTT TTCGTGTAGA AATGACCGAA GACAACGGGA ACCCGATTTG
Mca306          AA-TACTATT C-AAGAAAAA GAG-TTGATT ATTAAGCTCT AACTGCCCTC CTTCAATTTT TTCGTGTAGA AATGACCGAA GACAACGGGA ACCCGATTTG
Mca307          AA-TACTATT C-AAGAAAAA GAG-TTGATT ATTAAGCTCT AACTGCCCTC CTTCAATTTT TTCGTGTAGA AATGACCGAA GACAACGGGA ACCCGATTTG
Mca308          AA-TACTATT C-AAGACAAA AGAGTCGACT ATTAAGCTCT AACTGCCCTC CTTTGATGTT TTTGTGTAGA AATGACCGGA GACAACGGGA ACCCGATTTG
Mca309          AA-TACTATT C-AAGAAAAA GAG-TTGATT ATTAAGCTCT AACTGCCCTC CTTCAATTTT TTCGTGTAGA AATGACCGAA GACAACGGGA ACCCGATTTG
Mtr301          -------ATT C-AAGAAAAA AGAGTCTATT ATAAAGCTCT AACTGCCCTC CTTGGATGTT TTCGTGTAGA AATGACCGAA GACAACGGGA ACCCGATTTG
Mtr302          -------ATT C-AAGAAAAA AGAGTCTATT ATAAAGCTCT AACTGCCCTC CTTGGATGTT TTCGTGTAGA AATGACCGAA GACAACGGGA ATCCGATTTG
Mtr303          -------ATT C-AAGAAAAA AGAGTCTATT ATAAAGCTCT AACTGCCCTC CTTGGATGTT TTCGTGTAGA AATGACCGAA GACAACGGGA ACCCGATTTG
Mtr304          -------ATT C-AAGAAAAA AGAGTCTATT ATAAAGCTCT AACTGCCCTC CTTGGATGTT TTCGTGTAGA AATGACCGAA GACAACGGGA ACCCGATTTG
Mtr305          -------ATT C-AAGAAAAA AGAGTCTATT ATAAAGCTCT AACTGCCCTC CTTGGATGTT TTCGTGTAGA AATGACCGAA GACAACGGGA ACCCGATTTG
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Mtr306          -------ATT C-AAGAAAAA AGAGTCTATT ATAAAGCTCT AACTGCCCTC CTTGGATGTT TTCGTGTAGA AATGACCGAA GACAACGGGA ACCCGATTTG
Mae301          -------ATT C-AAGAAAAA AGAGTCTATT ATAAAGCTCT AACTGCCCTC CTTGGATGTT TTCGTGTAGA AATGACCGAA GACAACGGGA ACCCGATTTG
Mae302          -------ATT C-AAGAAAAA AGAGTCTATT ATAAAGCTCT AACTGCCCTC CTTGGATGTT TTCGTGTAGA AATGACCGAA GACAACGGGA ACCCGATTTG
Mae303          -------ATT C-AAGAAAAA AGAGTCTATT ATAAAGCTCT AACTGCCCTC CTTGGATGTT TTCGTGTAGA AATGACCGAA GACAACGGGA ACCCGATTTG
Mae304          -------ATT C-AAGAAAAA AGAGTCTATT ATAAAGCTCT AACTGCCCTC CTTGGATGTT TTCGTGTAGA AATGACCGAA GACAACGGGA ACCCGATTTG
Aro301          AA-TGCTGTT C-AAGAACAG AT--TTGACT ATAAAGCTCT AACTG-TCCC CTTCGATGTT TTCGTGTAGA AATGACCGAA GACAATGGGA ACCCGATTTG
Aro302          AA-TGCTGTT C-AAGAACAG AT--TCGACT ATAAAGCTCT AACTG-TCCC CTTCGATGTT TTCGTGTAGA AATGACCGAA GACAATGGGA ACCCAATTTG
Aro303          AA-TGCTGTT C-AAGAACAG AT--TCGACT ATAAAGCTCT AGCTG-TCCC CTTCGATGTT TTCGTGTAGA AATGACCGAA GACAATGGGA ACCCAATTTG
Aro304          AA-TGCTGTT C-AAGAACAG AT--TTGACT ATAAAGCTCT AACTG-TCCC CTTCGATGTT TTCGTGTAGA AATGACCGAA GACAATGGGA ACCCGATTTG
Aro305          AA-TGCTGTT C-AAGAACAG AT--TTGACT ATAAAGCTCT AACTG-TCCC CTTCGATGTT TTCGTGTAGA AATGACCGAA GACAATGGGA ACCCGATTTG
Aro306          AA-TGCTGTT C-AAGAACAG AT--TCGACT ATAAAGCTCT AACCG-TCCC CTTCGATGTT TTCGTGTAGA AATGACCGAA GACAATGGGA ACCCGATTTG
Aro307          AA-TGCTGTT C-AAGAACAG AT--TCGACT ATAAAGCTCT AACTG-TCCC CTTCGATGTT TTCGTGTAGA AATGACCGAA GACAATGGGA ACCCAATTTG
Aca301          AAATACTATT C-AAGAAAAG AT--TCGATT ATAAAGCTCT AACTG-TCTC CTTCGATGTT TTCGTGTAGA AATGACCGAA GACAATGGGA ATCCAATTTG
Aca302          AAATACTATT C-AAGAAAAG AT--TCGATT ATAAAGCTCT AACTG-TCTC CTTCGATGTT TTCGTGTAGA AATGACCGAA GACAATGGGA ATCCAATTTG
Aca303          AAATACTATT C-ATGAAAAG AT--TCGATT ATAAAGCTCT AACTG-TCTC CTTCGATGTT TTCGTGTAGA AATGACCGAA GACAATGGGA ATCCAATTTG
Kvi301          AA-TACTATT C-AAGAAAAG AT--TCGATT ATAAAGCTCT AACTG-CCTC CTTCGATGTT TTCGTGTAGA AATGACCGAA GACAATGGGA ACCCGATTTG
Kvi302          AA-TACTATT C-AAGAAAAG AT--TCGATT ATAAAGCTCT AACTG-CCTC CTTCGATGTT TTCGTGTAGA AATGACCGAA GACAATGGGA ACCCGATTTG
Kvi303          AATGTTCCTT C-AAGAAAAA AA--TCAATT CTAGAGATCT AATTG-TCTG GTTTGATGTT TTCGTGAAGA AATGACTGAA GACAATGGGA ACCCAATTTG


                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                       610        620        630        640        650        660        670        680        690        700
Ltr301          GAAGAACAGG GTGGAAAGTT GGAAGGAAAA GAAGAACAAG AAGAAAAAGC ATGCAACAAC TAAGGTTGAC AGAGAGGCTG AAGTCCCACC TGAGCAACAA
Ltp301          GAAGAACAGG GTGGAAAGTT GGAAGGAAAA GAAGAACAAG AAGAAAAAGC ATGCAACAAC TAAGGTTGAC AGAGAGGCTG AAGTCCCACC TGAGCAACAA
Ltp302          GAAGAACAGG GTGGAAAGTT GGAAGGAAAA GAAGAACAAG AAGAAAAAGC ATGCAACAAC TAAGGTTGAC AGAGAGGCTG AAGTCCCACC TGAGCAACAA
Lob301          GAAGAACAGG GTGGAAAGTT GGAAGGAAAA GAAGAACAAG AAGAAAAAGC ATGCAACAGC TAAGGTTGAC AGAGAGGCTG AAGTCCCACC TGAGCAACAA
Lcr301          GAAGAACAGG GTGGAAAGTT GGAAGGAAAA GAAGAACAAG AAGAAAAAGC ATGCAACAAC CAAGGTTGAC AAAGAGGCGG AAGTACCACC TGAGCAACAA
Lcr302          GAAGAACAGG GTGGAAAGTT GGAAGGAAAA GAAGAACAAG AAGAAAAAGC ATGCAACAAC CAAGGTTGAC AGAGAGGCTG AAGTACCACC TGAGCAACAA
Lcr303          GAAGAACAGG GTGGAAAGTT GGAAGGAAAG GAAGAACAAG AAGAAAAAGC ATGCAACAAC CAAGGTTGAC AGAGAGGCTG AAGTACCACC TGAGCAACAA
Lcr304          GAAGAACAGG GTGGAAAGTT GGAAGGAAAA GAAGAACAAG AAGAAAAAGC ATGCAACAAC CAAGGTTGAC AAAGAGGCGG AAGTACCACC TGAGCAACAA
Mve301          GAAGAACAGG GTGGAAAGTT GGAAGGAAAA GAAGAACAAG AAGAAAAAGC ATGCAACAAC CAAGGTTGAC AGAGAGGCGG AAGTACCACC TGAGCAACAA
Mve302          GAAGAACAGG GTGGAAAGTT GGAAGGAAAA GAAGAACAAG AAGAAAAAGC ATGCAACAAC CAAGGTTGAC AGAGAGGCTG AAGTACCACC TGAGCAACAA
Mve303          GAAGAACAGG GTGGAAAGTT GGAAGGAAAA GAAGAACAAG AAGAAAAAGC ATGCAACAAC CAAGGTTGAC AGAGAGGCTG AAGTACCACC TGAGCAACAA
Mne301          GAAGAACAGG GTGGAAAGTT GGAAGGAAAA GAAGAACAAG AAGAAAAAGC ATGCAACAAC CAAGGTTGAC AGAGAGGCTG AAGTCCCACC TGAGCAACAA
Mne302          GAAGAACAGG GTGGAAAGTT GGAAGGAAAA GAAGAACAAG AAGAAGAAGC ATGCAACAAC CAAGGTTGAC AGAGAGGCTG AAGTCCCACC TGAGCAACAA
Mne303          GAAGAACAGG GTGGAAAGTT GGAAGGAAAA GAAGAACAAG AAGAAAAAGC ATGCAACAAC CAAGGTTGAC AGAGAGGCTG AAGTCCCACC TGAGCAACAA
Mne304          GAAGAACAGG GTGGAAAGTT GGAAGGAAAA GAAGAACAAG AAGAAAAAGC ATGCAACAAC CAAGGTTGAC AGAGAGGCTG AAGTTCCACC TGAGCAACAA
Lac301          GAAGAACAGG GTGGAAAGTT GGAAGGAAAA GAAGAACAAG AAGAAAAAGC ATGCAACAAC CAAGGTTGAC AGAGAGGCTG AAGTCCCACC TGAGCAACAA
Lma301          GAAGAACAGG GTGGAAAGTT GGAAGGAAAA GAAAAACAAG AAGAAAAAGC ATGCAACAAC CAAGGTTGAC AGAGAGGCTG AAGTCCCACC TGAGCAACAA
Lma302          GAAGAACAGG GTGGAAAGTT GGAAGGAAAA GAAAAACAAG AAGAAAAAGC ATGCAACAAC CAAGGTTGAC AGAGAGGCTG AAGTCCCACC TGAGCAACAA
Lma303          GAAGAACAGG GTGGAAAGTT GGAAGGAAAA GAAAAACAAG AAGAAAAAGC ATGCAACAAC CAAGGTTGAC AGAGAGGCTG AAGTCCCACC TGAGCAACAA
Lma304          GAAGAACAGG GTGGAAAGTT GGAAGGAAAA GAAAAACAAG AAGAAAAAGC ATGCAACAAC CAAGGTTGAC AGAGAGGCTG AAGTCCCACC TGAGCAACAA
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Lma305        GAAGAACAGG GTGGAAAGTT GGAAGGAAAA GAAAAACAAG AAGAAAAAGC ATGCAACAAC CAAGGTTGAC AGAGAGGCTG AAGTCCCACC TGAGCAACAA
Lph301        GAAGAACAGG GTGGAAAGTT GGAAGGAAAA GAAGAACAAG AAGAAAAAGC ATGCAACAAC CAAGGTTGAC AGAGAGGCTG AAGTCCCACC TGAGCAACAA
Lph302        GAAGAACAGG GTGGAAAGTT GGAAGGAAAA GAAGAACAAG AAGAAAAAGC ATGCAACAAC CAAGGTTGAC AGAGAGGCTG AAGTCCCACC TGAGCAACAA
Mca301        GAAGAACAGG GTGGAAAGTT GGAAG----- ----AACAAG AAGAAAAAGC ATGCAACAAC TAATGTTGAC AGAGAGGCTC AAGTCCCACC TGAGCAACAA
Mca302        GAAGAACAGG GTGGAAAGTT GGAAG----- ----AACAAG AAGAAAAAGC ATGCAACAAC TAAGGTTGAC AGAGAGGCTC AAGTCCCACC TGAGCAACAA
Mca303        GAAGAACAGG GTGGAAAGTT GGAAG----- ----AACAAG AAGAAAAAGC ATGCAACAAC TAAGGTTGAC AGAGAGGCTC AAGTCCCACC TGAGCAACAA
Mca304        GAAGAACAGG GTGGAAAGTT GGAAGGAAAA GAAGAACAAG AAGAAAAAGC ATGCAACAAC TAATGTTGAC AGAGAGGCTG AAGTCCCACC TGAGCAACAA
Mca305        GAAGAACAGG GTGGAAAGTT GGAAGGAAAA GAAGAACAAG AAGAAAAAGC ATGCAACAAC TAAGGTTGAC AGAGAGGCTG AAGTCCCACC TGAGCAACAA
Mca306        GAAGAACAGG GTGGAAAGTT GGAAGGAAAA GAAGAACAAG AAGAAAAAGC ATGCAACAAC TAAGGTTGAC AGAGAGGCTG AAGTCCCACC TGAGCAACAA
Mca307        GAAGAACAGG GTGGAAAGTT GGAAGGAAAA GAAGAACAAG AAGAAAAAGC ATGCAACAAC TAAGGTTGAC AGAGAGGCTG AAGTCCCACC TGAGCAACAA
Mca308        GAAGAACAGG GTGGAAAGTT GGAAG----- ----AACAAG AAGAAAAAGC ATGCAACAAC TAAGGTTGAC AGAGAGGCTC AAGTCCCACC TGAGCAACAA
Mca309        GAAGAACAGG GTGGAAAGTT GGAAGGAAAA GAAGAACAAG AAGAAAAAGC ATGCAACAAC TAAGGTTGAC AGAGAGGCTG AAGTCCCACC TGAGCAACAA
Mtr301        GAAGAACAGG GTGGAAAGTT GGAAGGAAAA GAAGAACAAG AAGAAAAAGC ATGCAACAAC TAAGGTTGAC AGAGAGGCTC AAGTCCCACC TGAGCAACAA
Mtr302        GAAGAACAGG GTGGAAAGTT GGAAGGAAAA GAAGAACAAG AAGAAAAAGC ATGCAACAAC TAAGGTTGAC AGAGAGGCTC AAGTCCCACC TGAGCAACAA
Mtr303        GAAGAACAGG GTGGAAAGTT GGAAGGAAAA GAAGAACAAG AAGAAAAAGC ATGCAACAAC TAAGGTTGAC AGAGAGGCTC AAGTCCCACC TGAGCAACAA
Mtr304        GAAGAACAGG GTGGAAAGTT GGAAGGAAAA GAAGAACAAG AAGAAAAAGC ATGCAACAAC TAAGGTTGAC AGAGAGGCTC AAGTCCCACC TGAGCAACAA
Mtr305        GAAGAACAGG GTGGAAAGTT GGAAGGAAAA GAAGAACAAG AAGAAAAAGC ATGCAACAAC TAAGGTTGAC AGAGAGGCTC AAGTCCCACC TGAGCAACAA
Mtr306        GAAGAACAGG GTGGAAAGTT GGAAGGAAAA GAAGAACAAG AAGAAAAAGC ATGCAACAAC TAAGGTTGAC AGAGAGGCTC AAGTCCCACC TGAGCAACAA
Mae301        GAAGAACAGG GTGGAAAGTT GGAAGGAAAA GAAGAACAAG AAGAAAAAGC ATGCAACAAC TAAGGTTGAC AGAGAGGCTC AAGTCCCACC TGAGCAACAA
Mae302        GAAGAACAGG GTGGAAAGTT GGAAGGAAAA GAAGAACAAG AAGAAAAAGC ATGCAACAAC TAAGGTTGAC AGAGAGGCTC AAGTCCCACC TGAGCAACAA
Mae303        GAAGAACAGG GTGGAAAGTT GGAAGGAAAA GAAGAACAAG AAGAAAAAGC ATGCAACAAC TAAGGTTGAC AGAGAGGCTC AAGTCCCACC TGAGCAACAA
Mae304        GAAGAACAGG GTGGAAAGTT GGAAGGAAAA GAAGAACAAG AAGAAAAAGC ATGCAACAAC TAAGGTTGAC AGAGAGGCTC AAGTCCCACC TGAGCAACAA
Aro301        GAAGAACAGG GTGGAAAGTT GGAAGGAAAA GAAGAACAAG AAGAAAAAGG CTGCAACAAC TAAGGTTGAC AGAGAGGCTG AAGTCCCACC TGAGCAACAA
Aro302        GAAGAACAGG GTGGAAAGTT GGAAGGAAAA GAAGAACAAG AAGAAAAAGG CTGCAACAAC TAAGGTTGAC AGAGAGGCTG AAGTCCCACC TGAGCAACAA
Aro303        GAAGAACAGG GTGGAAAGTT GGAAGGAAAA GAAGAACAAG AAGAAAAAGG CTGCAACAAC TAAGGTTGAC AGAGAGGCTG AAGTCCCACC TGAGCAACAA
Aro304        GAAGAACAGG GTGGAAAGTT GGAAGGAAAA GAAGAACAAG AAGAAAAAGG CTGCAACAAC TAAGGTTGAC AGAGAGGCTG AAGTCCCACC TGAGCAACAA
Aro305        GAAGAACAGG GTGGAAAGTT GGAAGGAAAA GAAGAACAAG AAGAAAAAGG CTGCAACAAC TAAGGTTGAC AGAGAGGCTG AAGTCCCACC TGAGCAACAA
Aro306        GAAGAACAGG GTGGAAAGTT GGAAGGAAAA GAAGAACAAG AAGAAAAAGG CTGCAACAAC TAAGGTTGAC AGAGAGGCTG AAGTCCCACC TGAGCAACAA
Aro307        GAAGAACAGG GTGGAAAGTT GGAAGGAAAA GAAGAACAAG AAGAAAAAGG CTGCAACAAC TAAGGTTGAC AGAGAGGCTG AAGTCCCACC TGAGCAACAA
Aca301        GAAGAACAGG GTGGAAAGTT GGAAGGAAAA GAAGAACAAG AAGAAAAAGC CTGCAACAAC AAAGGTTGAC AGAGAGGCTG AAGTCCCACC TGAGCAACAA
Aca302        GAAGAACAGG GTGGAAAGTT GGAAGGAAAA GAAGAACAAG AAGAAAAAGC CTGCAACAAC TAAGGTTGAC AGAGAGGCTG AAGTCCCACC TGAGCAACAA
Aca303        GAAGAACAGG GTGGAAAGTT GGAAGGAAAA GAAGAACAAG AAGAAAAAGC CTGCAACAAC AAAGGTTGAC AGAGAGGCTG AAGTCCCACC TGAGCAACAA
Kvi301        GAAGAACAGG GTGGAAAGTT GGAAGGAAAA GAAGAACAAG AAGAAAAAGC CTGCAAAAAC TAAGGTTGAC AGAGAGGCTG AAATCCCACC TGAGCAACAA
Kvi302        GAAGAACAGG GTGGAAAGTT GGAAGGAAAA GAAGAACAAG AAGAAAAAGC CTGCAAAAAC TAAGGTTGAC AGAGAGGCTG AAATCCCACC TGAGCAACAA
Kvi303        GAAGAACAGG GTGGAAAGTT GGAAAGAAAA GAAGAACAAG AAGAAAAAGC CTGCAACAAC TAAGGCTGAC AGAGAGGCTG AAGTCCCACC TGAGCAACAA


              ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     710        720        730        740        750        760        770        780        790        800
Ltr301        ATGGAAGATA AACCGTAAGT ACAAAAAC-- ----GAAGCA -GATCAATGA TACGATTTTA CTTAGTGCAA TGT--TTTTG TTTATG-TTA AGTCTTACTG
Ltp301        ATGGAAGATA AACCGTAAGT ACAAAAAC-- ----GAAGCA -GATCGATGA TACGATTTTA CTTAGTGCAA TGT--TTTTG TTTATG-TTA AGTCTTACTG
Ltp302        ATGGAAGATA AACCGTAAGT ACAAAAAC-- ----GAAGCA -GATCGATGA TACGATTTTA CTTAGTGCAA TGT--TTTTG TTTATG-TTA AGTCTTACTG
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Lob301      ATGGAAGATA AACCGTAAGT ACAAAAAC-- ----GAAGCA -GATCGATGA TACGATTTTA CTTAGTGCAG TGT--TTTTG TTTATG-TTA AGTCTTACTG
Lcr301      ATGGAAGATA AACCGTAAGT ATAAAGAC-- ----GAAGCA -GATCAATGA TAAGATTTTA CTTGGTGCAA TGT--TTTTG TTTATATTTA AGTTTTACTG
Lcr302      ATGGAAGATA AACTGTAAGT ATAAAGGC-- ----GAAGCA -GATCAATGA TAAGATTTTA CTTGGTGCAA TGT--TTTTG TTTATATTTA AGTTTTACTG
Lcr303      ATGGAAGATA AACTGTAAGT ATAAAGGC-- ----GAAGCA -GATCAATGA TAAGATTTTA CTTGGTGCAA TGT--TTTTG TTTATATTTA AGTTTTACTG
Lcr304      ATGGAAGATA AACCGTAAGT ATAAAGAC-- ----GAAGCA -GATCAATGA TAAGATTTTA CTTGGTGCAA TGT--TTTTG TTTATATTTA AGTTTTACTG
Mve301      ATGGAAGATA AACCGTAAGT ATAAAGAC-- ----GAAGCA -GATCAATGA TAAGATTTTA CTTGGTGCAA TGT--TTTTG TTTATATTTA AGTTTTACTG
Mve302      ATGGAAGATA AACTGTAAGT ATAAAGGC-- ----GAAGCA -GATCAATGA TAAGATTTTA CTTGGTGCAA TGT--TTTTG TTTATATTTA AGTTTTACTT
Mve303      ATGGAAGATA AACTGTAAGT ATAAAGGC-- ----GAAGCA -GATCAATGA TAAGATTTTA CTTGGTGCAA TGT--TTTTG TTTATATTTA AGTTTTACTT
Mne301      ATGGAAGATA AACCGTAAGT ATAAAGAC-- ----GAAGCA -GATCAATGA TAAGATTTTA CTTGGTGCAA TGT--TTTTG TTTATATTCA AGTTTTACTG
Mne302      ATGGAAGATA AACCGTAAGT ATAAAGAC-- ----GAAGCA -GATCAATGA TAAGAGTTTA CTTGGTGCAA TGT--TTTTG TTTATATTCA AGTTTTACTG
Mne303      ATGGAAGATA AACCGTAAGT ATAAAGAC-- ----GAAGCA -GATCAATGA TAAGATTTTA CTTGGTGCAA TGT--TTTTG TTTATATTCA AGTTTTACTG
Mne304      ATGGAAGATA AACCGTAAGT ATAAAGAC-- ----GAAGCA -GATCAATGA TAAGATTTTA CTTGGTGCAA TGT--TTTTG TTTATATTCA AGTTTTACTG
Lac301      ATGGAAGATA AACCGTAAGT ATAAAGAC-- ----GAAGCA -GATCAATGA TAAGATTTTA CTTGGTGCAA TGT--TTTTG TTTATATTTA AGTTTTACTG
Lma301      ATGGAAGATA AACCGTAAGT ATAAAGAC-- ----GAAGCA -GATCAATGA TAAGATTTTT CTTGGTGCAA TGT--TTTTG TTTATATTTA AGTTTTACTG
Lma302      ATGGAAGATA AACCGTAAGT ATAAAGAC-- ----GAAGCA -GATCAATGA TAAGATTTTT CTTGGTGCAA TGT--TTTTG TTTATATTTA AGTTTTACTG
Lma303      ATGGAAGATA AACCGTAAGT ATAAAGAC-- ----GAAGCA -GATCAATGA TAAGATTTTT CTTGGTGCAA TGT--TTTTG TTTATATTTA AGTTTTACTG
Lma304      ATGGAAGATA AACCGTAAGT ATAAAGAC-- ----GAAGCA -GATCAATGA TAAGATTTTT CTTGGTGCAA TGT--TTTTG TTTATATTTA AGTTTTACTG
Lma305      ATGGAAGATA AACCGTAAGT ATAAAGAC-- ----GAAGCA -GATCAATGA TAAGATTTTT CTTGGTGCAA TGT--TTTTG TTTATATTTA AGTTTTACTG
Lph301      ATGGAAGATA AACCGTAAGT ATAAAGAC-- ----GAAACA -GATCAATGA TAAGATTTTA CTTGGTGCAA TGT--TTTTG TTTATATTTA AGTTTTACTG
Lph302      ATGGAAGATA AACCGTAAGT ATAAAGAC-- ----GAAACA -GATCAATGA TAAGATTTTA CTTGGTGCAA TGT--CTTTG TTTATATTTA AGTTTTACTG
Mca301      ATGGAAGATA AACCGTAAGT ACAAAAAAC- ----GAAGCA -GATCGATGA GAAGATTTTA TTTAGTGCAA TGT-TTTTTG TTT------- ----------
Mca302      ATGGAAGATA AACCGTAAGT ACAAAAAAC- ----GAAGCA -GATCGGTGA TAAGATTTTA TTTAGTGCAA TGT-TTTTTG TTT------- ----------
Mca303      ATGGAAGATA AACCGTAAGT ACAAAAAAC- ----GAAGCA -GATCGATGA TAAGATTTTA TTTAGTGCAA TGT-TTTTTG TTT------- ----------
Mca304      ATGGAAGATA AACCGTAAGT ATAAGAAC-- ----GAAGCT -GATCGATGA TAAGATTTTA CTTAATGCAA TGT-TTATTG TTT------- ----------
Mca305      ATGGAAGATA AACCGTAAGT ATAAGAAC-- ----GAAGCT -GATCGATGA TAAGATTTTA CTTAGTGCAA TGT-TTATTG TTT------- ----------
Mca306      ATGGAAGATA AACCGTAAGT ATAAGAAC-- ----GAAGCT -GATCGATGA TAAGATTTTA CTTAGTGCAA TGT-TTATTG TTT------- ----------
Mca307      ATGGAAGATA AACCGTAAGT ATAAGAAC-- ----GAAGCT -GATCGATGA TAAGATTTTA CTTAGTGCAA TGT-TTATTG TTT------- ----------
Mca308      ATGGAAGATA AACCGTAAGT ACAAAAAAC- ----GAAGCA -GATCGATGA TAAGATTTTA TTTAGTGCAA TGT-TTTTTG TTT------- ----------
Mca309      ATGGAAGATA AACCGTAAGT ATAAGAAC-- ----GAAGCT -GATCGATGA TAAGATTTTA CTTAGTGCAA TGT-TTATTG TTT------- ----------
Mtr301      ATGGAAGATA AACTGTAAGC ACGAAAAC-- ----GAAGCA AGATCAATGA TAAGATTCTA CT-AGTGCAA TGTTTTTTTG TTTACATTCA AGTCTTACTG
Mtr302      ATGGAAGATA AACCGTAAGC ACGAAAAC-- ----GAAGCA AGATCAATGA TAAGATTCTA CT-AGTGCAA TGTTTTTTTG TTTACATTCA AGTCTTACTG
Mtr303      ATGGAAGATA AACCGTAAGC ACGAAAAC-- ----GAAGCA AGATCAATGA TAAGATTCTA CT-AGTGCAA TGTTTTTTTG TTTACATTCA AGTCTTACTG
Mtr304      ATGGAAGATA AACCGTAAGC ACGAAAAC-- ----GAAGCA AGATCAATGA TAAGATTCTA CT-AGTGCAA TGTTTTTTTG TTTACATTCA AGTCTTACTG
Mtr305      ATGGAAGATA AACCGTAAGC ACGAAAAC-- ----GAAGCA AGATCAATGA TAAGATTCTA CT-AGTGCAA TGTTTTTTTG TTTACATTCA AGTCTTACTG
Mtr306      ATGGAAGATA AACCGTAAGC ACGAAAAC-- ----GAAGCA AGATCAATGA TAAGATTCTA CT-AGCGCAA TGTTTTTTTG TTTACATTCA AGTCTTACTG
Mae301      ATGGAAGATA AACCGTAAGC ACGAAAAC-- ----GAAGCA -GATCAATGA TAAGATTCTA CT-AGTGCAA TGTTTTTTTG TTTACATTCA AGTCTTACTG
Mae302      ATGGAAGATA AACCGTAAGC ACGAAAAC-- ----GAAGCA -GATCAATGA TAAGATTCTA CT-AGTGCAA TGTTCTTTTG TTTACATTCA AGTCTTACTG
Mae303      ATGGAAGATA AACCGTAAGC ACGAAAAC-- ----GAAGCG -GATCAATGA TAAGATTCTA CT-AGTGCAA TGTTTTTTTG TTTACATTCA AGTCTTACTG
Mae304      ATGGAAGATA AACCGTAAGC ACGAAAAC-- ----GAAGCA -GATCAATGA TAAGATTCTA CT-AGTGCAA TGTTTTTTTG TTTACATTCA AGTCTTACTG
Aro301      ATGGAAGATA AACCGTAAGT ATAAAAAC-- ----GAAGCA -GATCAATGA TAAGATTCTA CTTAGTGCAA TGT-TTTTTG TTTATG-TTA AGTCTTACTG
Aro302      ATGGAAGATA AACCGTTAGT ATAAAAAC-- ----GAAGCA -GATCAATGA TAAGATTCTA CTTAGTGCAA TGT-GTTTTG TTTATG-TTA AGTCTTACTG
Aro303      ATGGAAGATA AACCGTAAGT ATAAAAAC-- ----GAAGCA -GATCAATGA TAAGATTCTA CTTAGTGCAA TGT-GTTTTG TTTATG-TTA AGTCTTACTG
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Aro304          ATGGAAGATA AACCGTAAGT GTATATATAT ATAT-ATGTA -GATCAATGA TAAGATTCGA CTTAGTGCTA TGT--TTTTG TTTATG-TTA AGTCTTACTG
Aro305          ATGGAAGATA AACCGTAAGT ATAAAAAC-- ----GAAGCA -GATCAATGA TAAGATTCTA CTTAGTGCAA TGT-TTTTTG TTTATG-TTA AGTCTTACTG
Aro306          ATGGGAGATA AACCGTAAGT ATAAAAAC-- ----GTAGCA -GATCAATGA TAAGATTCTA CTTAGTGCAA TGT-TTTTTG TTTATG-TTA AGTCTTACTG
Aro307          ATGGAAGATA AACCGTAAGT ATAAAAAC-- ----GAAGCA -GATCAATGA TAAGATTCTA CTTAGTGCAA TGT-GTTTTG TTTATG-TTA AGTCTTACTG
Aca301          ATGGAAGATA AACCGTAC-- ---------- ----GAAGCA -GATCAATGA TAAGAGTCTA CTTAGTGCAA TGT--TTTTG TATATG-TTA AGTCTTACTG
Aca302          ATGGAAGATA AACCGTAC-- ---------- ----GAAGCA -GATCAATGA TAAGATTCTA CTTAGTGCAA TGT--TTTTG TATATG-TTA AGTCTTACTG
Aca303          ATGGAAGATA AACCGTAC-- ---------- ----GAAGCA -GATCAATGA TAAGATTCTA CTTAGTGCTA TGT--TTTTG TTTATG-TTA AGTCTTACTG
Kvi301          ATGGAAGATA AACCGTATGT ATAAAAAC-- ----GAAGCA -GATCAATGA TAAGATTCTA CTTAGTGCAA TGT--TTTTG TTTATG-TTA AGTCTTACTG
Kvi302          ATGGGAGATA AACCGTATGT ATAAAAAC-- ----GAAGCA -GATCAATGA TAAGATTCTA CTTAGTGCAA TGT--TTTTG TTTATG-TTA AGTCTTACTG
Kvi303          ATGGAAGATA AACCGTAAGT ATAAAAAC-- ----GAAGCA -GATCAATGA TAAGATTCTA CTTAGTGCAA TGT--TTTTG TTTATG-TTA AGTCTTACTG


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                       810        820        830        840        850        860        870        880        890        900
Ltr301          ATATGTAAAA TTTGCATTTG AAGAGCACCA GATGCTTCCC AGCCCCTATC CACTATAATT CCGATTCCGA AAAGCAAACT TGCACCGTAC CGAACTGTGA
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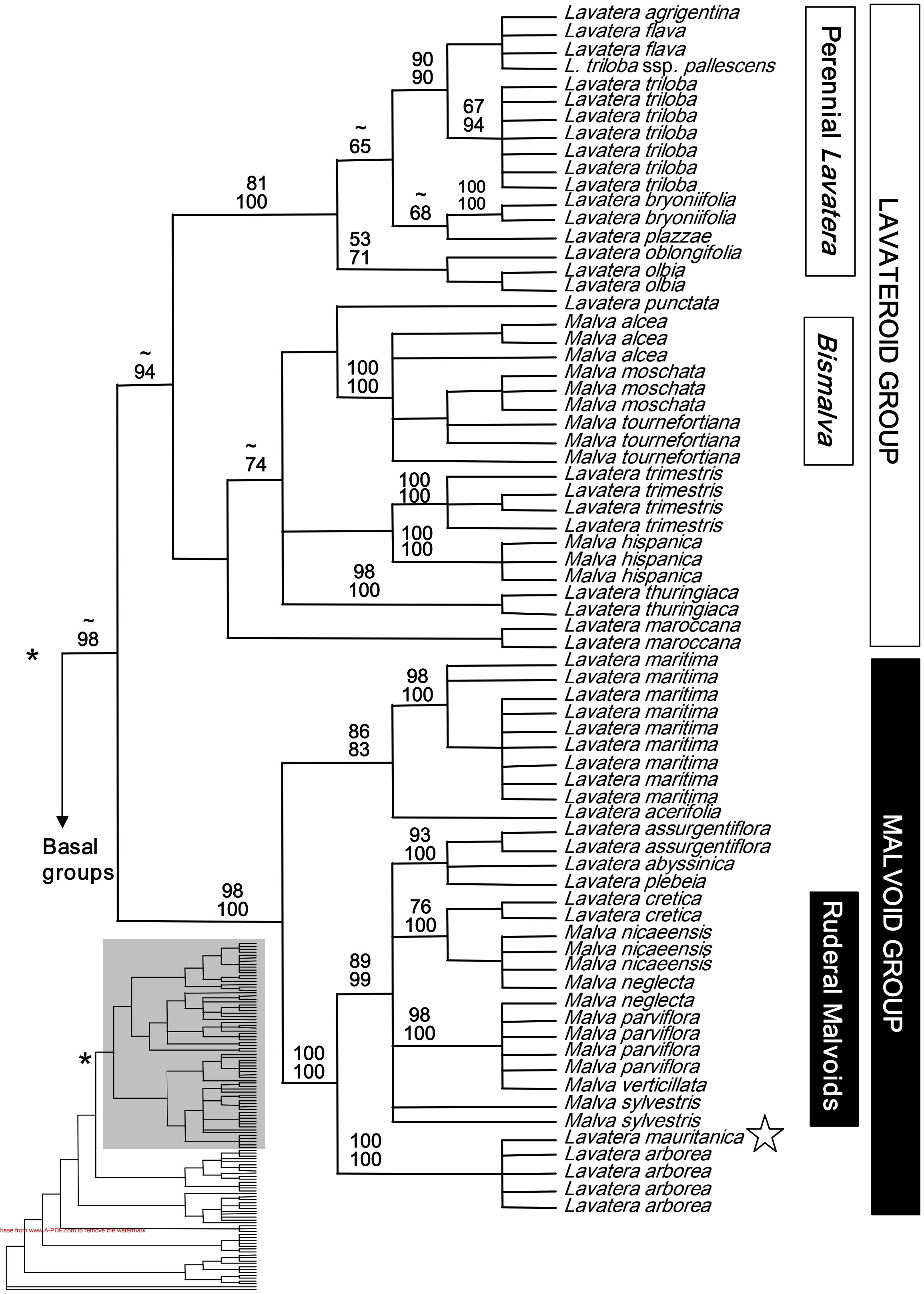


Fig 1a. ITS strict consensus of 3150 MPT. Stars indicate hybrid speciation events. The triangle marks the isolated position of *L. phoenicea*. Values above clades indicate bootstap support (only when higher than 50%) and bayesian posterior probability.

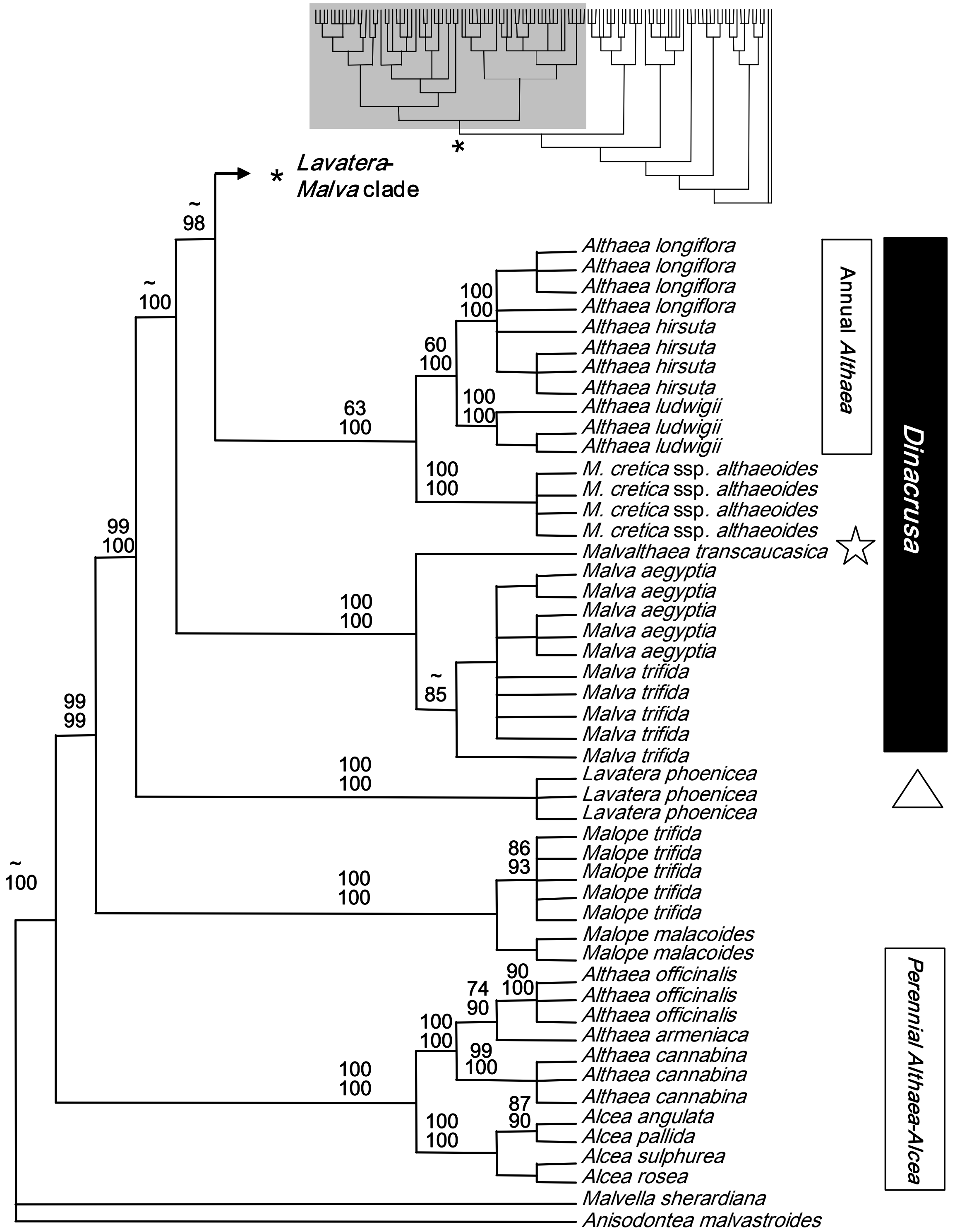


Fig 1b. ITS strict consensus of 3150 MPT. Stars indicate hybrid speciation events. The triangle marks the isolated position of *L. phoenicea*. Values above clades indicate bootstap support (only when higher than 50%) and bayesian posterior probability.

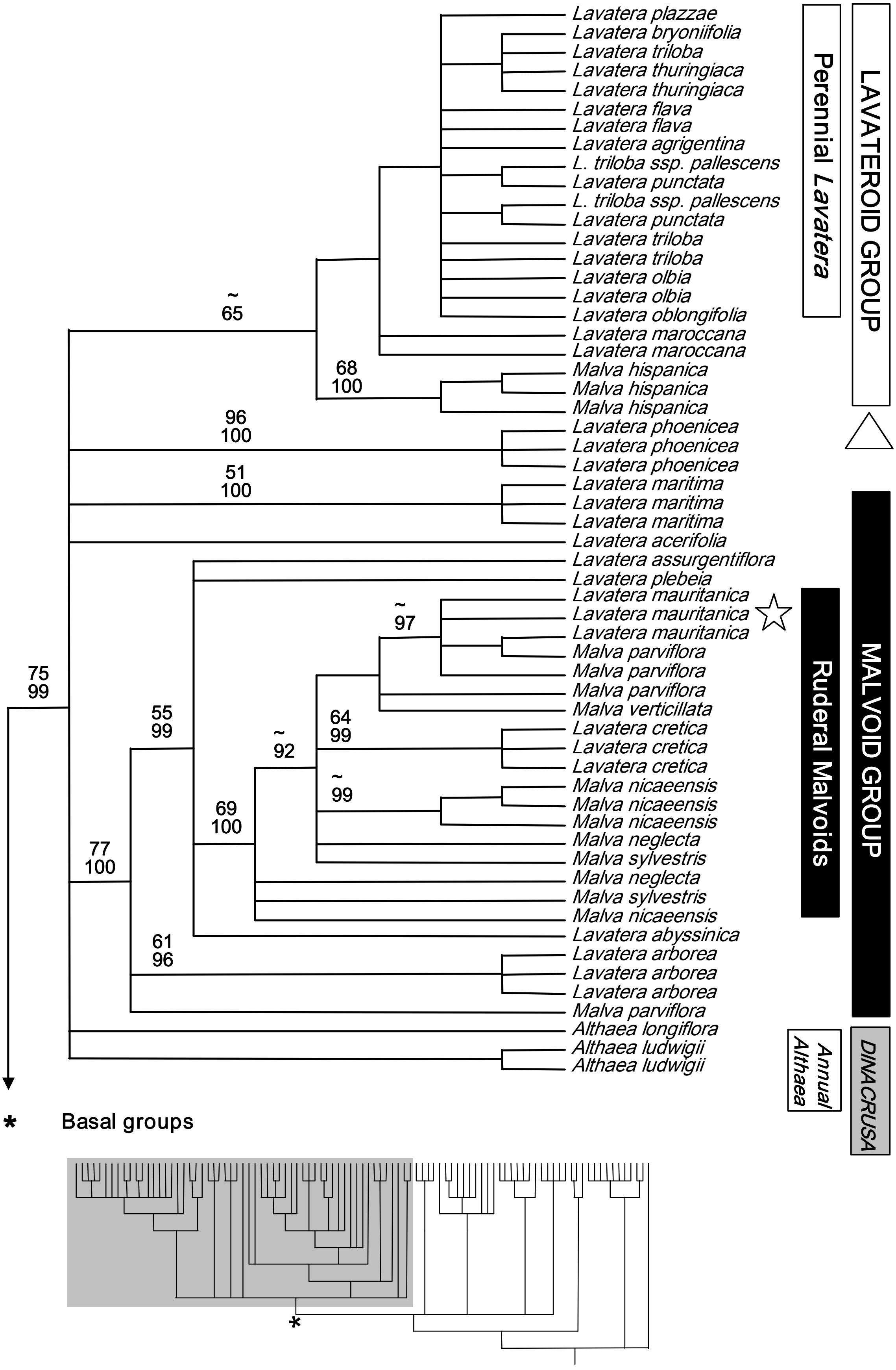


Fig 2a. *psb*A-*trn*H plus *trn*L-*trn*F Strict consensus of 7700 MPT. Stars indicate hybrid speciation events. The triangle marks the isolated position of *L. phoenicea*. Values above clades indicate bootstap support (only when higher than 50%) and bayesian posterior probability.

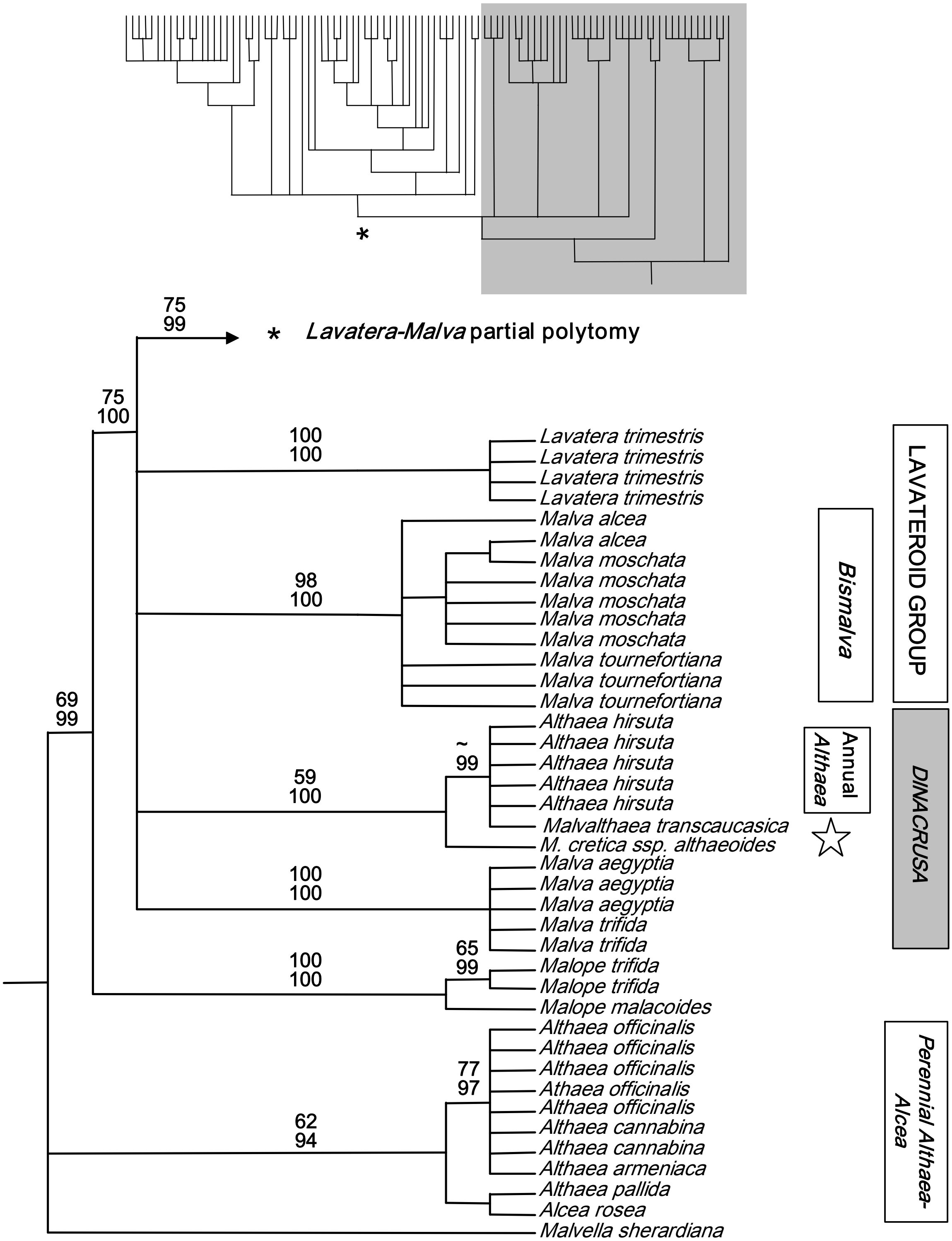


Fig 2b. *psb*A-*trn*H plus *trn*L-*trn*F Strict consensus of 7700 MPT. Stars indicate hybrid speciation events. The triangle marks the isolated position of *L. phoenicea*. Values above clades indicate bootstap support (only when higher than 50%) and bayesian posterior probability.

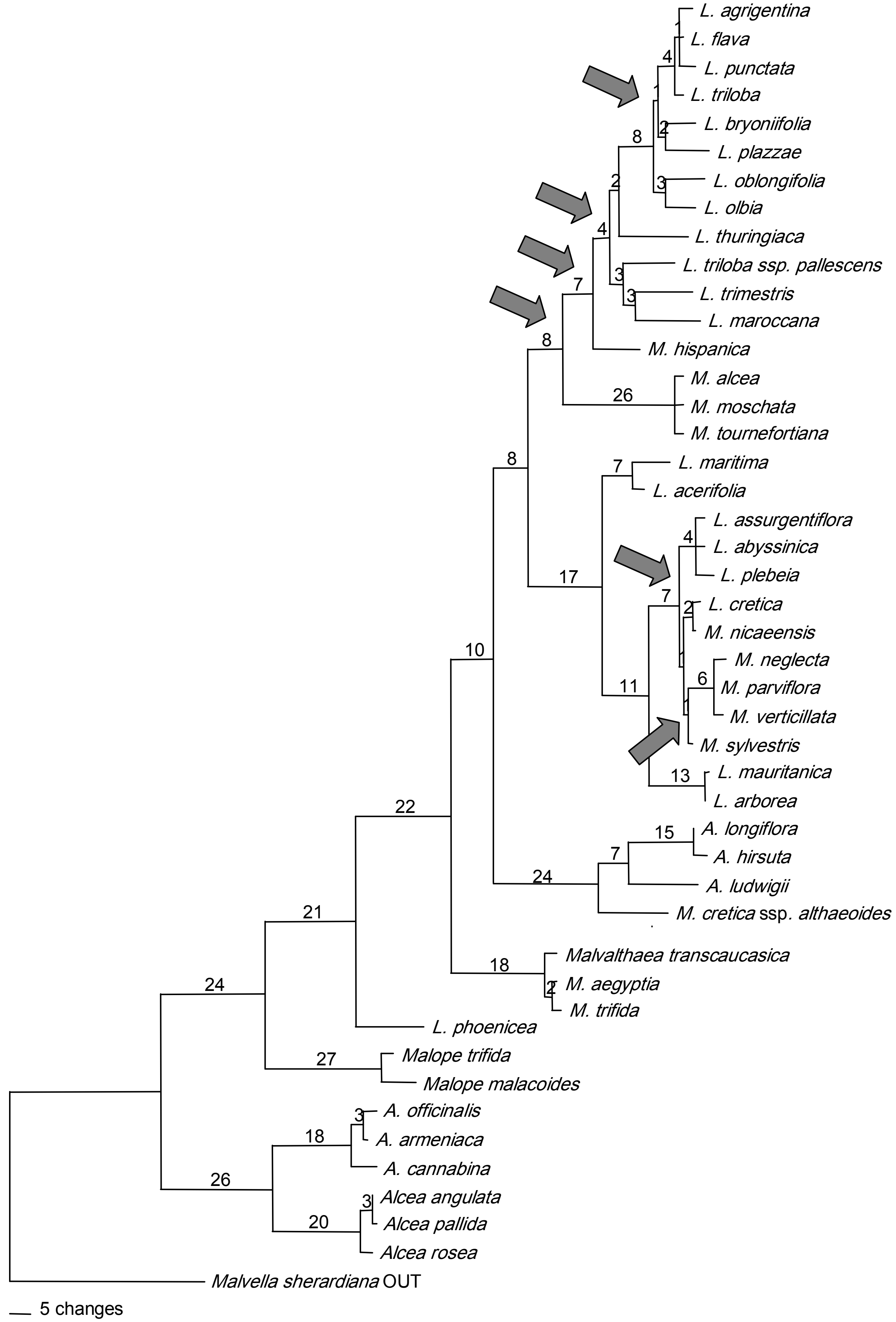


Fig. 3. ITS, one of the 3150 MPT, phylogram. The arrows indicate critical short branches. Above clade lines branch length in number of changes.

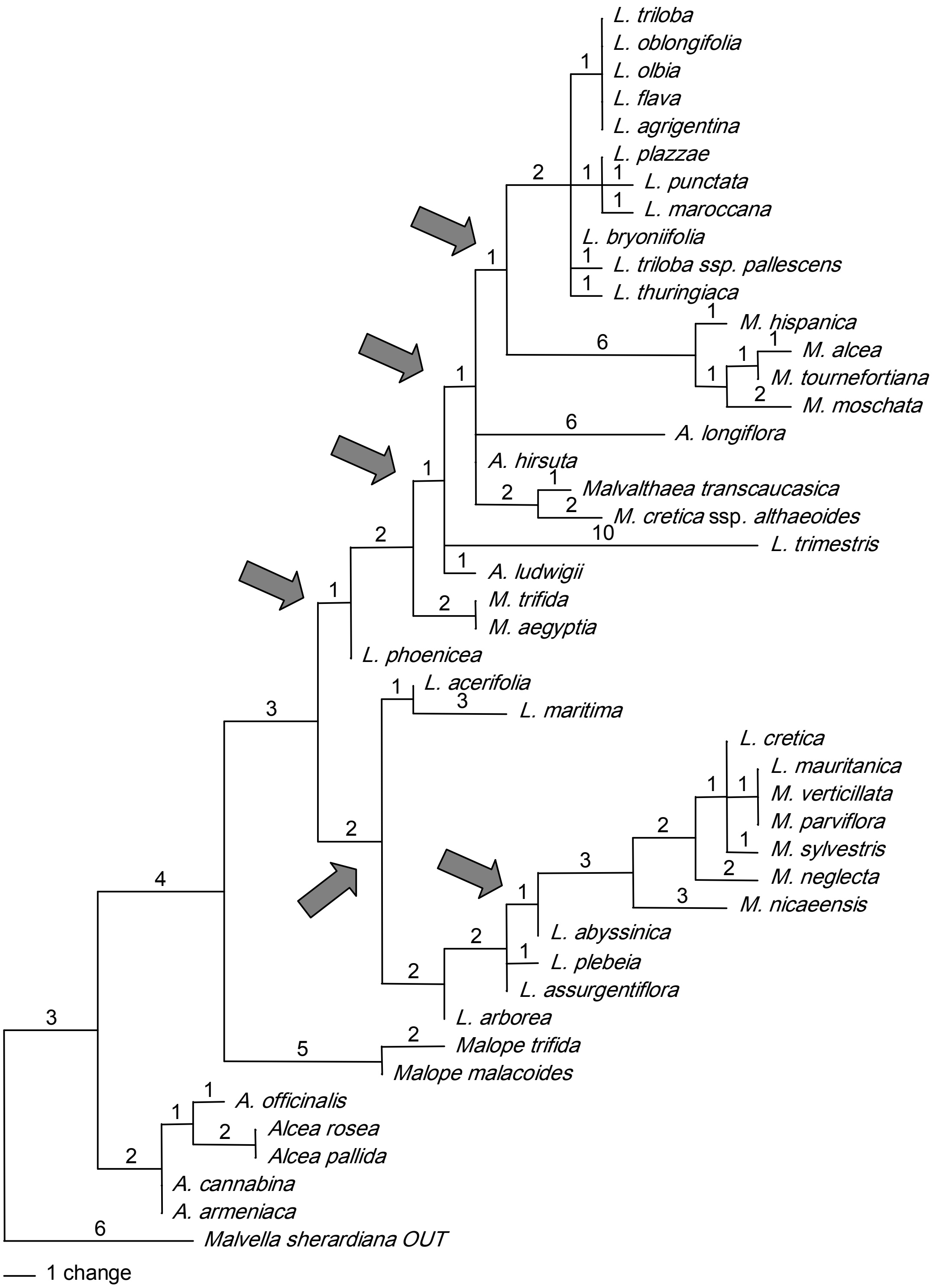


Fig. 4. *trn*L-*trn*F plus *psb*A-*trn*H, one of the 7700 MPT, phylogram. The arrows indicate critical short branches. Above lines branch length in number of changes.

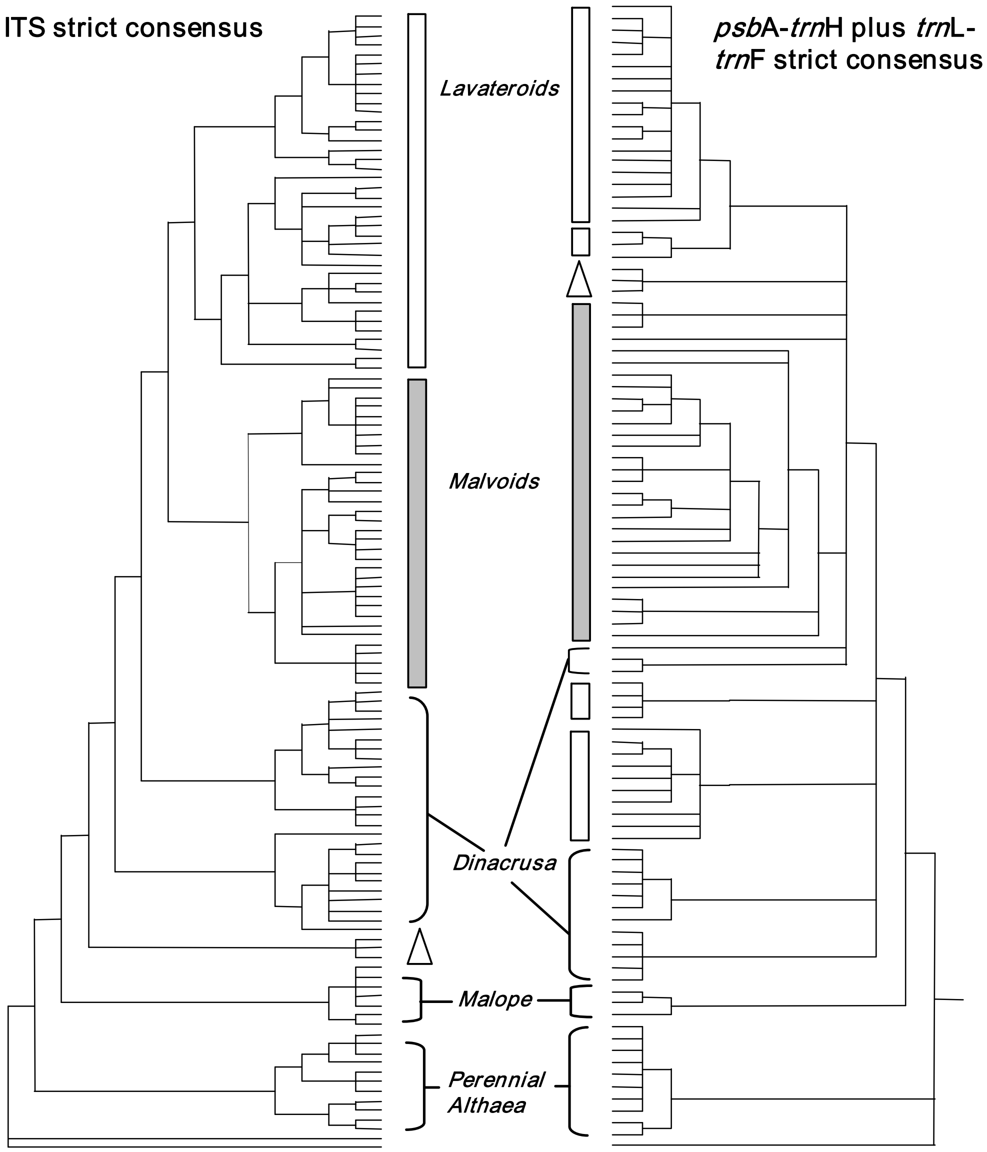


Fig. 5. ITS and plastid strict consensus tree comparison. The triangle marks the position of the Canary Islands isolated endemic *L. phoenicea*.

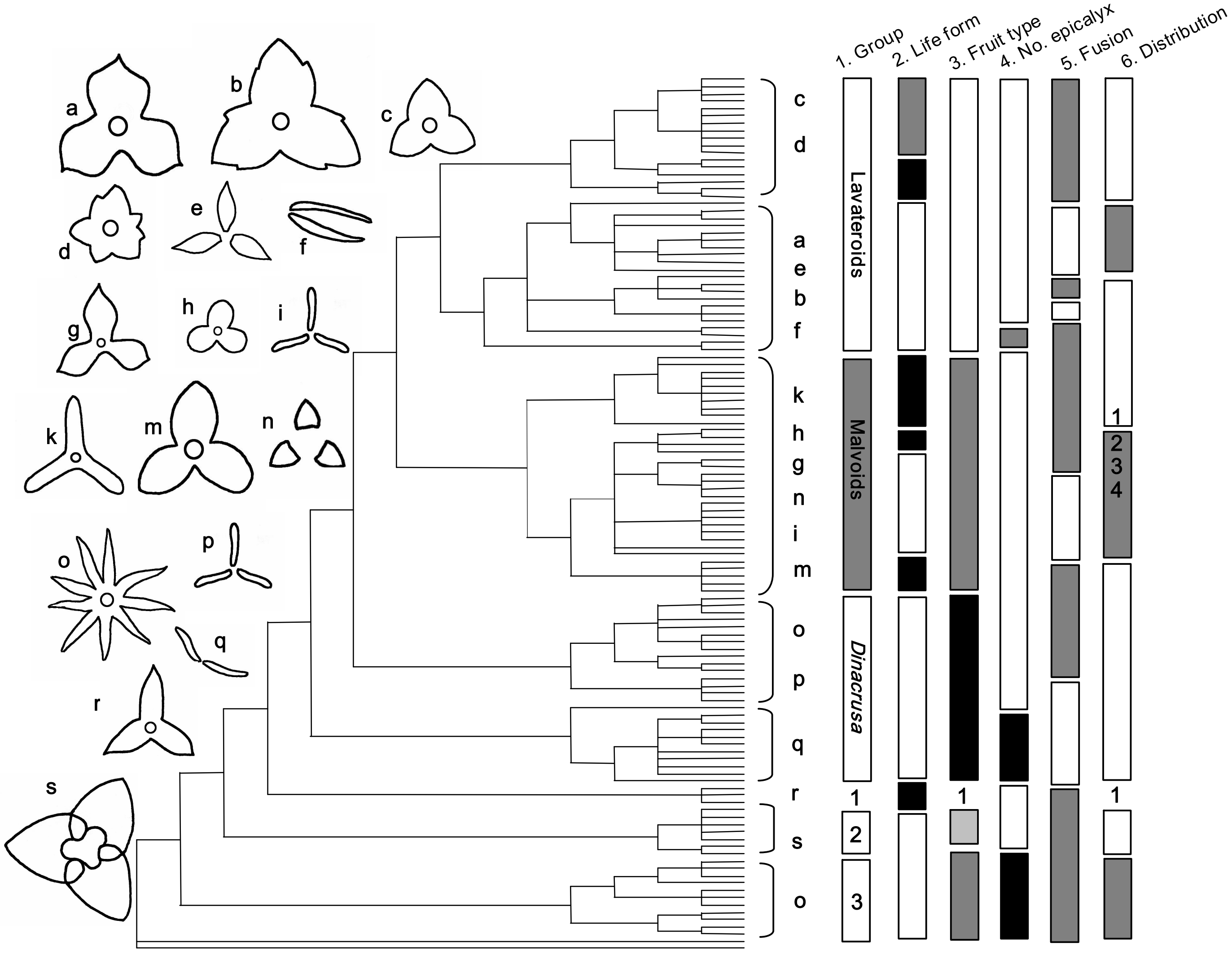


Fig 6. Character distribution: a, epicalyx type *Lavatera punctata*, **b**, *L. trimestris*, **c**, *L. thuringiaca*, **d**, *L. plazzae*, **e**, *Malva alcea*, **f**, *M. hispanica*, **g**, *L. cretica*, **h**, *L. plebeia*, **i**, *M. sylvestris*, **k**, *L. acerifolia*, **m**, *L. arborea*, **n**, *M. nicaeensis*, **o**, *Althaea hirsuta*, **p**, *M. cretica*, **q**, *M. aegyptia*, **r**, *L. phoenicea*, **s**, *Malope trifida*. **1. Group**: 1, *Lavatera* (*Navaea*) *phoenicea*; 2, *Malope*; 3, perennial *Althaea-Alcea* **2. Life form**: in grey, perennials lignified at base; in black, shrubs; in white, herbs. **3. Fruit type**: white, lavateroid; dark grey, malvoid; black, *Dinacrusa*; light grey, *Malope*; 1, *L. phoenicea*. **4. Number of epicalyx bracts**: white, three; black, more than three; grey, two. **5. Epicalyx bracts fusion degree**: grey, fused at least at base; white, free. **6. Plant Distribution**: white, Mediterranean; grey, widely distributed through temperate Europe and Asia; 1, Canary Islands endemic; 2 Californian Channel Islands endemic; 3, Australian endemic; 4, Somalian endemic.

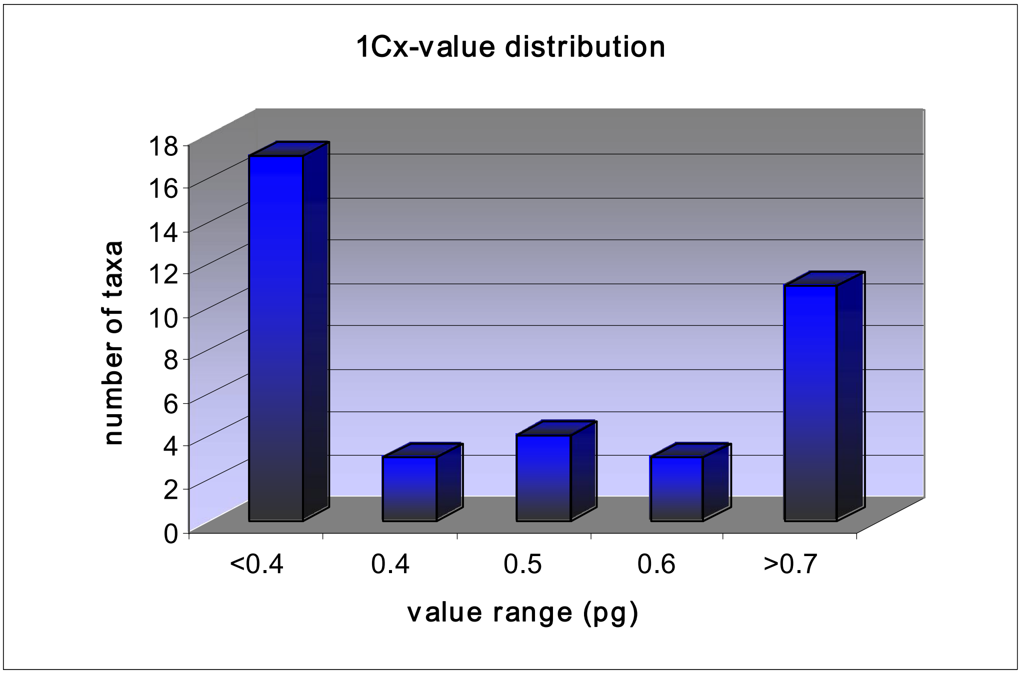
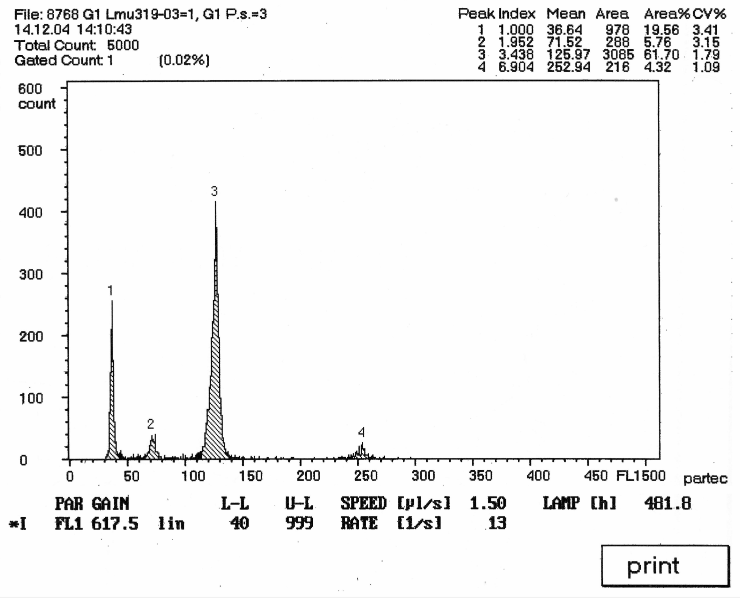


Fig. 1. Bimodal distribution of 1Cx-values among the representatives of the *Malva* alliance.



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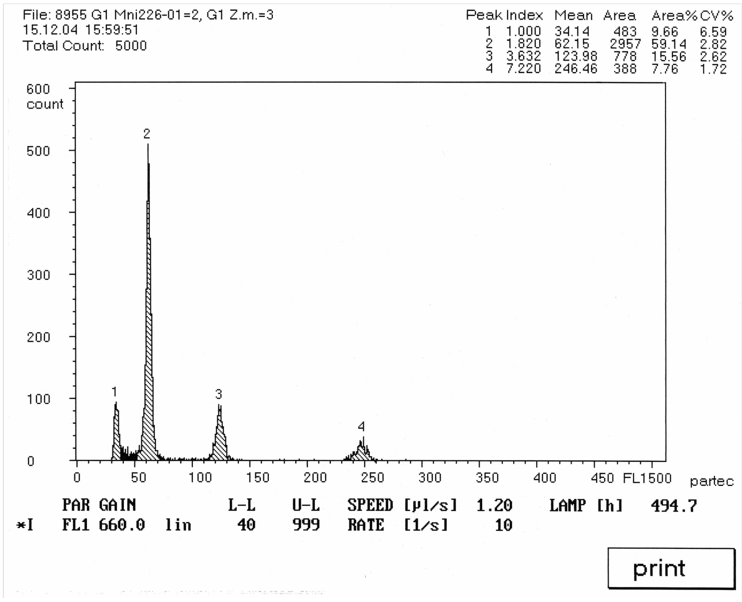
Total Count:  5000                                         2  1.952  71.52   288  5.76   3.15
Gated Count: 1        (0.02%)                              3  3.438  125.97  3085 61.70  1.79
                                                           4  6.904  252.94  216  4.32   1.09

     PAR GAIN          L-L    U-L   SPEED [µl/s]  1.50     LAMP [h]    481.8
*I   FL1 617.5  lin     40    999   RATE  [1/s]     13
```

Fig. 3. Examples of flow cytometry diagrams generated by the PARTEC Cell Analyzer. Above: *Lavatera mauritanica* (peaks 1 and 2) with *Pisum sativum* 'Kleine Rheinländerin' as standard organism (peaks 3 and 4). Below: *Malva nicaeensis* (peaks 1 ans 2) with *Zea mays* as standard (peaks 3 and 4).



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                                                           3  3.632  123.98  778  15.56  2.62
                                                           4  7.220  246.46  388  7.76   1.72

     PAR GAIN          L-L    U-L   SPEED [µl/s]  1.20     LAMP [h]    494.7
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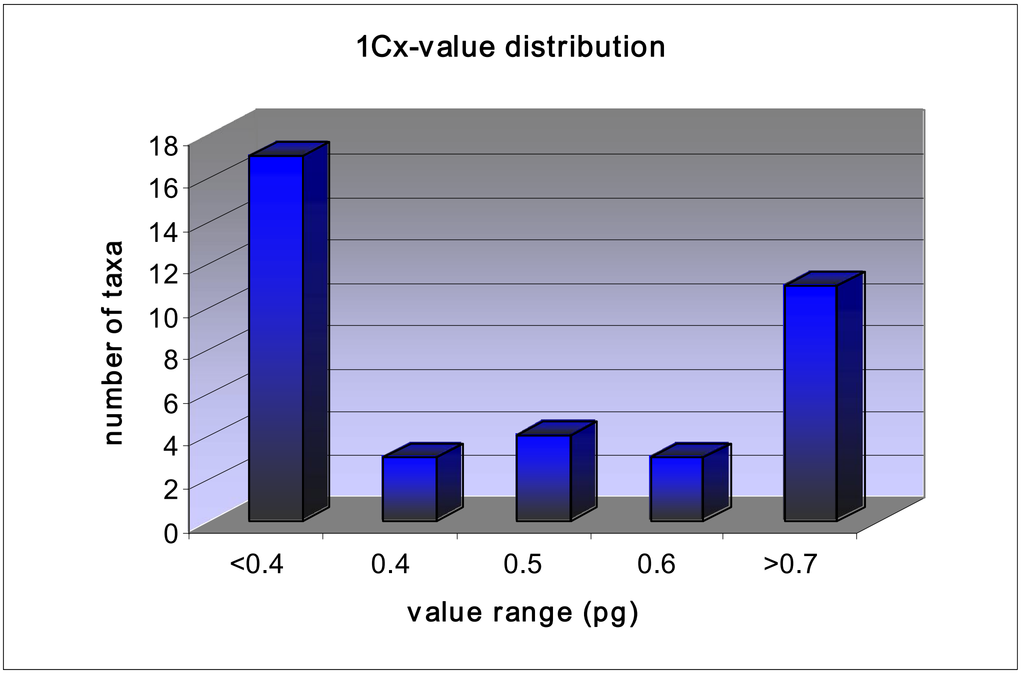
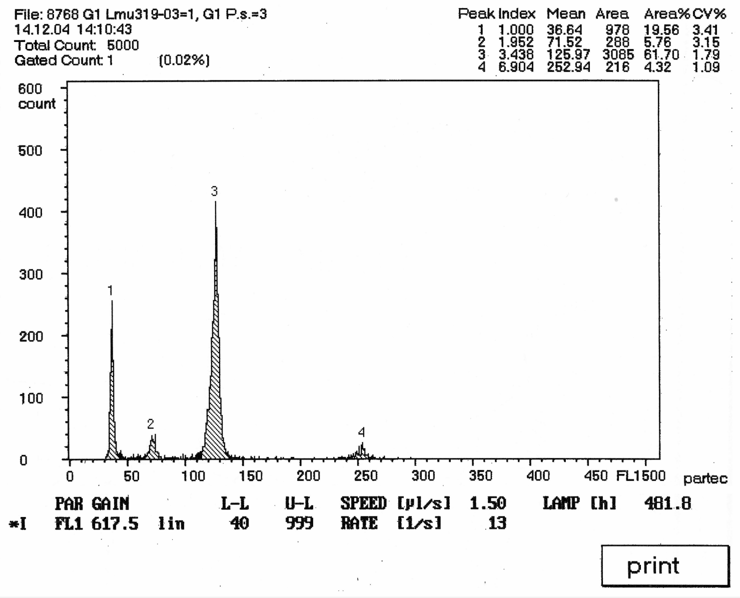


Fig. 1. Bimodal distribution of 1Cx-values among the representatives of the *Malva* alliance.



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File: 8768 G1 Lmu319-03=1, G1 P.s.=3                    Peak Index  Mean   Area  Area% CV%
14.12.04 14:10:43                                          1 1.000  36.64   978  19.56  3.41
Total Count:  5000                                         2 1.952  71.52   288  5.76   3.15
Gated Count: 1         (0.02%)                             3 3.438  125.97 3085  61.70  1.79
                                                           4 6.904  252.94  216  4.32   1.09
```

```
    PAR GAIN           L-L   U-L   SPEED [µl/s]  1.50    LAMP [h]   481.8
*I  FL1 617.5  lin     40    999   RATE  [1/s]    13
```

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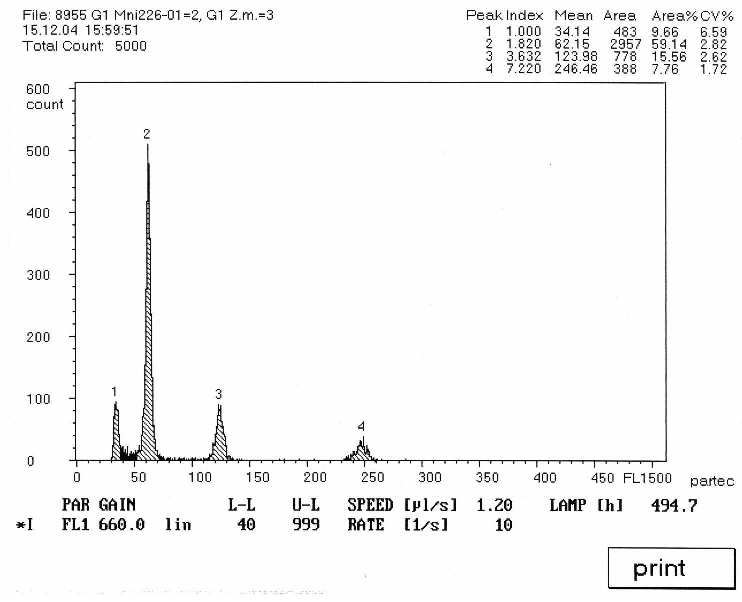

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File: 8955 G1 Mni226-01=2, G1 Z.m.=3                    Peak Index  Mean    Area  Area% CV%
15.12.04 15:59:51                                          1  1.000  34.14    483  9.66   6.59
Total Count:  5000                                         2  1.820  62.15   2957  59.14  2.82
                                                           3  3.632  123.98   778  15.56  2.62
                                                           4  7.220  246.46   388  7.76   1.72
```

```
    PAR GAIN           L-L   U-L   SPEED [µl/s]  1.20    LAMP [h]   494.7
*I  FL1 660.0  lin     40    999   RATE  [1/s]    10
```

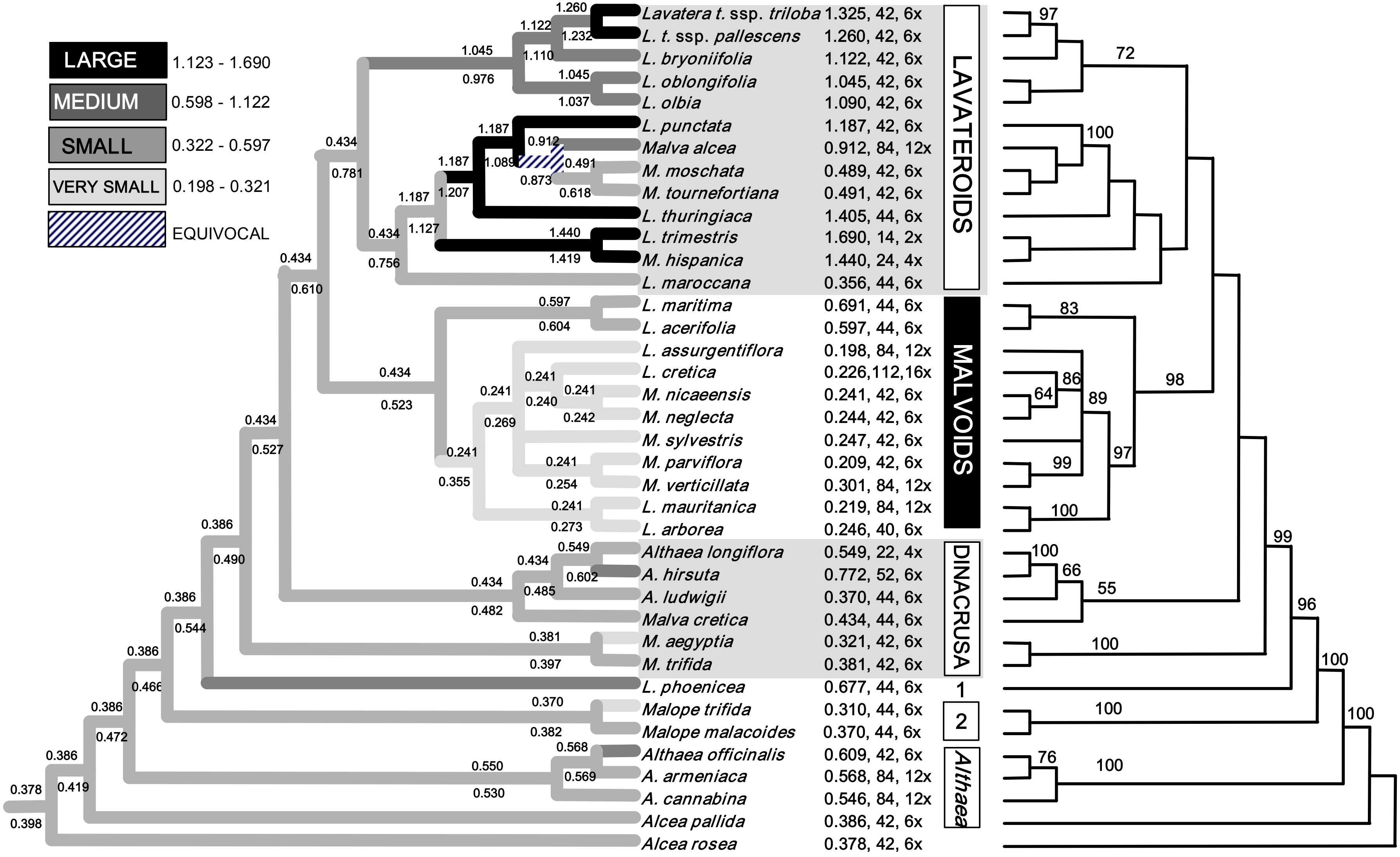


Fig. 2. Phylogenetic tree and character optimization. **Left tree: character optimization.** Values displayed above clade lines represent 1Cx-values inferred by linear parsimony (MINSTATES), below cladogram lines squared change parsimony inferred 1Cx-values. In the middle column, 1Cx values for each species, chromosome counts and ploidy levels are displayed. **Right tree: bayesian 50% majority-rule ITS topology** with bootstrap support displayed above clade lines. Only figures higher than 50% are present. 1 = *Lavatera* (*Navaea*) *phoenicea*. 2 = *Malope* group.

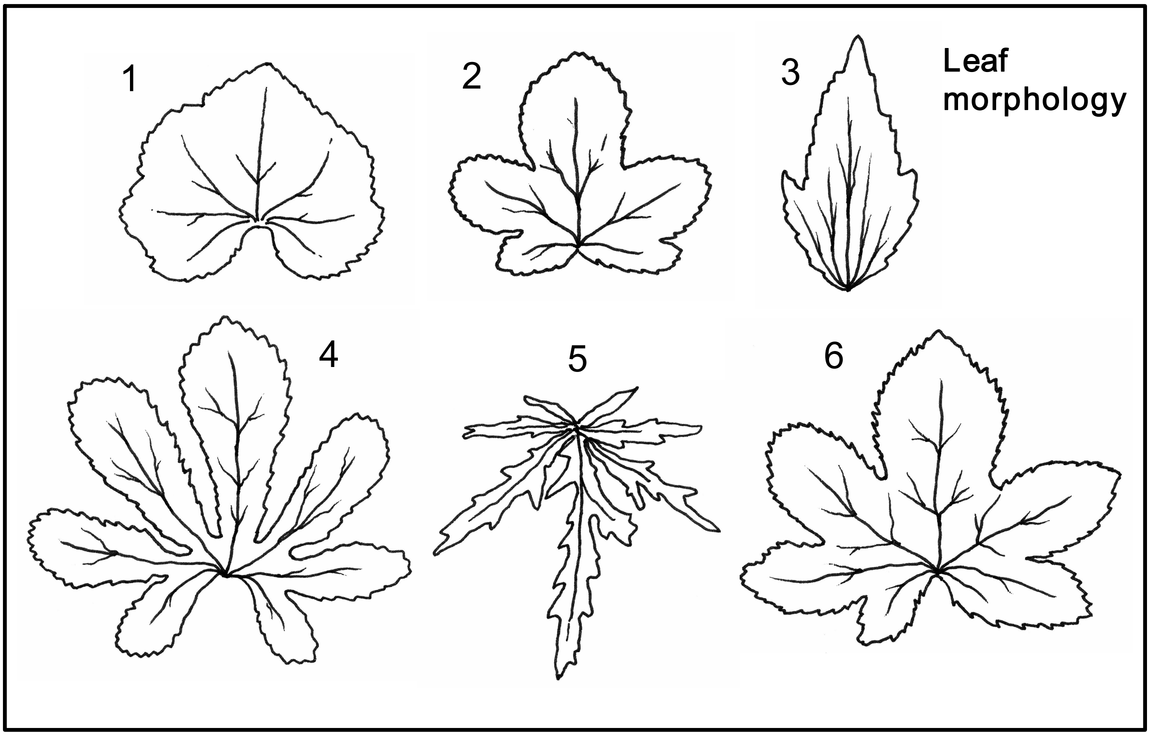
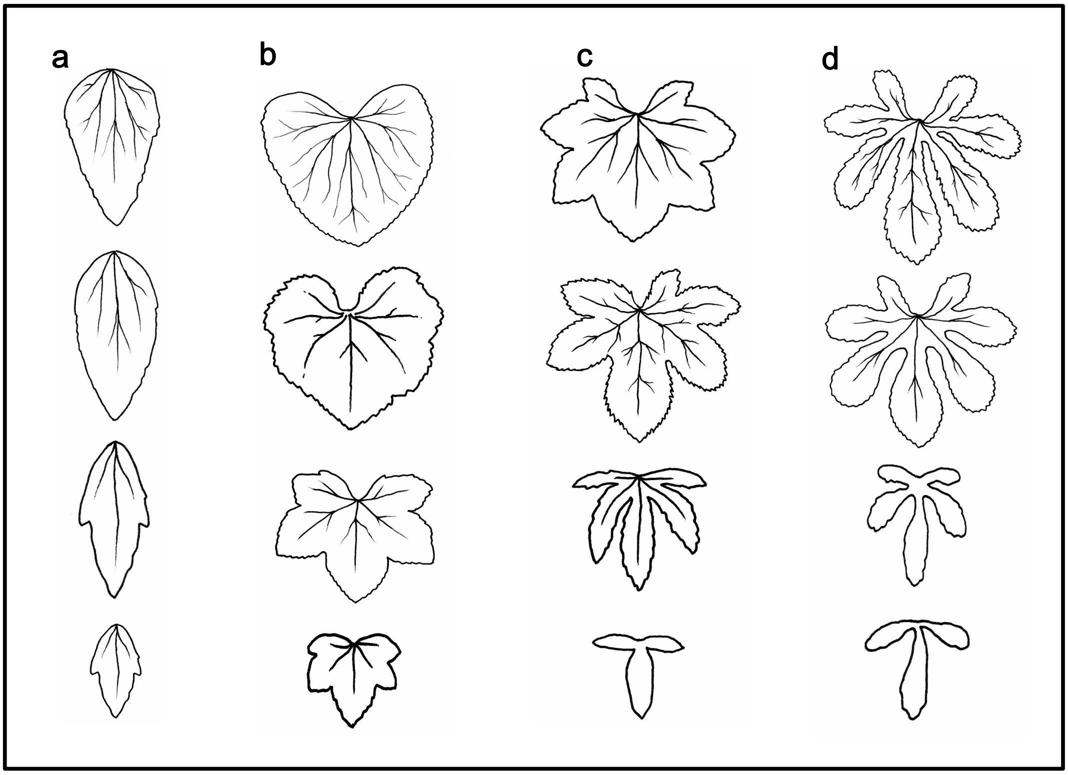


Fig. 1. Above: **Leaf morphology types. 1. ‘pallida’** type. **2. ‘longipedicellata’** type. **3. ‘sulphurea’** type. **4. ‘sachsachanica’** type. **5. ‘wilhelminae’** type. **6. ‘rugosa’** type. Species with types 1, 3 and 5 present a tendency to be homophyllous (1 and 3 with undissected leaves and 5 with all leaves profoundly dissected), while species displaying types 2 and 4 are slightly heterophyllous. Below: **Leaf sequence types**, from basal leaves to inflorescence bracts. **a. ‘sulphurea’**, homophyllous with entire leaves. **b. ‘rufescens’**, slightly heterophyllous. **c. ‘kurdica’**, heterophyllous. **d. ‘flavovirens’** heterophyllous with all leaves profoundly dissected.



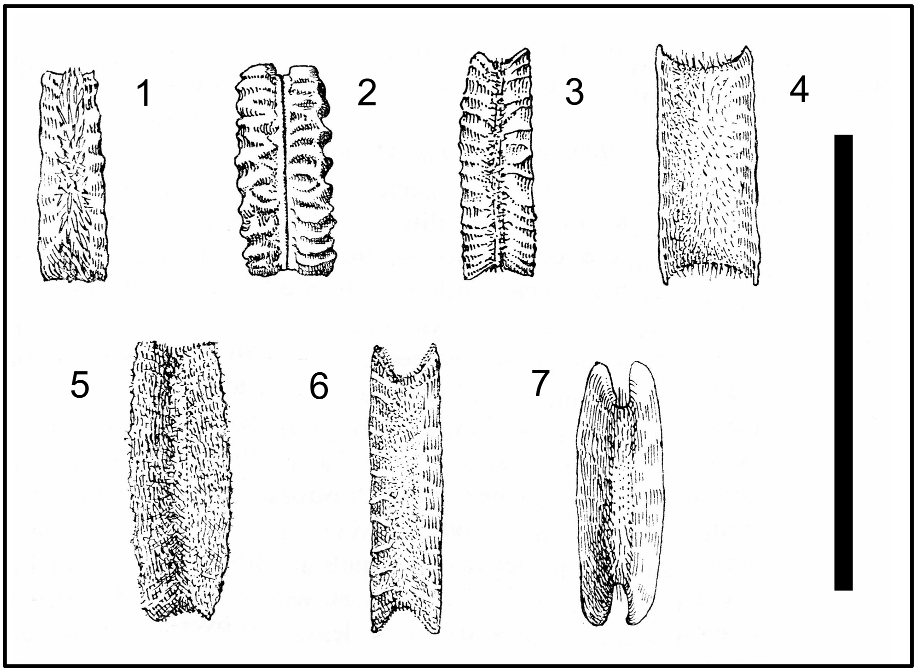
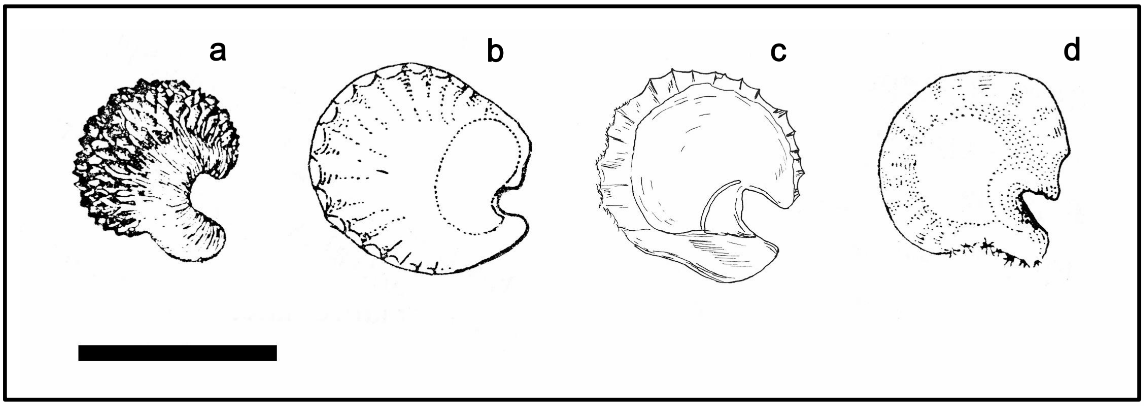


Fig. 2. Above: **Mericarp morphology** (after Zohary, 1963b). **1. Planocot**, plain. 2. Planocot, furrowed. **3. Plagionot**. **4. Plagiopterous** with wrinkled wings. 5. Plagiopterous with smooth wings. **6. Orthopterous** with wrinkled wings. 7. Orthopterous with smooth wings. Scale bar = 1.5 cm. Below: Mericarp morphology, lateral view. **a. Planocot** (*A. galilaea*). **b. Plagionot** (*A. sulphurea*). **c. Plagiopterous** (*A. flavovirens*). **d. Orthopterous** (*A. arbelensis*). Scale bar = 1 cm.



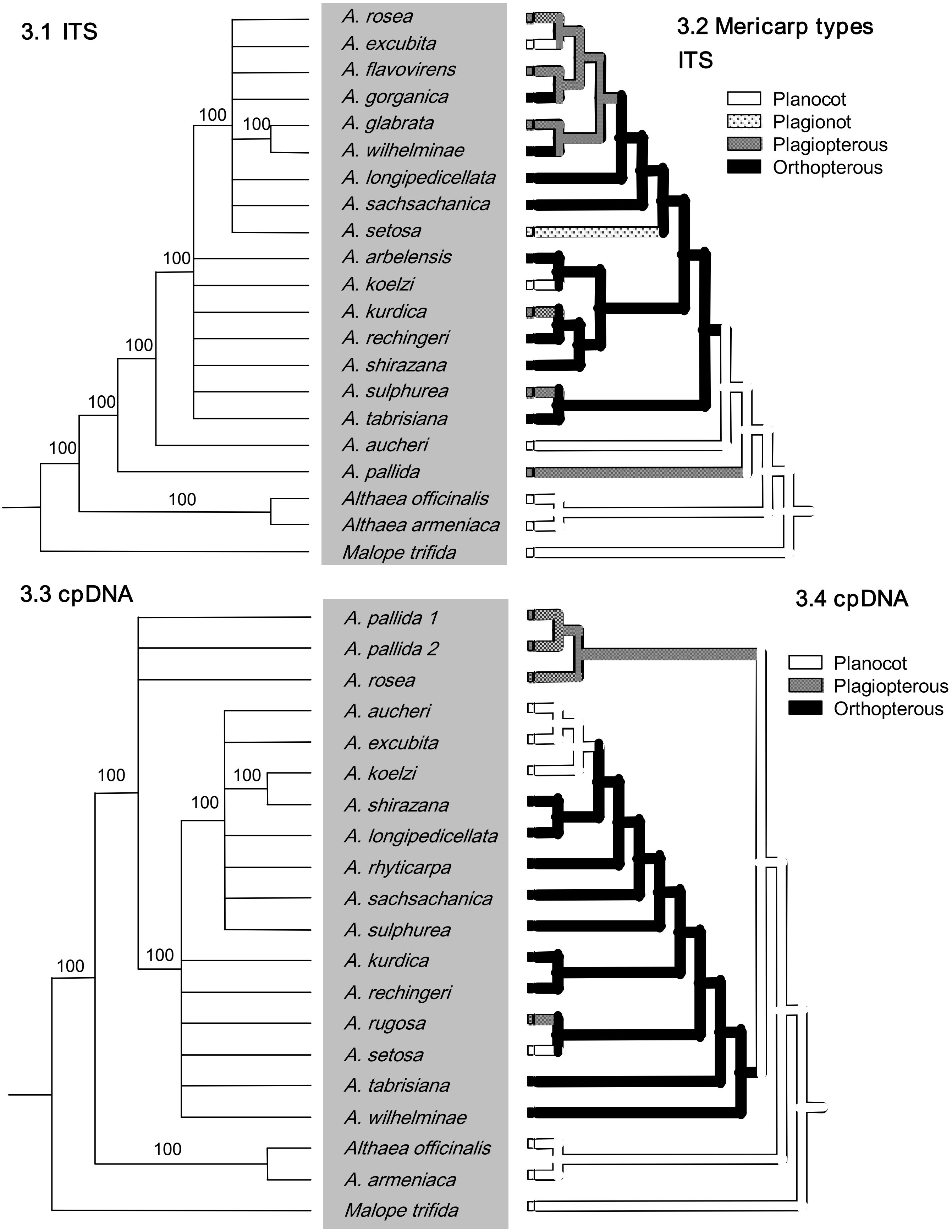


Fig. 3. Character optimization. **3.1 ITS** bootstrap consensus tree. Only probabilities higher than 50% are displayed. **3.2. Mericarp types** mapped on an ITS bayesian 50% majority rule consensus tree. Posterior probabilities were 100 for all clades. **3.3. Plastid *psb*A-*trn*H plus *trn*L-*trn*F** bootstrap consensus tree. Only probabilities higher than 50% are displayed. **3.4. Mericarp types** mapped on a plastid bayesian 50% majority rule consensus tree. Posterior probabilities were 100 for all clades.

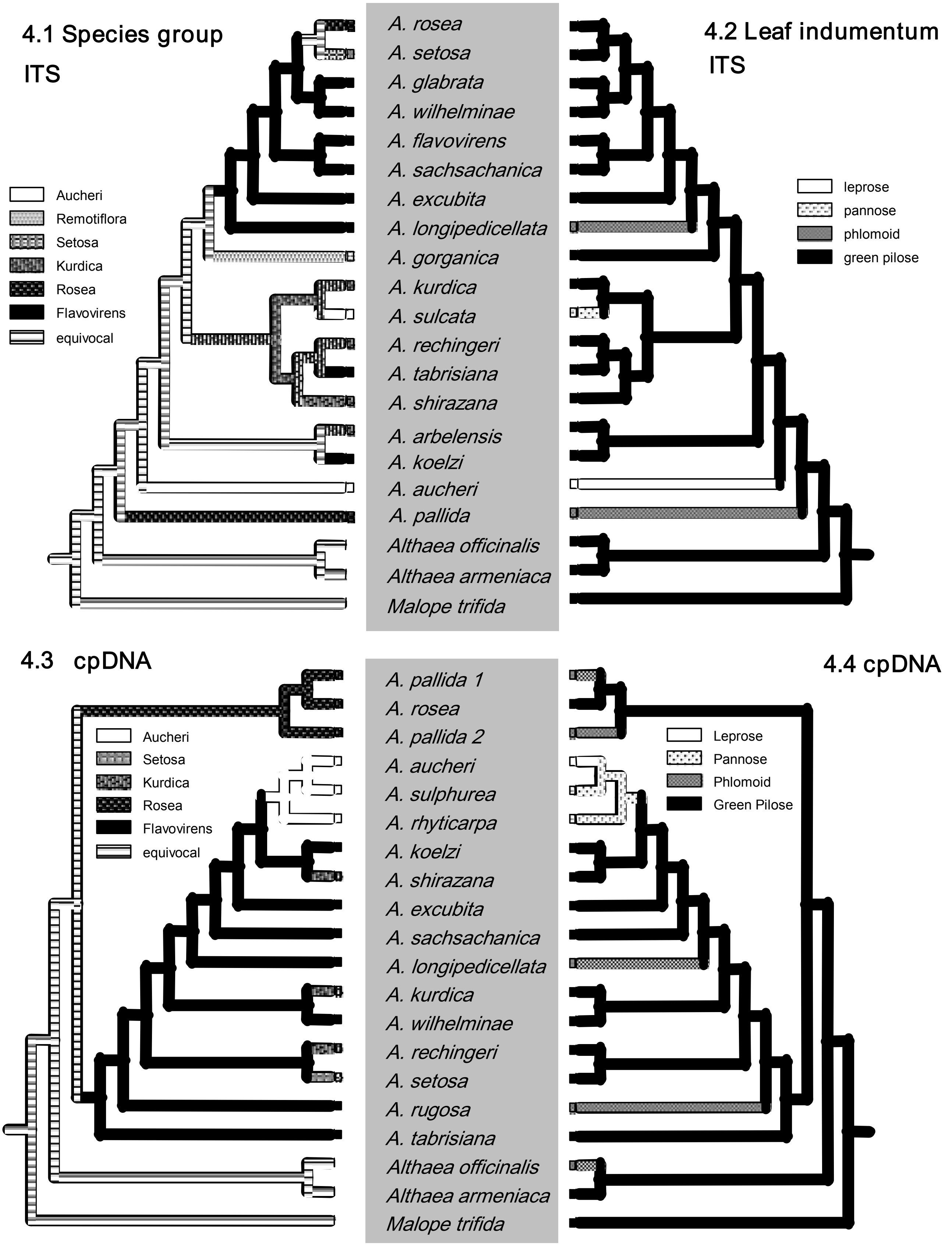


Fig. 4. Character optimization. **4.1 Zohary´s (1963a) species groups** mapped on an ITS bayesian 50% majority rule consensus tree. Posterior probabilities were 100 for all clades. **4.2. Leaf indumentum types** mapped on an ITS bayesian 50% majority rule consensus tree. **4.3. Zohary´s (1963a) species groups** mapped on an plastid *psb*A-*trn*H plus *trn*L-*trn*F bootstrap consensus tree. Posterior probabilities were 100 for all clades. **4.4. Leaf indumentum** mapped on a plastid bayesian 50% majority rule consensus tree.

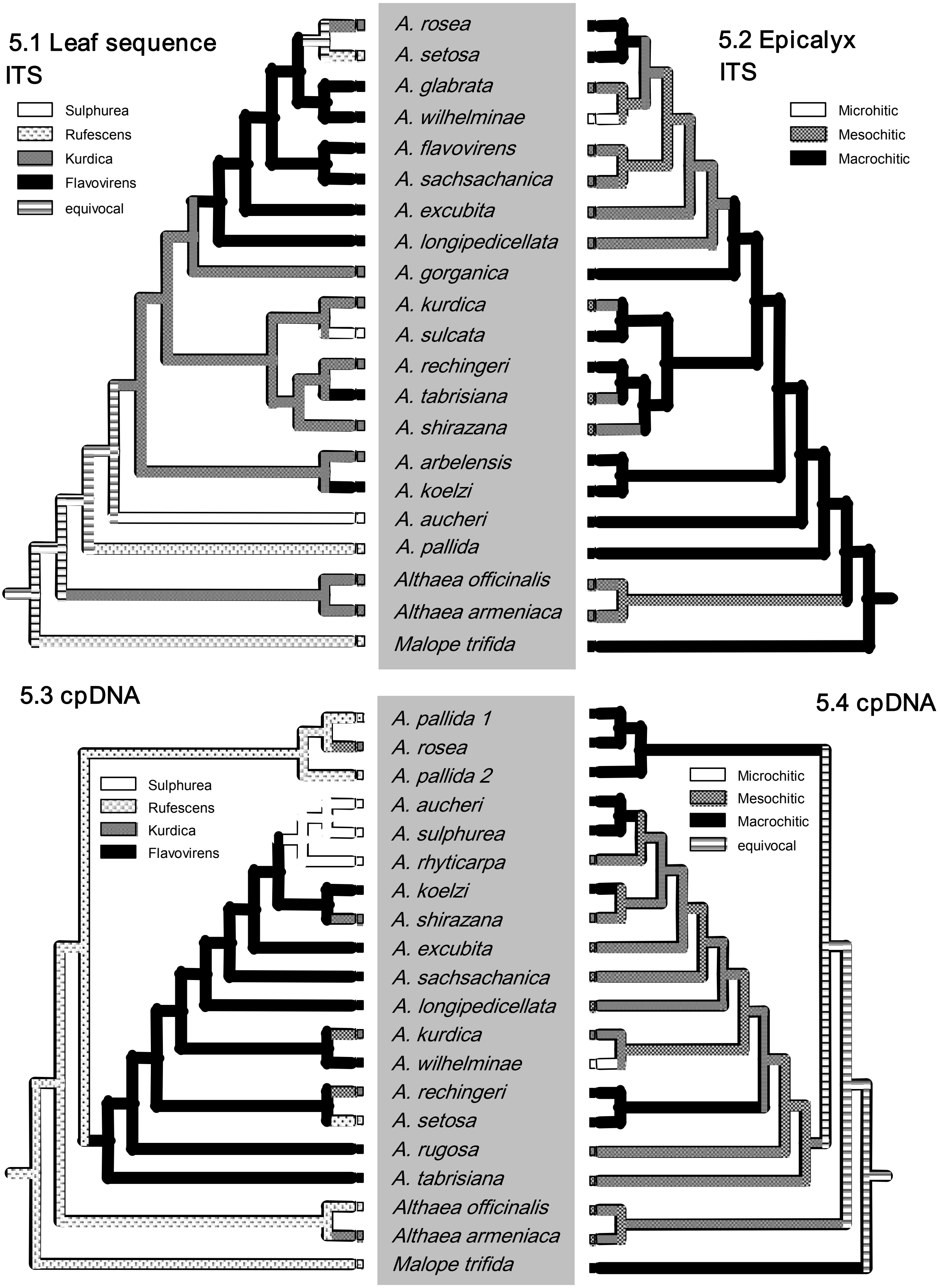


Fig. 5. Character optimization. **5.1 Leaf sequence** mapped on an ITS bayesian 50% majority rule consensus tree. Posterior probabilities were 100 for all clades. **5.2. Epicalyx types** mapped on an ITS bayesian 50% majority rule consensus tree. **5.3. Leaf sequence** mapped on an plastid *psb*A-*trn*H plus *trn*L-*trn*F bootstrap consensus tree. Posterior probabilities were 100 for all clades. **5.4. Epicalyx types** mapped on a plastid bayesian 50% majority rule consensus tree.

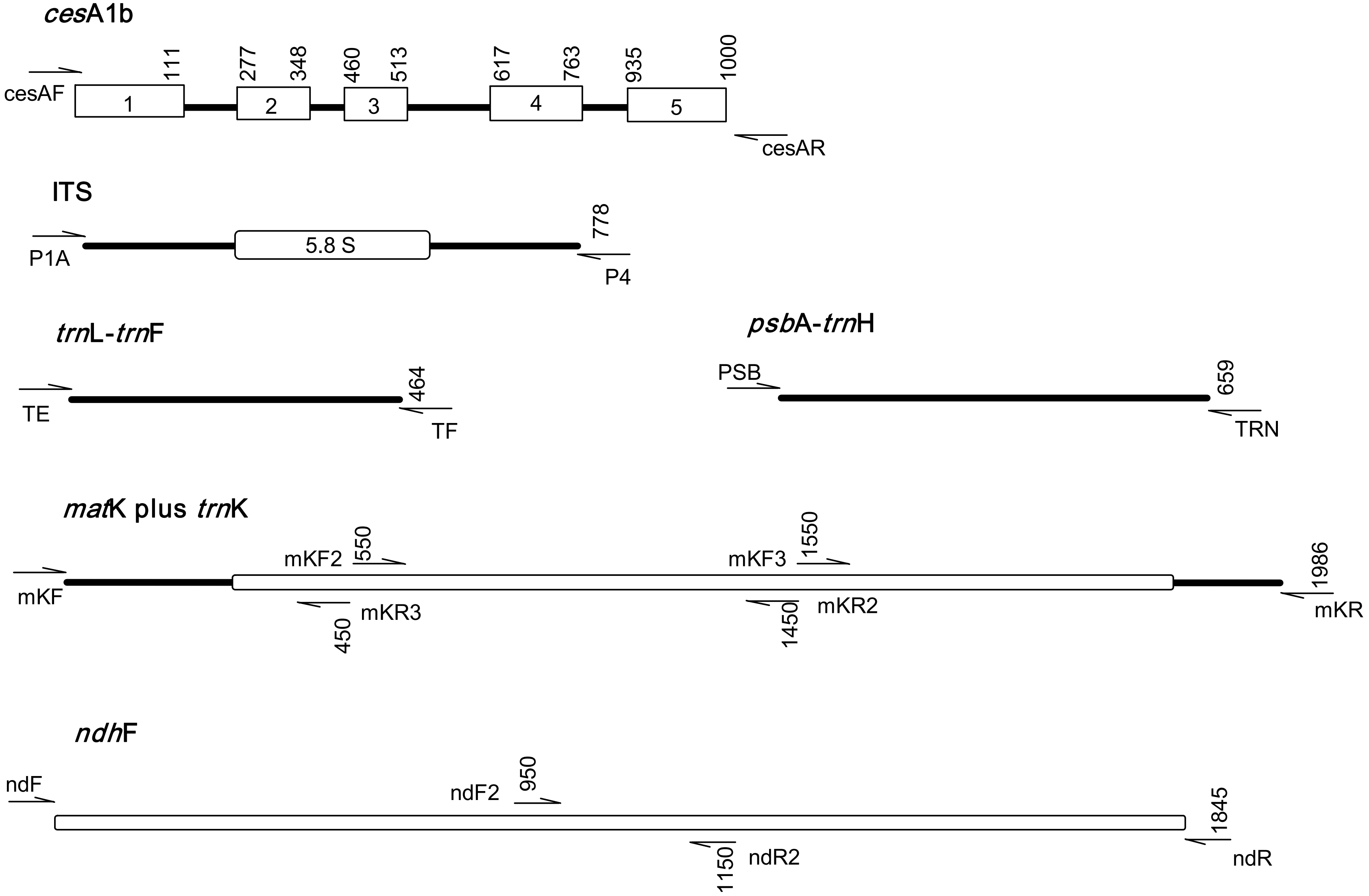


Figure 1. Markers amplified for this study.

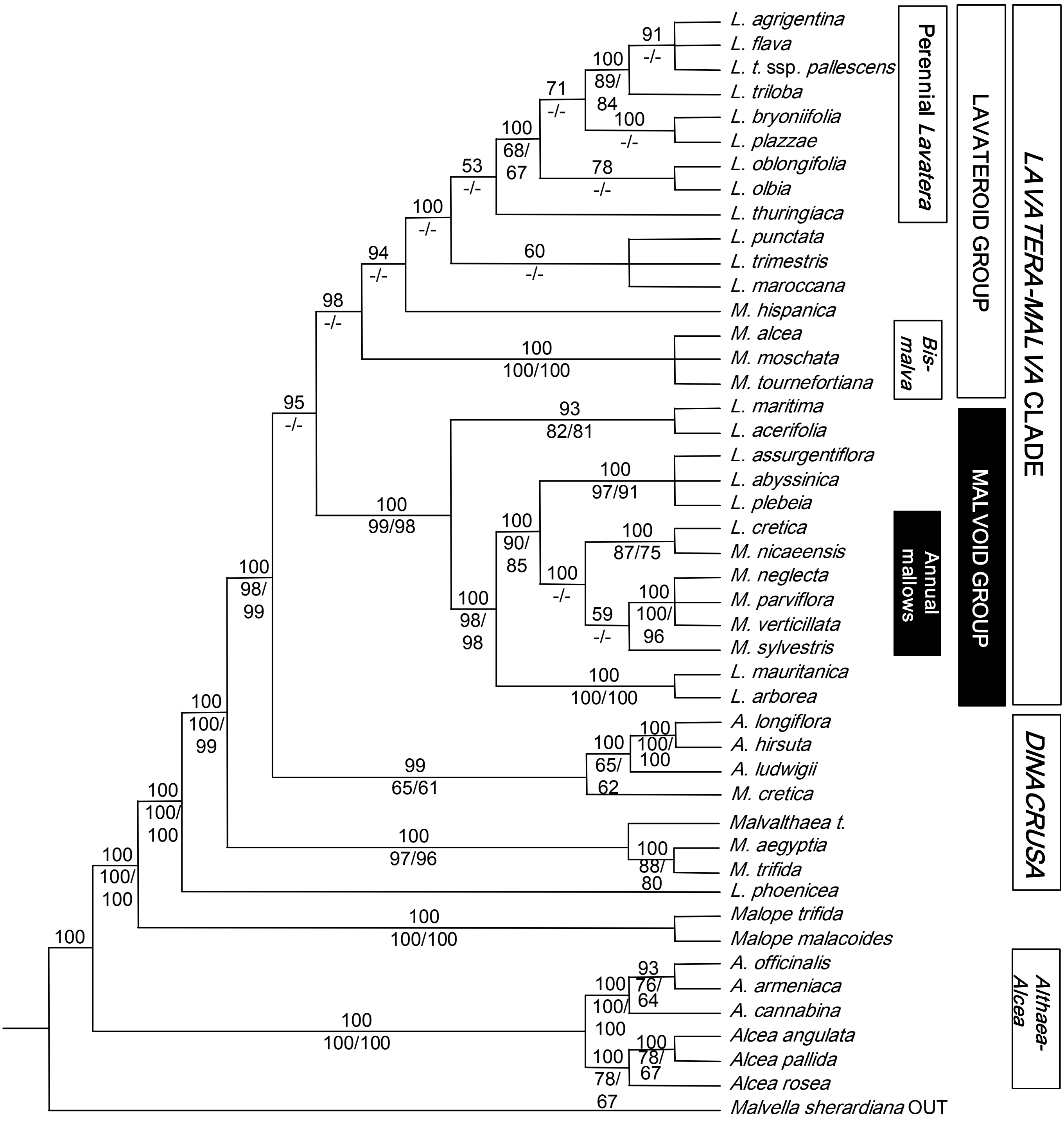


Fig 2. **ITS** 50% majority rule bayesian topology. Values displayed above clade lines represent bayesian posterior probability. Values under clade lines: left, bootstrap support; right, jackknife support (only values higher than 50% are displayed).

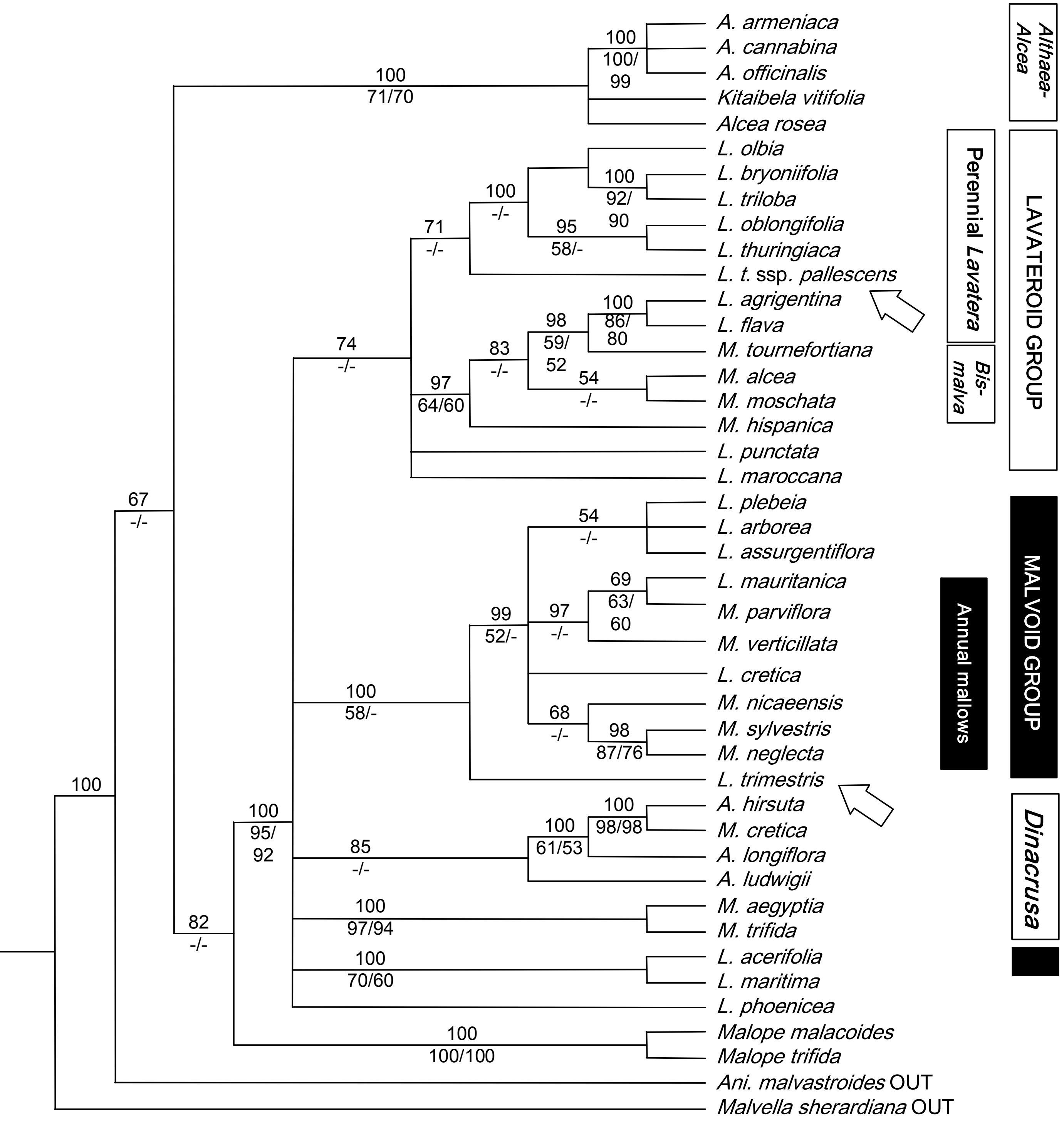


Fig 3. *mat*K plus *trn*K strict consensus from 7520 MPT. Black boxes mark malvoid taxa. Arrows indicate species of labile phylogenetic position. Values displayed above clade lines represent bayesian posterior probabilities. Values under clade lines: left, bootstrap support; right, jackknife support (only values higher than 50% are displayed).

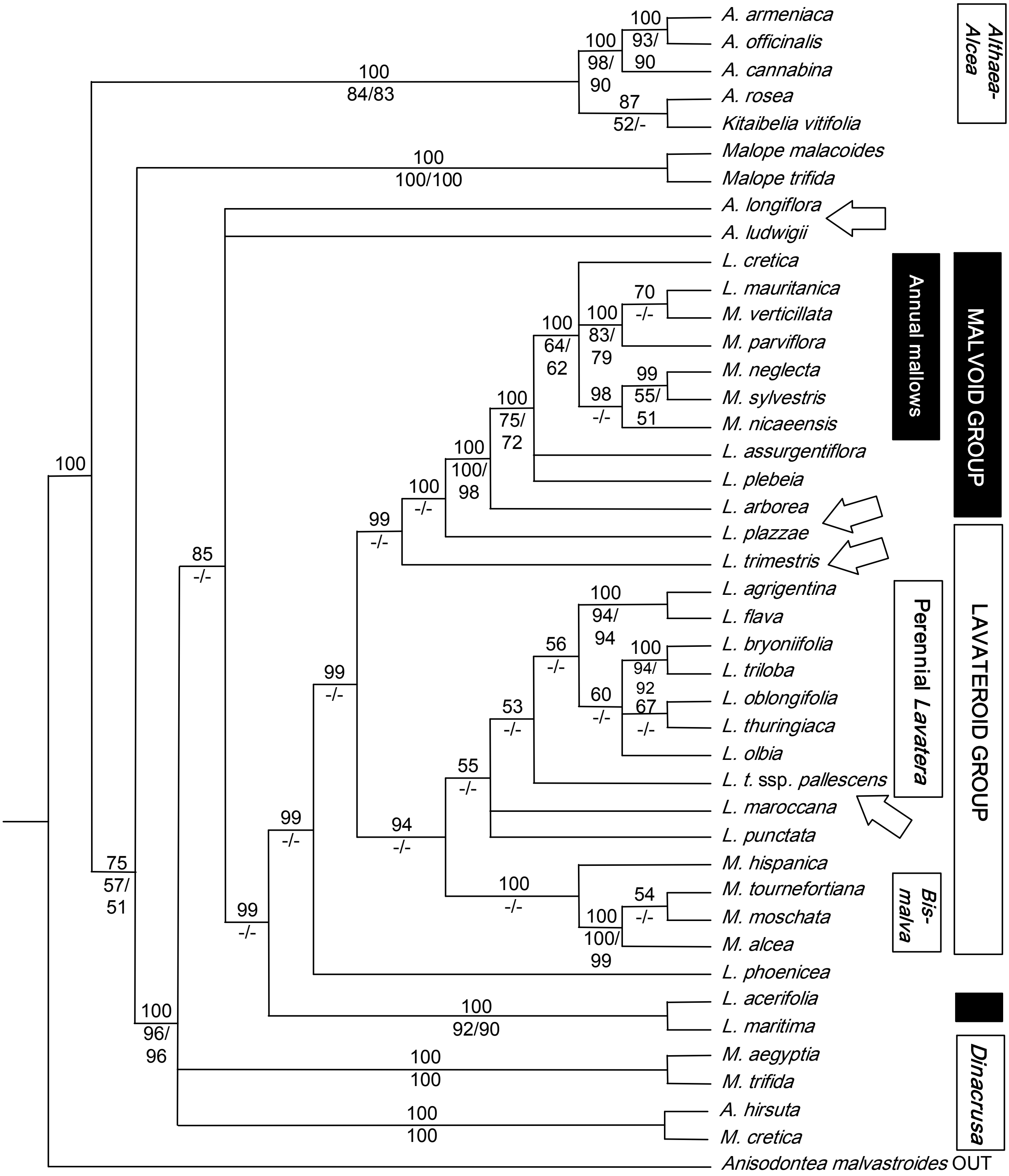


Fig 4. Joint plastid (*trn*L-*trn*F, *psb*A-*trn*H, *mat*K plus *trn*K, *ndh*F) analysis. Strict consensus from 10 MPT. Black boxes mark malvoid taxa. Arrows indicate species of labile phylogenetic position. Values displayed above clade lines represent bayesian posterior probabilities. Values under clade lines: left, bootstrap support; right, jackknife support (only values higher than 50% are displayed).

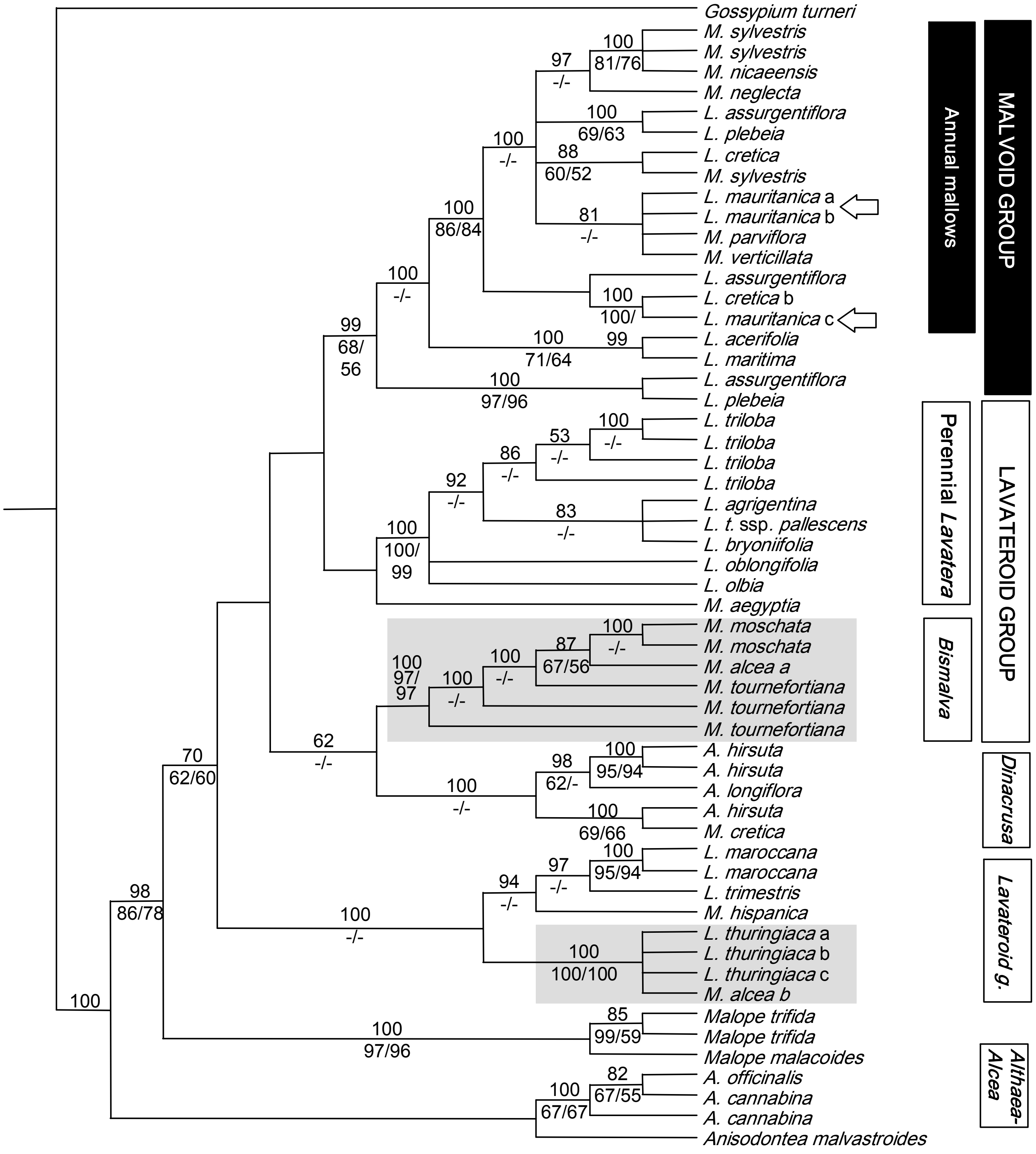


Fig 5a. *ces*A1b **P1** strict consensus from 7370 MPT. Arrows indicate the position of the allopolyploid *Lavatera mauritanica*. Grey boxes mark the position of the allopolyploid *Malva alcea*. Values displayed above clade lines represent bayesian posterior probabilities. Values under clade lines: left, bootstrap support; right, jackknife support (only values higher than 50% are displayed).

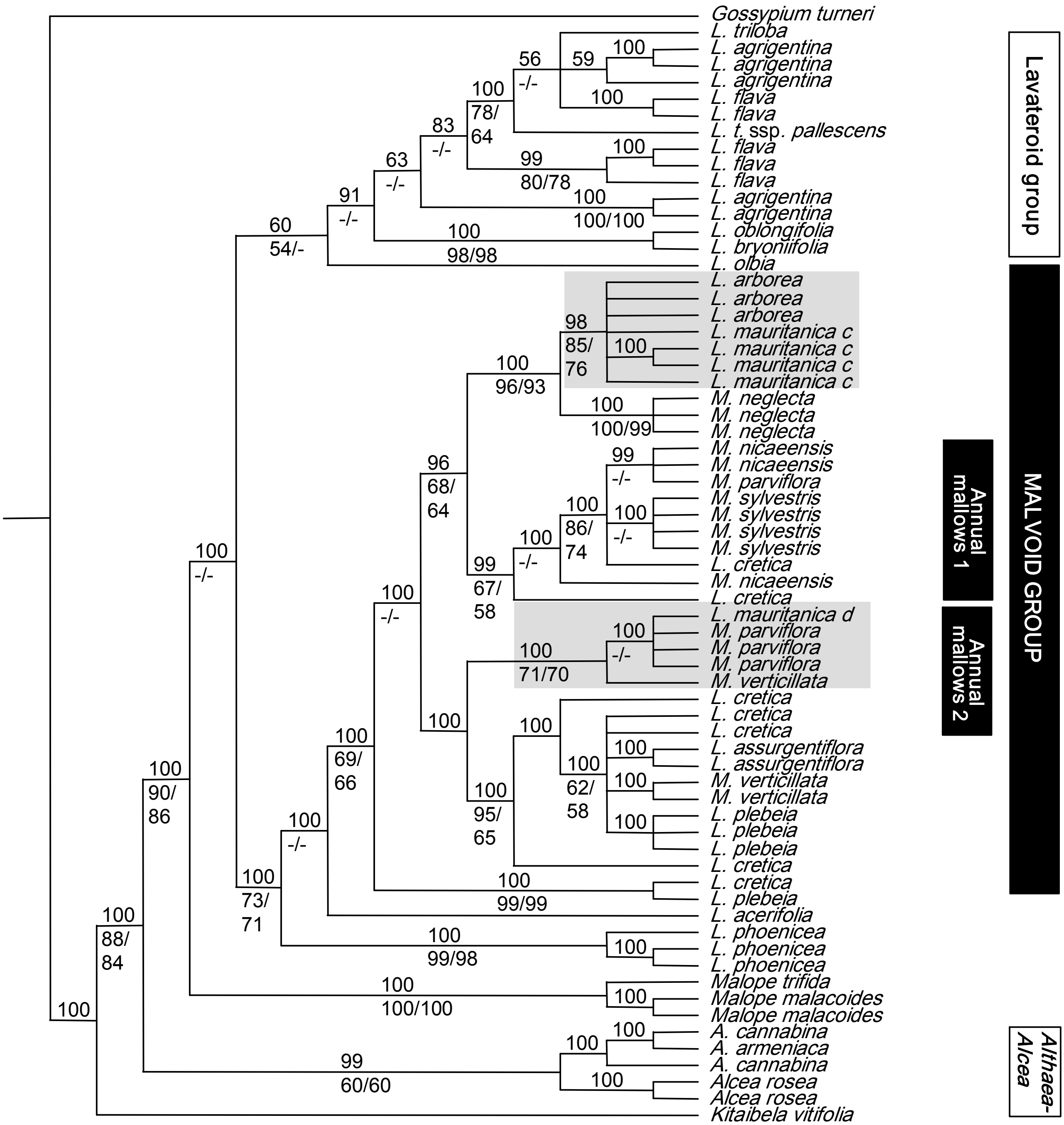


Fig 5b. ***ces*A1b P2** strict consensus from 5865 MPT. Grey boxes mark the position of the allopolyploid *Lavatera mauritanica*. Values displayed above clade lines represent bayesian posterior probabilities. Values under clade lines: left, bootstrap support; right, jackknife support (only values higher than 50% are displayed).

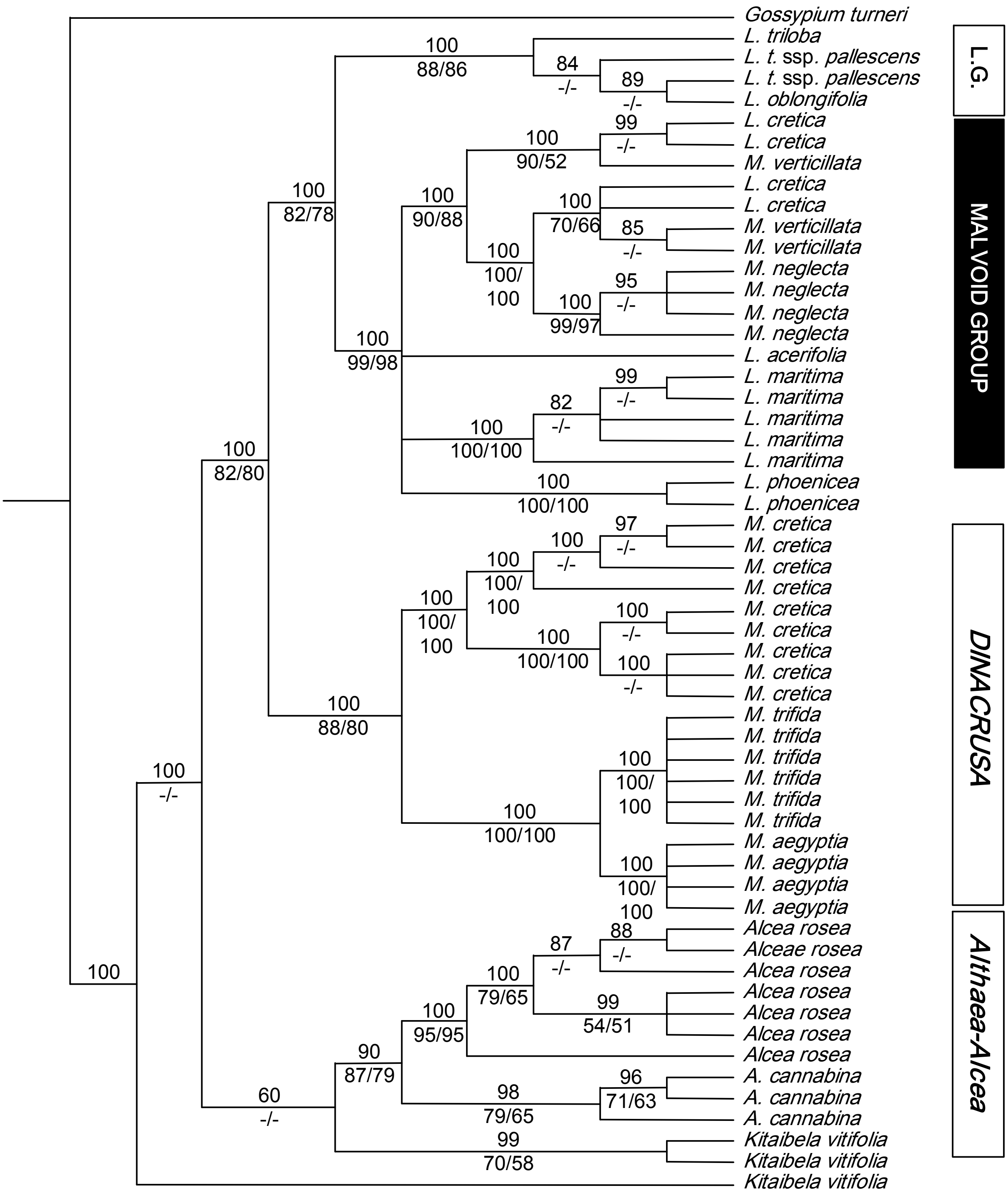


Fig 5c. ***ces*A1b P3** strict consensus from 149 MPT. Values displayed above clade lines represent bayesian posterior probabilities. Values under clade lines: left, bootstrap support; right, jackknife support (only values higher than 50% are displayed).

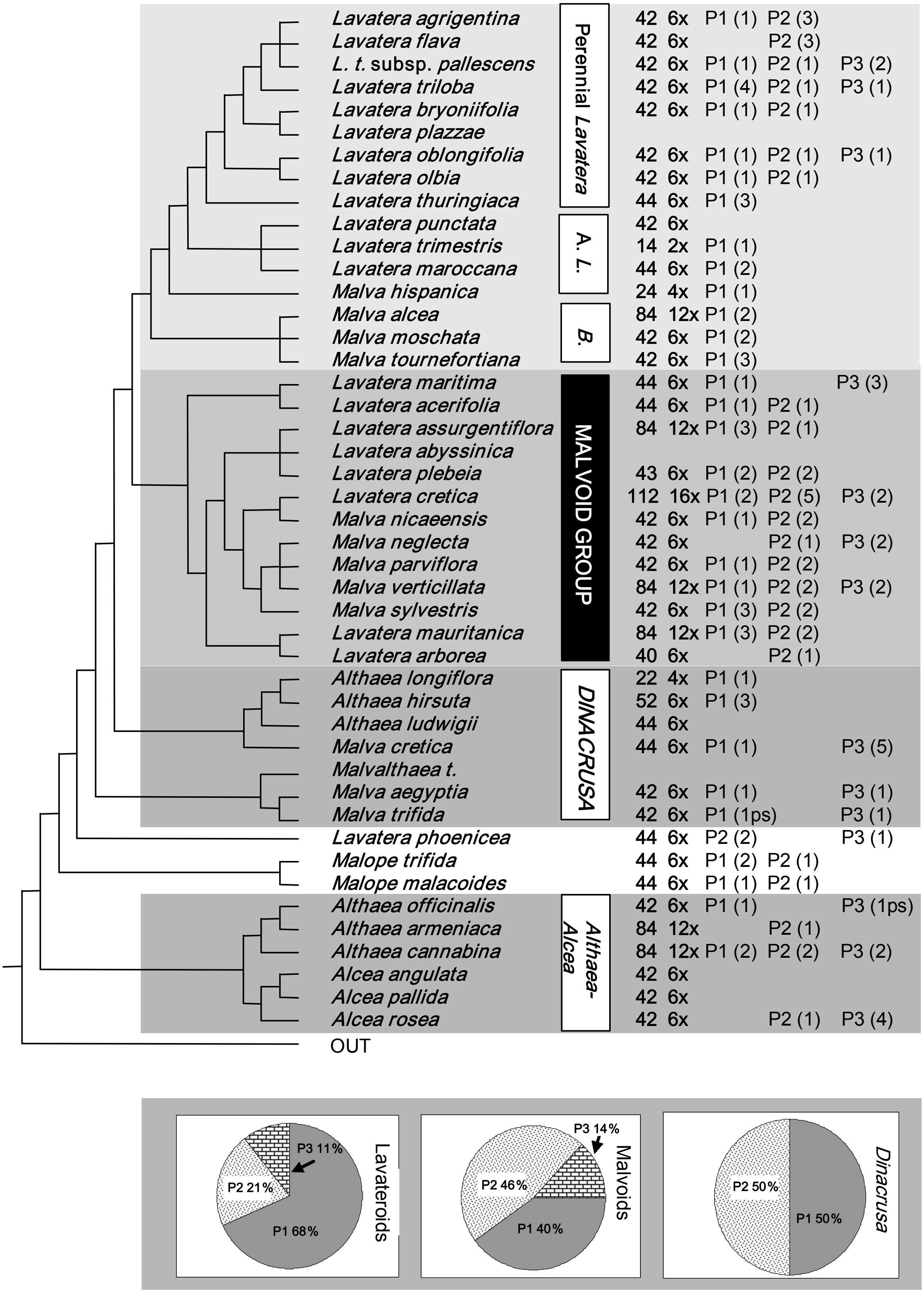


Figure 6. Chromosome numbers, ploidy levels and *ces*A1b paralogues (P1, P2 and P3) present in each taxon. **ps.** = pseudogene, not included in analyses. The data are displayed on the ITS phylogeny of figure 2. A. L. = Annual *Lavatera*, B. = *Bismalva*.